

Feb 20 09:21:41 2003

us-09-636-259b-3.rpt

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 15, 2003, 16:56:00 : Search time 24.5 seconds
(without alignments)
1765.734 Million cell updates/sec

US-09-636-259b-3

Title: 2381
Perfect score: 1 MGSLOPDAGNASWNGTEAPG.....HDFRRAFKKILCRGDRKRIV 450
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues 283224

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2227	93.5	450	2	A38316	alpha-2-adrenergic
2	2222	93.3	450	2	A34169	alpha-2a-adrenergic
3	2199	92.4	450	2	I49481	alpha-2-adrenergic
4	2132	89.5	450	2	B40392	alpha-2-adrenergic
5	2111	88.7	450	2	JH0190	alpha-2-adrenergic
6	1175	49.3	458	2	A40392	alpha-2C4 adrenoce
7	1175	49.3	458	2	I49480	alpha-2B-adrenergic
8	1169	49.1	458	2	A48392	alpha-2C-adrenergic
9	1169	49.1	458	2	A37869	alpha-2C-adrenocept
10	1165.5	47.5	450	2	A31237	alpha-2B-adrenergic
11	1130.5	47.3	450	2	I50829	alpha-2B-adrenergic
12	1125.5	47.0	455	2	A37223	alpha-2-C2 adrener
13	1119.5	46.6	448	2	I51883	alpha-2B-adrenergic
14	1110.5	46.1	453	2	A35642	alpha-2B-adrenergic
15	1098.5	29.1	484	2	S58868	G protein-coupled
16	693.5	28.6	379	2	JC6178	serotonin receptor
17	681.5	27.3	476	2	JC5042	G protein-coupled
18	651	27.2	601	2	S12004	tyramine receptor
19	648	27.2	601	2	JH0170	octopamine receptor
20	648	27.2	601	2	JH0170	dopamine receptor
21	629	26.4	444	1	DYHUD2	dopamine receptor
22	626.5	25.9	444	1	DYMSD2	dopamine receptor
23	616	25.9	444	1	S08146	dopamine receptor
24	612	25.7	511	2	C56849	G protein-coupled
25	612	25.7	377	2	B30341	dopamine receptor
26	606.5	25.5	442	1	DYXLD2	hypothetical prote
27	596.5	25.1	430	2	T16079	serotonin receptor
28	594	24.9	422	2	I38209	

30	586.5	24.6	377	2	S68423	serotonin receptor
31	585.5	24.6	377	2	A53279	serotonin receptor
32	585	24.6	421	2	I49375	dopamine receptor
33	578.5	24.3	514	2	D56849	serotonin receptor
34	577.5	24.3	390	2	JN0268	serotonin receptor
35	577	24.2	422	2	JH0315	alpha-1B adrenergic
36	573.5	24.1	517	2	A45121	serotonin receptor
37	564	23.7	374	2	I77467	serotonin receptor
38	563	23.6	564	2	A38271	dopamine receptor
39	561.5	23.6	389	2	S68422	alpha-1-adrenergic
40	561	23.6	387	2	DYHUD4	serotonin receptor
41	560	23.5	515	2	A40491	serotonin receptor
42	559.5	23.5	390	2	S58126	hypothetical prote
43	558	23.4	386	2	A42688	alpha-1B-adrenergic
44	557.5	23.4	501	2	T18863	
45	556.5	23.4	515	2	JC1525	

ALIGNMENTS

RESULT 1
A38316
alpha-2-adrenergic receptor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C:Accession: A38316
R:Guyer, C.A.; Horstman, D.A.; Wilson, A.L.; Clark, J.D.; Craoe Jr., E.J.; Limbird, J. Biol. Chem. 265, 17307-17317, 1990
A:Title: Cloning, sequencing, and expression of the gene encoding the porcine alpha-2
A:Reference number: A38316; MUID:91009167; PMID:2170371
A:Accession: A38316
A:Molecule type: DNA
A:Residues: 1-450 <GVY>
A:Cross-references: GB:J05652; NID:g164303; PIDN:AAA30984.1; PID:g164304
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
Query Match 93.5%; Score 2227; DB 2; Length 450; Indels 0; Gaps 0;
Best Local Similarity 94.0%; Pred. No. 4.7e-136; Mismatches 24;
Matches 423; Conservative 3;

QY	1	MGSLOPDAGNASWNGTEAPGARATPSLOVTLTLVCLAGLMLTFVGNVLTAVFT	60
DB	1	MGSLOPDAGNASWNGTEAPGARATPSLOVTLTLVCLAGLMLTFVGNVLTAVFT	60
QY	61	SRALKAPQNLFLVSLASADILVATVIPSLEANEVGMWYFGKAWCEIYLADVLECTSS	120
DB	61	SRALKAPQNLFLVSLASADILVATVIPSLEANEVGMWYFGKAWCEIYLADVLECTSS	120
QY	121	IVHLCAISLDKRWSTQAIENYLNKTRPRRIKAITVWVISAVISFPPLISIEKKAGGG	180
DB	121	IVHLCAISLDKRWSTQAIENYLNKTRPRRIKAITVWVISAVISFPPLISIEKKAGGG	180
QY	181	PQPAEPRCEINDOKWYVSSCIGSFAPCLIMLVYVRIYQIAKRTRVPPSRGPDAAA	240
DB	181	PQPAEPRCEINDOKWYVSSCIGSFAPCLIMLVYVRIYQIAKRTRVPPSRGPDAAA	240
QY	241	APPGTERRRPNGIGPERSAGPGGAEPPLTQNGAPGEPAPAGPRDTALDLESSSSD	300
DB	241	ALPGAERPNGLGPERGVGRVGAEEPLPVQNGAPGEPAPAGPRDADGLDESSSSSE	300
QY	301	HAERPPGPRRBERGPRGKARASQVKBGDSLPRRGPGATGTPAAGPEERVGAAKAS	360
DB	301	HAERPPGPRRBERGPRGKARASQVKBGDSLPRRGPGATGTPAAGPEERVGAAKAS	360
QY	361	RWRGRONREKRTFVLAIVGVVCMFPFFFTYTLTAVGCSVPRTLKFFFWGVCNSS	420
DB	361	RWRGRONREKRTFVLAIVGVVCMFPFFFTYTLTAVGCSVPRTLKFFFWGVCNSS	420
QY	421	LNPVITYTFNHFRRRAFKKILCRGDRKRIV	450
DB	421	LNPVITYTFNHFRRRAFKKILCRGDRKRIV	450

RESULT 2
alpha-2A-adrenergic receptor - human
A34169

N/Alternate names: alpha-2C10-adrenergic receptor
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence
C/Accession: A34169; A40132; S14311
R/Fraser, C.M.; Arakawa, S.; McCormbie, W.R.; Venter, J.C.
J. Biol. Chem. 264, 11754-11761, 1989
A/Title: Cloning, sequence analysis, and permanent expression of a human alpha2-adrenergic
cyclase attenuation and activation.
A/Reference number: A34169; MUID:89308571; PMID:2568356
A/Accession: A34169
A/Molecule type: DNA
A/Residues: 1-450 <FRA>
R/Kobilka, B.K.; Matsui, H.; Kobilka, T.S.; Yang-Feng, T.L.; Francke, U.; Caron, M.G.; I
Science 238, 650-656, 1987
A/Title: Cloning, sequencing, and expression of the gene coding for the human platelet a
A/Reference number: A40132; MUID:88042789; PMID:2823383
A/Accession: A40132
A/Molecule type: DNA
A/Residues: 1-103, 'T', 105-156, 'C', 158-367, 'L', 369-450 <KOB>
A/Cross-references: GB:M18415; NID:9178195; PIDN:AAA51665.1; PID:9178196
A/Note: the authors translated the codon TGT for residue 157 as Val, and CTC for residue
R/Chahjani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.
FEBS Lett. 280, 241-244, 1991
A/Title: Identification of an additional gene belonging to the alpha(2) adrenergic recep
A/Reference number: S14311; MUID:91192139; PMID:1849485
A/Accession: S14311
A/Molecule type: DNA
A/Residues: 77-123, 'P', 125-209 <CHH>
A/Genetics: GDB:ADRA2A; ADRA2; ADRA2R
A/Cross-references: GDB:ADRA2; ADRA2; ADRA2R
A/Map position: GDB:120538; OMIM:104210
A/Introns: #status absent
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 93.3%; Score 2222; DB 2; Length 450;
Matches 425; Conservative 1; Mismatches 24; Indels 0; Gaps 0;

QY 1 MGSLQPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLTVFGNVLIIVFT 60
DB 1 MGSLQPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLTVFGNVLIIVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEMVGYWFGKAWCEIYLALDVLEFCTSS 120
DB 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEMVGYWFGKAWCEIYLALDVLEFCTSS 120
QY 121 IVHCAISLDRYWSITQAIENLKRTPRIKAIITVWVISAVISFPPLISTIEKKGGGG 180
DB 121 IVHCAISLDRYWSITQAIENLKRTPRIKAIITVWVISAVISFPPLISTIEKKGGGG 180
QY 181 POPAEPRCETINDOKWYVIVSSCISGFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDAYA 240
DB 181 POPAEPRCETINDOKWYVIVSSCISGFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDAYA 240
QY 241 APPGGERRRPGLGPERSGAGPGAELPTQNLGAPGEPAPAGPRDLDLLESSSSD 300
DB 241 APPGGERRRPGLGPERSGAGPGAELPTQNLGAPGEPAPAGPRDLDLLESSSSD 300
QY 301 HAERPPGRRPGRGKAKARASQVKKPGDSLPRRGPGATGIGTPAAGPEEERVGAAKAS 360
DB 301 HAERPPGRRPGRGKAKARASQVKKPGDSLPRRGPGATGIGTPAAGPEEERVGAAKAS 360
QY 361 RWRGRONREKRTFVLAVVIGVFWCFPEFFFTYTLTAVGCSVPRTLFFKFFWFGYCNS 420
DB 361 RWRGRONREKRTFVLAVVIGVFWCFPEFFFTYTLTAVGCSVPRTLFFKFFWFGYCNS 420

DB 361 AGAGQONREKRTFVLAVVIGVFWCFPEFFFTYTLTAVGCSVPRTLFFKFFWFGYCNS 420
QY 421 LNPVIYTIENHDFRAFKKILCRGDRKRIY 450
DB 421 LNPVIYTIENHDFRAFKKILCRGDRKRIY 450

RESULT 3

149481

alpha-2 adrenergic receptor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence
C/Accession: I49481
R/Link, R.; Daut, D.; Barsh, G.S.; Chruscinski, A.; Kobilka, B.
Mol. Pharmacol. 42, 16-27, 1992
A/Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and
in antagonist binding.
A/Reference number: I49480; MUID:92342131; PMID:1353249
A/Accession: I49481
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-450 <RES>
A/Cross-references: GB:M99377; NID:9191882; PIDN:AAA37213.1; PID:9191883
C/Superfamily: vertebrate rhodopsin
C/Keywords: neurotransmitter receptor

Query Match

Best Local Similarity 92.4%; Score 2199; DB 2; Length 450;
Matches 415; Conservative 8; Mismatches 27; Indels 0; Gaps 0;

QY 1 MGSLQPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLTVFGNVLIIVFT 60
DB 1 MGSLQPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLTVFGNVLIIVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEMVGYWFGKAWCEIYLALDVLEFCTSS 120
DB 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEMVGYWFGKAWCEIYLALDVLEFCTSS 120
QY 121 IVHCAISLDRYWSITQAIENLKRTPRIKAIITVWVISAVISFPPLISTIEKKGGGG 180
DB 121 IVHCAISLDRYWSITQAIENLKRTPRIKAIITVWVISAVISFPPLISTIEKKGGGG 180
QY 181 POPAEPRCETINDOKWYVIVSSCISGFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDAYA 240
DB 181 POPAEPRCETINDOKWYVIVSSCISGFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDAYA 240
QY 241 APPGGERRRPGLGPERSGAGPGAELPTQNLGAPGEPAPAGPRDLDLLESSSSD 300
DB 241 APPGGERRRPGLGPERSGAGPGAELPTQNLGAPGEPAPAGPRDLDLLESSSSD 300
QY 301 HAERPPGRRPGRGKAKARASQVKKPGDSLPRRGPGATGIGTPAAGPEEERVGAAKAS 360
DB 301 HAERPPGRRPGRGKAKARASQVKKPGDSLPRRGPGATGIGTPAAGPEEERVGAAKAS 360
QY 361 RWRGRONREKRTFVLAVVIGVFWCFPEFFFTYTLTAVGCSVPRTLFFKFFWFGYCNS 420
DB 361 RWRGRONREKRTFVLAVVIGVFWCFPEFFFTYTLTAVGCSVPRTLFFKFFWFGYCNS 420
QY 421 LNPVIYTIENHDFRAFKKILCRGDRKRIY 450
DB 421 LNPVIYTIENHDFRAFKKILCRGDRKRIY 450

RESULT 4

B40392

alpha-2-adrenergic receptor (clone RG10) - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 06-Dec-1991 #sequence
C/Accession: B40392
R/Lanier, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.
J. Biol. Chem. 266, 10470-10478, 1991
A/Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic
A/Reference number: A40392; MUID:91244823; PMID 1645350

A;Accession: B40392
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 <LAN>
A;Cross-references: GB:M62372; NID:g206615; PIDN:AAA42034.1; PID:g206616
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match	89.5%;	Score 2132;	DB 2;	Length 450;
Best Local Similarity	89.8%;	Pred. NO. 6e-130;		
Matches 404;	Conservative 10;	Mismatches 36;	Indels 0;	Gaps 0;

Qy	1	MGSLÖP	DAGNASWNGTEAPGGGARATPYSLÖVTLTVCLAGLIMLTVFGANLVII	AVFT	60	
Db	1	MGSLÖP	DAGNASWNGTEAPGGGTRATPYSLÖVTLTVCLAGLIMLTVFGANLVII	AVFT	60	
Qy	61	SRALKAPÖN	FLVSLASADILVATLVIIPFSLANEVMGYFGKAWCEIY	LMDLV	ECTSS 120	
Db	61	SRALKAPÖN	FLVSLASADILVATLVIIPFSLANEVMGYFGKAWCEIY	LMDLV	ECTSS 120	
Qy	121	IVHLCAISLDR	WYSITQAIIEYNLKRTPRRIKAIITVWVISA	VISFPPLISTE	KGGGGG 180	
Db	121	IVHLCAISLDR	WYSITQAIIEYNLKRTPRRIKAIITVWVISA	VISFPPLISTE	KGGAGG 180	
Qy	181	POPAEPRCEI	NDOKWYVIVISSCIGSEFAPCLIMILVYRITQIAKRRTRVPPSRKGP	DAVA	240	
Db	181	QOPAEPSCKI	NDOKWYVIVISSSIGSEFAPCLIMILVYRITQIAKRRTRVPPSRKGP	DACS	240	
Qy	241	APPGCTERRP	NGLGPERSAGPGGAEAEP	LQTÖLNGAPGEPADAP	PRD	TALDLESSSSD 300
Db	241	APPGADRRP	NAVGPERGAGTAGAEAEPL	QTÖLNGAPGEPAP	TRPRDGDALDLESSSSE	300
Qy	301	HAERPPGRPR	PERPGRGKARASQVKKPGDSLPRRG	PATGIGTIPPAAGPGEER	VAKAKAS	360
Db	301	HAERÖGPGK	PERGPRAKGKTAKASQVKKPGDSLRRRG	PAGAPGASGSÖGGEER	AGAKAS	360
Qy	361	RWRGRONREK	RFTFVLAVVIGVFCWPEPFEFTYTLTAVGCSV	PRTLKFFFWFGYCNSS	420	
Db	361	RWRGRONREK	RFTFVLAVVIGVFCWPEPFEFTYTLTAVGCPV	YÖLNFFFWFGYCNSS	420	
Qy	421	LNPNVYITIF	NHDFRRAEKKILCRGDR	KRIV	450	
Db	421	LNPNVYITIF	NHDFRRAEKKILCRGDR	KRIV	450	

RESULT 5

alpha-2-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
C:Accession: JH0190
R:Chalberg, S.C.; Duda, T.; Rhine, J.A.; Sharma, R.K.
Mol. Cell. Biochem. 97, 161-172, 1990
A:Title: Molecular cloning, sequencing and expression of an alpha2-adrenergic receptor
A:Reference number: JH0190; MUID:91125329; PMID:2177834
A:Accession: JH0190
A:Molecule type: mRNA
A:Residues: 1-450 <CHA>
A:Experimental source: brain
C:Comment: Alpha-2-adrenergic receptor is a predominant catecholamine receptor. It mediates
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:34-59/Domain: hydrophobic <HDI>
F:71-96/Domain: hydrophobic <HII>
F:106-131/Domain: hydrophobic <III>
F:150-175/Domain: hydrophobic <HIV>
F:193-218/Domain: hydrophobic <HDV>
F:375-400/Domain: hydrophobic <HVI>
F:405-430/Domain: hydrophobic <VII>

Query Match	88.7%;	Score 2111;	DB 2;	Length 450;
Best Local Similarity	89.3%;	Pred. No. 1.3e-128;		
Matches 402; Conservative	9;	Mismatches 39;	Indels 0;	Gaps 0;

QY	1	M	G	S	L	Q	P	D	A	G	N	A	S	W	N	G	T	E	A	P	G	G	A	R	A	T	P	S	L	O	V	T	L	L	V	C	L	A	G	L	M	L	T	F	E	G	N	V	L	I	A	V	F	T	60				
Db	1	M	G	S	L	Q	P	D	A	G	N	A	S	W	N	G	T	E	A	P	G	G	T	R	A	T	P	S	L	Q	V	T	L	L	V	C	L	A	G	L	M	L	T	F	E	G	N	V	L	I	A	V	F	T	60				
QY	61	S	R	A	L	K	A	P	Q	N	L	F	L	V	S	L	A	S	A	D	I	L	V	A	T	L	V	I	P	F	S	L	A	N	E	W	G	Y	F	G	K	A	W	C	E	I	Y	L	A	D	V	L	F	C	T	S	120		
Db	61	S	R	A	L	K	A	P	Q	N	L	F	L	V	S	L	A	S	A	D	I	L	V	A	T	L	V	I	P	F	S	L	A	N	E	W	G	Y	F	G	K	A	W	C	E	I	Y	L	A	D	V	L	F	C	T	S	120		
QY	121	I	V	H	L	C	A	I	S	L	D	R	Y	W	S	T	Q	A	I	E	Y	N	L	K	R	T	P	R	R	I	K	A	I	I	T	T	W	V	I	S	A	V	I	S	E	P	P	L	I	S	I	E	K	K	G	G	G	180	
Db	121	I	V	H	L	C	A	I	S	L	D	R	Y	W	S	T	Q	A	I	E	Y	N	L	K	R	T	P	R	R	I	K	A	I	H	C	H	C	V	I	S	A	V	I	S	E	P	P	L	I	S	I	E	K	K	G	A	G	G	180
QY	181	P	Q	P	A	E	P	R	C	E	I	N	D	Q	K	W	Y	I	S	S	C	I	G	S	F	E	A	P	C	L	I	M	I	L	Y	V	R	I	Q	I	A	K	R	T	R	V	P	P	S	R	G	P	D	A	V	A	240		
Db	181	Q	P	A	E	P	R	S	C	K	I	N	D	Q	K	W	Y	I	S	S	S	I	G	S	F	E	A	P	C	L	I	M	I	L	Y	V	R	I	Q	I	A	K	R	T	R	V	P	P	S	R	G	P	D	A	C	S	240		
QY	241	A	P	P	G	T	E	R	R	P	N	G	L	G	P	E	R	S	A	G	P	G	A	E	A	E	P	L	P	T	Q	L	N	G	A	G	E	P	A	P	A	G	P	R	D	T	D	A	L	D	I	E	S	S	S	S	300		
Db	241	A	P	P	G	A	D	R	R	P	N	G	L	G	P	E	R	G	A	G	T	A	G	E	A	E	P	L	P	T	Q	L	N	G	A	G	E	P	A	P	T	R	P	R	D	G	D	A	L	D	I	E	S	S	S	S	300		
QY	301	H	A	E	R	P	G	P	R	R	P	E	R	G	P	R	G	K	A	R	A	S	Q	Y	K	P	G	D	S	L	P	R	G	P	G	A	T	G	I	G	T	P	A	G	P	G	E	E	R	V	A	K	A	S	360				
Db	301	H	A	E	R	P	G	P	G	K	P	E	R	G	P	R	A	K	T	A	S	Q	Y	K	P	G	D	S	L	P	R	G	P	G	A	G	P	G	A	S	G	S	G	Q	G	E	E	R	A	G	A	K	A	S	360				
QY	361	R	W	R	G	R	O	N	E	K	R	E	T	F	L	V	A	V	I	G	V	Y	C	W	E	P	F	E	T	T	L	A	V	G	S	V	P	R	T	L	F	K	F	F	W	E	G	Y	C	N	S	420							
Db	361	R	W	R	G	R	O	N	E	K	R	E	T	F	L	V	A	V	I	G	V	Y	C	W	E	P	F	E																															

RESULT 6

alpha-2-adrenergic receptor (clone RG10) - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
C/Accession: A40392
R/Lanier, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.
J. Biol. Chem. 266, 10470-10478, 1991
A/Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic
A/Reference number: A40392; MUID:91244823; PMID:1645350
A/Accession: A40392
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-458 <LAN>
A/Cross-references: GB:M62371; NID:g206612; PIDN:AAA42033.1; PID:g206613
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match	49.3%;	Score 1175;	DB 2;	Length 458;
Best Local Similarity	54.1%;	Pred. NO. 1.9e-68;		
Matches 252;	Conservative 48;	Mismatches 104;	Indels 62;	Gaps 12;

[illegible]

Db 252 RPDGASPTTENGIG--KAAGENGHCAPP-RTEV-----EP-----DESSAAE 290
QY 301 HAERPPGRRPERGPRGKGKARASQVKGPSLPRRGDGTGIGTPAAGPEERVGAAKAS 360
Db 291 RRRRRGAVRRGGRREGAEGDGTGSADGPGGLAAEQARTASRSP--GPGRLSRASSRS 348
QY 361 -----RWGR-----QNRKRTFVLAVVIGVFVVCWPFPEFTYTLTAV---GC 401
Db 349 VEEFLSRRRRARSSVCRKRYAQAAREKRTFVLAVVMGVFVLCWPFPEFSYSLGICREAC 408
QY 402 SVPRTLKFFEFWEGYCNSSLNPVITYTFNHDFRRAFKKILCRGDRK 447
Db 409 QLPEPLKFFFWIGYCNSSLNPVITYTFNODFRRSFKHILFRRRR 454

RESULT 7
149480
alpha-2 adrenergic receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I49480
R:Link, R.; Daunt, D.; Barsb, G.S.; Chruscinski, A.; Kobilka, B.
Mol. Pharmacol. 42, 16-27, 1992
A:Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and its
in antagonist binding.
A:Reference number: I49480; MUID:92342131; PMID:1353249
A:Accession: I49480
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-458 <RES>
A:Cross-references: GB:M99376; NID:g191880; PIDN:AAA37212.1; PID:g191881
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match 49.3%; Score 1175; DB 2; Length 458;
Best Local Similarity 54.1%; Pred. No. 1.9e-68;
Matches 252; Conservative 48; Mismatches 104; Indels 62; Gaps 12;

QY 14 NGTEA----PGGARAT-----PYSLQVTLTVCLAGLIMLTVFGNVLVIAVFT 60
Db 19 NSDAGEWGS GGAGANASGTDWVPPGQYSAGAVAGLAAVGLIVFTVGNVLVIAVLT 78
QY 61 SRALKAPQNLFLVSLASADILVATLVIPEFLANVMGYWFGKAWCEIYLAIDLVECTSS 120
Db 79 SRALRAPQNLFLVSLASADILVATLVMFSLANELMAWYFGQVWCGVYLAIDLVECTSS 138
QY 121 IVHLCAISLDRYWSITQAIENYLNKTRPRRIKALITVWVISAVISFPPLISIEKKGGGG 180
Db 139 IVHLCAISLDRYWSVTQAVEYNLKRTPRRKATIVAWLISAVISFPPLVSFYRRPDGA- 197
QY 181 PQPAEPRCEINDQKWYVYSSCIGSFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDVA 240
Db 198 ---AYPQGLNDETWYILSSCIGSFAPCLIMGLVYARIYVAKLRTLSEKRG---A 251
QY 241 APPGTERRPNGLGPERSAGPGAEEPLPTQLNGAPGEPAPAGPRDLDLDESSSSD 300
Db 252 GPDGASPTTENGIG--KAAGENGHCAPP-RTEV-----EP-----DESSAAE 290
QY 301 HAERPPGRRPERGPRGKGKARASQVKGPSLPRRGDGTGIGTPAAGPEERVGAAKAS 360
Db 291 RRRRGALRRGGRREGAEGDGTGSADGPGGLAAEQARTASRSP--GPGRLSRASSRS 348
QY 361 -----RWGR-----QNRKRTFVLAVVIGVFVVCWPFPEFTYTLTAV---GC 401
Db 349 VEEFLSRRRRARSSVCRKRYAQAAREKRTFVLAVVMGVFVLCWPFPEFSYSLGICREAC 408
QY 402 SVPRTLKFFEFWEGYCNSSLNPVITYTFNHDFRRAFKKILCRGDRK 447
Db 409 QLPEPLKFFFWIGYCNSSLNPVITYTFNODFRRSFKHILFRRRR 454

RESULT 8

A48392
alpha 2C4 adrenoceptor subtype - mouse
N:Alternate names: alpha 2C4 isoceptor
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C:Accession: A48392
R:Chang, Y.H.; Chang, N.C.; Chen, W.M.; Chang, A.C.
Biochem. Mol. Biol. Int. 29, 467-474, 1993
A:Title: Molecular characterization of a murine homologue of alpha 2C4 adrenoceptor s
A:Reference number: A48392; MUID:93250567; PMID:8387367
A:Accession: A48392
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-458 <CHA>
A:Cross-references: GB:M97516; NID:g191728; PIDN:AAA37183.1; PID:g191729
A:Experimental source: DBA/2, liver
A>Note: sequence extracted from NCBI backbone (NCBIN:131475, NCBIIP:131476)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 49.1%; Score 1169; DB 2; Length 458;
Best Local Similarity 54.0%; Pred. No. 4.6e-68;
Matches 252; Conservative 48; Mismatches 103; Indels 64; Gaps 13;

QY 14 NGTEA----PGGARAT-----PYSLQVTLTVCLAGLIMLTVFGNVLVIAVFT 60
Db 19 NSDAGEWGS GGAGANASGTDWVPPGQYSAGAVAGLAAVGLIVFTVGNVLVIAVLT 78
QY 61 SRALKAPQNLFLVSLASADILVATLVIPEFLANVMGYWFGKAWCEIYLAIDLVECTSS 120
Db 79 SRALRAPQNLFLVSLASADILVATLVMFSLANELMAWYFGQVWCGVYLAIDLVECTSS 138
QY 121 IVHLCAISLDRYWSITQAIENYLNKTRPRRIKALITVWVISAVISFPPLISIEKKGGGG 180
Db 139 IVHLCAISLDRYWSVTQAVEYNLKRTPRRKATIVAWLISAVISFPPLVSFYRR----- 193
QY 181 PQ-PAEPRCEINDQKWYVYSSCIGSFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDVA 239
Db 194 PDVAAYPQGLNDETWYILSSCIGSFAPCLIMGLVYARIYVAKLRTLSEKRG--- 250
QY 240 AAPPGTERRPNGLGPERSAGPGAEEPLPTQLNGAPGEPAPAGPRDLDLDESSSS 299
Db 251 AGPDGASPTTENGIG--KAAGENGHCAPP-RTEV-----EP-----DESSAA 289
QY 300 DHAERPPGRRPERGPRGKGKARASQVKGPSLPRRGDGTGIGTPAAGPEERVGAAKA 359
Db 290 ERRRRRAAVRRGGRREGAEGDGTGSADGPGGLAAEQARTASRSP--GPGRLSRASSR 347
QY 360 S-----RWGR-----QNRKRTFVLAVVIGVFVVCWPFPEFTYTLTAV---G 400
Db 348 SVEEFLSRRRRARSSVCRKRYAQAAREKRTFVLAVVMGVFVLCWPFPEFSYSLGICREA 407
QY 401 CSVPRTLKFFEFWEGYCNSSLNPVITYTFNHDFRRAFKKILCRGDRK 447
Db 408 QLPEPLKFFFWIGYCNSSLNPVITYTFNODFRRSFKHILFRRRR 454

RESULT 9
A37869
alpha-2B-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C:Accession: A37869; S13023
R:Flordellis, C.S.; Handy, D.E.; Bresnahan, M.R.; Zannis, V.I.; Gavras, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 1019-1023, 1991
A:Title: Cloning and expression of a rat brain alpha-2B-adrenergic receptor.
A:Reference number: A37869; MUID:91126047; PMID:1704126
A:Accession: A37869
A:Molecule type: mRNA
A:Residues: 1-458 <FLO>
A:Cross-references: GB:M58316; NID:g202585; PIDN:AAA40634.1; PID:g202586
A>Note: the authors translated the codon ACC for residue 69 as Asn and GCG for residu
R.Voigt, M.M.; McCune, S.K.; Kanterman, R.Y.; Felder, C.C.


```

Db      69  LFLVSLATADILVATLVMPFSLANELMGWYFGKVMCGIYALADVLFCTSSIVHLCALISL 128
QY     130  DRYWSITQAEYENLKRTPRRIKAILITVWVISAVISFPPLISIEKKGGGGPQDAEPCE 189
Db     129  DRYWSVTQAEYENLKRTPKRVKCIIVWLISAFISSPPLSID----SNNTISSQPCM 184
QY     190  INDQKWYVISSICGSEFAPCLIMILVYRITYQIAKRRTVRPSSRRGPDVAADPGTERR 249
Db     185  LNDDTWYILSSMASFAPCLIMILYIRIYQVAKTRTR--SMSGKE--PRPDGVTQT 238
QY     250  PNGLGPERSA PGGAE-----AEPITQUNGAPGEPAPAGPRDLDLESSSSSDHAER 304
Db     239  ENGLNKANSPECHGDRENGHCQCPTPSPQRTVTIGQ-----QTDADMDESEFSSEGGKH 291
QY     305  PPGRRRPERGDRGKGKARASQYVPGDSLPRRPGATGIGTPAAGPGGEERVGAAKASRWRG 364
Db     292  KPQRQDSQRAKR-PGLKKSSISIKQASARISRVSNKSYVDLFASRRKRRRSSIAEKKVS---- 346
QY     365  RQNRKRETFVLAVVIGVFVVCWEPPEFFTYTLTAV---GCSVPRTLFEKFEWEGYCNSSL 421
Db     347  -QAREKRETFVLAVVMGVFVVCWEPPEFFSYSLHAYCRDYCKIPDTLFK-FEWIGYCNSSL 404
QY     422  NPVIYTIENHDFERRAFKKILCRGDRK 447
Db     405  NPAIYTIENRDFERRAFQKILCKSWK 430

```

RESULT 12

A37223

alpha-2B-adrenergic receptor - human

N;Alternate names: alpha-2C2-adrenergic receptor

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 29-Oct-1999

C;Accession: A37223; I39407; S14308; A36158

R;Welnshank, R.L.; Zgombick, J.M.; Macchi, M.; Adham, N.; Lichtblau, H.; Branchek, T.A.; Mol. Pharmacol. 38, 681-688, 1990

A;Title: Cloning, expression, and pharmacological characterization of a human alpha-2B-adrenergic receptor

A;Reference number: A37223; MUID:91042469; PMID:2172775

A;Accession: A37223

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-450 <WEI>

R;Lomasney, J.W.; Lorenz, W.; Allen, L.F.; King, K.; Regan, J.W.; Yang-Feng, T.L.; Caron, M.G.; Proc. Natl. Acad. Sci. U.S.A. 87, 5094-5098, 1990

A;Title: Expansion of the alpha-2-adrenergic receptor family: cloning and characterization

A;Reference number: I39407; MUID:90311349; PMID:2164221

A;Accession: I39407

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-450 <LOM>

A;Cross-references: GB:M34041; NID:g178197; PIDN:AAA51666.1; PID:g178198

R;Chajland, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S. FEBS Lett. 280, 241-244, 1991

A;Title: Identification of an additional gene belonging to the alpha(2) adrenergic receptor family

A;Reference number: S14308; MUID:91192139; PMID:1849485

A;Accession: S14308

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 56-185 <CHH>

A;Cross-references: GB:X59684; NID:g228635

A;Note: this translation is not annotated in GenBank entry HSA1PH218, release 111.0

R;Chang, A.C.; Ho, T.F.; Chang, N.C. Biochem. Biophys. Res. Commun. 172, 817-823, 1990

A;Title: In vitro amplification by polymerase chain reaction of a partial gene encoding alpha-2B-adrenergic receptor

A;Reference number: A36158; MUID:91054503; PMID:2173582

A;Accession: A36158

A;Molecule type: DNA

A;Residues: 95-361, 'QL', 364-389 <CHA>

A;Cross-references: GB:M38742; NID:g177867; PIDN:AAA62823.1; PID:g177868

C;Genetics:

A;Gene: GDB:ADRA2B; ADRA2B; ADRA2L1; ADRA2RL1

A;Cross-references: GDB:120539; OMIM:104260

A;Map position: 2p13-2q13
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match	47.3%;	Score 1125.5;	DB 2;	Length 450;
Best Local Similarity	53.2%;	Pred. No. 2.8e-65;		
Matches 243; Conservative	50;	Mismatches 105;	Indels 59;	Gaps 14;

```

QY 27 PYSQVTLTVCLAGLMLLTVEGNVYIIAVFTSRALKAPONLFLVSLASADILAVTLV 86
   |||:| | : |||:| | |||:| | |||:| | |||:| | |||:| | |||:| |
Db 6 PYSVQATAIAAIAITFLILFTIEGNALVILAVLTSRSLRAPONLFLVSLAAADILAVTLI 65
QY 87 IPFSLANEVWGIVYFGKAWCEIYALDVLFTCTSSIVHLCAISLDRYWSITOAEYNLKR 146
   ||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 IPFSLANELLGWYFRRTWCEVYALDVLFTCTSSIVHLCAISLDRYWAVSRALAEYNSKRT 125
QY 147 PRRIKAILITVWVISAVISFPPLISTIEKKGGGGGPQ-ABPCEINDQKWYISSCIGSF 205
   ||| ||| : ||| : ||| ||| | ||| | ||| : ||| : ||| : ||| |||
Db 126 PRRIKCIILTWLIAAVISLPLI-----YKGDQPQPRGRPQCKLNQEAWYIIASSIGSF 181
QY 206 FAPCLIMLIVYVRIYQIAKRTRVPSRGRPDAAVAPPGTERPNGLGPEERSADGGAE 265
   ||| ||| ||| ||| ||| ||| : ||| | | : ||| : |||
Db 182 FAPCLIMLIVYLRILYIAKR-----SNRGRPRAKGGPGQGESKQPR--PDHGALASAK 233
QY 266 AEP LPT-----QLNG---APGEPAPA-GPRD TALDLEES-----SS 298
   | : : ||| : ||| | ||| | |||
Db 234 LPALASVASAREVNGHSHKSTGEKEGETPEDTGTRALPPSWAALLPNSGGQKEGVCASP 293
QY 299 SDHAERPGRPRPERGPRGKGAKASOVKPGD--SLPRRGPB-----ATGIGTPAAGPGE 351
   | ||| | | : | : : | | | | | | | | | | | | | | | | | |
Db 294 EDEAE-----EEEEEEEECEPDVAVSPASACSPPLQOPQGSRYLATLRGQVYLLGRG- 348
QY 352 ERVGAAKASRMGRGRON--REKRTFVLAVVIGVFVVCWFPEFFTYTLTAV--GCSVPRT 406
   ||| | | | : | | | | | | | | | | | | | | | | | : | |
Db 349 --VGAIGGQWWRRAHAYTREREKRTFVLAVVIGVFVLCWFPFFFSYSLGAICPRHKCKVPHG 406
QY 407 LFKFEFEGYCNSSLNPVITYITFNHDFRAFKKILCR 443
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 407 LFOFEFWIGYCNSSLNPVITYITFNQDFRRAFRRIICR 443

```

RESULT 13
S28221
alpha-2-C2 adrenergic receptor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 13-Aug-1999
C/Accession: S28221; JH06933
R/Chen, W.M.; Chang, A.C.; Shle, B.J.; Chang, Y.H.; Chang, N.C.A.
Biochim. Biophys. Acta 1171, 219-223, 1992
A/Title: Molecular cloning and characterization of a mouse alpha(2)C2 adrenoceptor su
A/Reference number: S28221; MUID:93129625; PMID:1336396
A/Accession: S28221
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-455 <CHE>
A/Cross-references: EMBL:M94583
A/Note: the authors translated the codon CCA for residue 161 as Phe, ACT for residue
R/Chruscinski, A.J.; Link, R.E.; Daunt, D.A.; Barsh, G.S.; Kobilka, B.K.
Biochem. Biophys. Res. Commun. 186, 1280-1287, 1992
A/Title: Cloning and expression of the mouse homolog of the human alpha2-C2 adrenergi
A/Reference number: JH06933; MUID:92378586; PMID:1354956
A/Accession: JH06933
A/Molecule type: DNA
A/Residues: 6-228,231-455 <CHR>
A/Cross-references: GB:L00979; NID:g191547; PIDN:AAA37131.1; PID:g191548
C/Superfamily: vertebrate rhodopsin
F/Keywords: G protein-coupled receptor; transmembrane protein
F/18-43/Domain: transmembrane #status predicted <TM1>
F/55-81/Domain: transmembrane #status predicted <TM2>
F/90-115/Domain: transmembrane #status predicted <TM3>
F/134-158/Domain: transmembrane #status predicted <TM4>
F/173-199/Domain: transmembrane #status predicted <TM5>
F/377-402/Domain: transmembrane #status predicted <TM6>

Db 411 FQFFWIGYCNSLNPVIYTFVNODFRRAFRRILCR 446

Search completed: February 15, 2003, 18:08:03
Job time : 26.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 15, 2003, 14:14:47 ; Search time 13.5 Seconds
(without alignments)
1382.544 Million cell updates/sec

Title: US-09-636-259B-3
Perfect score: 2381
Sequence: 1 MGSLOPDAGNASWNGTEAPG.....HDFRRAFKKILCRGDKRKRIY 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2381	100.0	450	1 A2AA_HUMAN	P08913 homo sapien
2	2227	93.5	450	1 A2AA_PIG	P18871 sus scrofa
3	2199	92.4	450	1 A2AA_MOUSE	Q01338 mus musculu
4	2188	91.9	450	1 A2AA_CAVPO	Q60474 cavia porce
5	2166	91.0	450	1 A2AA_RAT	P22909 rattus norv
6	2120	89.0	452	1 A2AA_BOVIN	Q28838 bos taurus
7	1188	49.9	462	1 A2AC_HUMAN	P18825 homo sapien
8	1177.5	49.5	455	1 A2AC_CAVPO	Q60476 cavia porce
9	1175	49.3	458	1 A2AC_MOUSE	Q01337 mus musculu
10	1175	49.3	458	1 A2AC_RAT	P22086 rattus norv
11	1171.5	49.2	448	1 A2AB_CAVPO	Q60475 cavia porce
12	1147	48.2	469	1 A2AC_DIDMA	P35405 didelphis m
13	1130.5	47.5	432	1 A2AR_LABOS	Q91081 labrus ossi
14	1125.5	47.3	450	1 A2AB_HUMAN	P18089 homo sapien
15	1119.5	47.0	455	1 A2AB_MOUSE	P30545 mus musculu
16	1098.5	46.1	453	1 A2AB_RAT	P19328 rattus norv
17	1015.5	42.7	436	1 A2AR_CARAU	P32251 carassius a
18	946	39.7	382	1 A2AB_DIDMA	Q77715 didelphis m
19	936	39.3	384	1 A2AB_ELEMA	O19014 elephas max
20	933	39.2	386	1 A2AB_AMBHO	O18935 amblysomus
21	931	39.1	390	1 A2AB_DUGDU	O77713 dugong dugo
22	930	39.1	388	1 A2AB_ORYAF	O19032 orycteropus
23	927.5	39.0	389	1 A2AB_PROHA	O19054 procavia ca
24	926	38.9	394	1 A2AB_RABRT	O77830 oryctolagus
25	923	38.8	389	1 A2AB_BOVSE	O77721 equus cabal
26	922	38.7	392	1 A2AB_BOVIN	O77700 bos taurus
27	919.5	38.6	387	1 A2AB_MACPR	O19025 macrotscelid
28	917.5	38.5	391	1 A2AB_ERIEU	O19012 erinaceus e
29	898	37.7	384	1 A2AB_ECHTE	O77723 echinops te
30	896.5	37.7	397	1 A2AB_TALEU	O19091 talpa europ
31	693.5	29.1	484	1 OAR1_LOCMU	Q25321 locusta mig
32	692.5	29.1	484	1 OAR2_LOCMU	Q25322 locusta mig
33	681.5	28.6	379	1 GRE2_BALAM	Q93127 balanus amp

34	651	27.3	476	1 GRE1_BALAM	Q93126 balanus amp
35	648	27.2	601	1 OAR_DROME	P22270 drosophila
36	640.5	26.9	477	1 OAR_HELVI	O25188 heliothis v
37	632.5	26.6	479	1 OAR_BOMMO	O17232 bombyx mori
38	631.5	26.5	443	1 D2DR_CERAE	P52702 cercopithec
39	629	26.4	444	1 D2DR_BOVIN	P20288 bos taurus
40	626.5	26.3	443	1 D2DR_HUMAN	P14416 homo sapien
41	619	26.0	463	1 D2DR_FUGRU	P53453 fugu rubrip
42	616	25.9	444	1 D2DR_MOUSE	P13953 mus musculu
43	611	25.7	377	1 SH1D_CANFA	P11614 canis famli
44	606.5	25.5	442	1 D2D1_XENLA	P24628 xenopus lae
45	605	25.4	376	1 SH1D_CAVPO	Q60484 cavia porce

ALIGNMENTS

RESULT 1
A2AA_HUMAN
ID A2AA_HUMAN STANDARD; PRT; 450 AA.

AC P08913;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR subtype C10).
GN ADRA2A OR ADRA2R OR ADRAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89308571; PubMed=2568356;
RA Fraser C.M., Arakawa S., McComble W.R., Venter J.C.;
RT "Cloning, sequence analysis, and permanent expression of a human alpha 2-adrenergic receptor in Chinese hamster ovary cells. Evidence for independent pathways of receptor coupling to adenylate cyclase attenuation and activation."
RL J. Biol. Chem. 264:11754-11761(1989).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Platelet;
RX MEDLINE=88042789; PubMed=2823383;
RA Kobilka B.K., Matsui H., Kobilka T.S., Yang-Feng T.L., Francke U., Caron M.G., Lefkowitz R.J., Regan J.W.;
RT "Cloning, sequencing, and expression of the gene coding for the human platelet alpha 2-adrenergic receptor."
RL Science 238:650-656(1987).
RN [3]
RP REVISIONS TO 333-365.
RX MEDLINE=91009167; PubMed=2170371;
RA Guyer C.A., Horstman D.A., Wilson A.L., Clark J.D., Kragoe E.J. Jr., Limbird L.E.;
RT "Cloning, sequencing, and expression of the gene encoding the porcine alpha 2-adrenergic receptor. Allosteric modulation by Na⁺, H⁺, and amiloride analogs."
RL J. Biol. Chem. 265:17307-17317(1990).
RN [4]
RP MUTAGENESIS OF PHE-412.
RX MEDLINE=91332079; PubMed=1678390;
RA Suryanarayana S., Daunt D.A., von Zastrow M., Kobilka B.K.;
RT "A point mutation in the seventh hydrophobic domain of the alpha 2 adrenergic receptor increases its affinity for a family of beta receptor antagonists."
RL J. Biol. Chem. 266:15488-15492(1991).
RN [5]
RP MUTAGENESIS OF ASPARTIC ACID AND SERINE RESIDUES.
RX MEDLINE=91342598; PubMed=1678850;
RA Wang C.-D., Buck M.A., Fraser C.M.;
RT "Site-directed mutagenesis of alpha 2a-adrenergic receptors: Identification of amino acids involved in ligand binding and receptor activation by agonists."

RL Mol. Pharmacol. 40:168-179(1991).
CC -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS. THE RANK ORDER OF POTENCY FOR AGONISTS OF THIS RECEPTOR
CC IS OXYMETAZOLINE > CLONIDINE > EPINEPHRINE > NOREPINEPHRINE >
CC PHENYLEPHRINE > DOPAMINE > P-SYNEPHRINE > P-TYRAMINE > SEROTONIN =
CC P-OCTOPAMINE. FOR ANTAGONISTS, THE RANK ORDER IS YOHIMBINE >
CC PHENTOLAMINE = MANSERINE > CHLORPROMAZINE = SPIPERONE = PRAZOSIN
CC > PROPRANOLOL > ALPRENOLOL = PINDOLOL.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M23533; AAA51655.1; -.
DR EMBL; M18415; AAA51664.1; -.
DR PIR; A34169; A34169.
DR PIR; A40132; A40132.
DR HSSP; P29274; 1MMH.
DR GeneW; HGNC:281; ADRA2A.
DR MIM; 104210; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33
FT TRANSMEM 34 59
FT DOMAIN 60 70
FT TRANSMEM 71 96
FT DOMAIN 97 106
FT TRANSMEM 107 129
FT DOMAIN 130 149
FT TRANSMEM 150 173
FT DOMAIN 174 192
FT TRANSMEM 193 217
FT DOMAIN 218 374
FT TRANSMEM 375 399
FT DOMAIN 400 406
FT TRANSMEM 407 430
FT DOMAIN 431 450
FT CARBOHYD 10 10
FT CARBOHYD 14 14
FT DISULFID 106 188
FT LIPID 442 442
FT SITE 113 113
FT SITE 200 200
FT SITE 204 204
FT SITE 79 79
FT MUTAGEN 113 113
FT MUTAGEN 130 130
FT MUTAGEN 200 200
FT MUTAGEN 204 204
FT MUTAGEN 412 412

AGONIST BINDING.
S->A: LOWER AFFINITY FOR AGONISTS. NO
CHANGE IN GUANINE NUCLEOTIDE-SENSITIVE
AGONIST BINDING.
S->A: LOWER AFFINITY FOR AGONISTS.
REDUCED GUANINE NUCLEOTIDE-SENSITIVE
AGONIST BINDING.
F->N: 350X REDUCED AFFINITY FOR ALPHA-2

FT ANTAGONIST YOHIMBINE, 3000X INCREASE FOR
FT BETA-ANTAGONIST ALPRENOLOL.
FT CONFLICT 104 104 A -> T (IN REF. 2).
FT CONFLICT 157 157 V -> C (IN REF. 2).
FT CONFLICT 333 365 PRRGPGATGIGTPAAGPGEERVGAKASRWGR ->
FT RGAGRGGRSGRRLOGRGRSASGLPRRRAGAG
FT (IN REF. 1 AND 2).
FT R -> L (IN REF. 2).
SQ CONFLICT 368 368
SQ SEQUENCE 450 AA; 48956 MW; A703CF262F04E8AC CRC64;
Query Match 100.0%; Score 2381; DB 1; Length 450;
Best Local Similarity 100.0%; Pred. No. 6.3e-103;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSLOPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLLMLLTVFGNVLIIVFT 60
Db 1 MGSLOPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLLMLLTVFGNVLIIVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEMGYWFGKAWCEIYALDVLCTSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEMGYWFGKAWCEIYALDVLCTSS 120
QY 121 IVHLCALSLDRWSTQATEYNLKTTPRIKAIITVWVISAVISFPPLISIEKKGGGG 180
Db 121 IVHLCALSLDRWSTQATEYNLKTTPRIKAIITVWVISAVISFPPLISIEKKGGGG 180
QY 181 POPAEPCEINDQKWYVSSCIGSEFAPCLIMILYVRIYQIAKRRTRVPSRRGPDAYA 240
Db 181 POPAEPCEINDQKWYVSSCIGSEFAPCLIMILYVRIYQIAKRRTRVPSRRGPDAYA 240
QY 241 APPGCTERRPNGLGPERSAGPGAFAEPLPTQNGAPGEPAPAGPRDLDLESSSSD 300
Db 241 APPGCTERRPNGLGPERSAGPGAFAEPLPTQNGAPGEPAPAGPRDLDLESSSSD 300
QY 301 HAERPPGRRRPERGPRGCKARASQVKPGDSLPRRPGATGIGTPAAGPGEERVGAKAS 360
Db 301 HAERPPGRRRPERGPRGCKARASQVKPGDSLPRRPGATGIGTPAAGPGEERVGAKAS 360
QY 361 RWRGRONREKRFTEFLAVVIGVFWCWFPEFFTYTLTAVGCSVPRTLEKFFWFGYCNS 420
Db 361 RWRGRONREKRFTEFLAVVIGVFWCWFPEFFTYTLTAVGCSVPRTLEKFFWFGYCNS 420
QY 421 LNPVIYTIFFNHDFRRAFKKILCRGDKRRIY 450
Db 421 LNPVIYTIFFNHDFRRAFKKILCRGDKRRIY 450
RESULT 2
A2AA_PIG STANDARD; PRT; 450 AA.
ID A2AA_PIG
AC P18871;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
GN ADRA2A OR A2AR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 212-232.
RC TISSUE=Liver;
RX MEDLINE=91009167; PubMed=2170371;
RA Guyer C.A., Horstman D.A., Wilson A.L., Clark J.D., Kragoe E.J. Jr.,
RA Limbird L.E.;
RT "Cloning, sequencing, and expression of the gene encoding the porcine
RT alpha 2-adrenergic receptor. Allosteric modulation by Na+, H+, and
RT amiloride analogs.";
RL J. Biol. Chem. 265:17307-17317(1990).
RP [2]
RP MUTAGENESIS OF CYS-442.
RX MEDLINE=93216775; PubMed=8385131;

RA Kennedy M.E., Limbird L.E.;
RT "Mutations of the alpha 2a-adrenergic receptor that eliminate
RT detectable palmitoylation do not perturb receptor-G-protein
RT coupling."
RL J. Biol. Chem. 268:8003-8011(1993).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: ALPHA2-ADRENERGIC RECEPTOR SHOWS AN ALLOSTERIC
CC MODULATION BY NA+, H+, AND AMILORIDE ANALOGS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: J05652; AAA30984.1; -.
DR PIR: A38316; A38316.
DR HSSP: P29274; 1MMH.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 59 1 (POTENTIAL).
FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 96 2 (POTENTIAL).
FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 173 4 (POTENTIAL).
FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 374 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 375 399 6 (POTENTIAL).
FT DOMAIN 400 409 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 410 430 7 (POTENTIAL).
FT DOMAIN 431 450 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 188 BY SIMILARITY.
FT LIPID 442 442 PALMITATE.
FT SITE 113 113 IMPLICATED IN LIGAND BINDING (BY
FT SITE 200 200 IMPLICATED IN CATECHOL AGONIST BINDING
FT SITE 204 204 (BY SIMILARITY).
FT SITE 204 204 IMPLICATED IN CATECHOL AGONIST BINDING
FT SITE 204 204 (BY SIMILARITY).
FT MUTAGEN 442 442 C->A,S: LOSS OF PALMITOYLATION.
FT SEQUENCE 450 AA; 48975 MM; 79D7D5B47372074E CRC64;
Query Match 93.5%; Score 2227; DB 1; Length 450;
Best Local Similarity 94.0%; Pred. No. 7e-96;
Matches 423; Conservative 3; Mismatches 24; Indels 0; Gaps 0;

QY 1 MGSLOPDAGNASMNGTEAPGGARATPYSLOVTLTVCLAGLMLTVFNGNLVIIVFT 60
DB 1 MGSLOPEAGNASMNGTEAPGGARATPYSLOVTLTVCLAGLMLTVFNGNLVIIVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPSLANEVMGYWFGKAWCEIYIALDVLCTSS 120
DB 61 SRALKAPQNLFLVSLASADILVATLVIPSLANEVMGYWFGKAWCEIYIALDVLCTSS 120
QY 121 IVHLCAISLDRYWSITQAIIEYNLKRTPRRIKAIITVWVISAVISPPPLISIEKKGGGG 180
DB 121 IVHLCAISLDRYWSITQAIIEYNLKRTPRRIKAIITVWVISAVISPPPLISIEKKGGGG 180

DB 121 IVHLCAISLDRYWSITQAIIEYNLKRTPRRIKAIITVWVISAVISPPPLISIEKKAGGG 180
QY 181 PQPAEPRCEINDQKWYVISSCIGSFAPCLIMLVYRIYQIAKRRTRVPPSRGPDAA 240
DB 181 QQPAEPRCEINDQKWYVISSCIGSFAPCLIMLVYRIYQIAKRRTRVPPSRGPDAA 240
QY 241 APPGTERPNGLGERSAGPGAEEPLTQNLNGAPGEPAPAGPRDTALDLESSSSD 300
DB 241 ALPGAERRPNGLGERGVGVAEAEPLVQLNGAPGEPAPAGPRADGLDLESSSSSE 300
QY 301 HAERPPGPRRPERGPRGKAKARASQVKGDSLPBRGPGATGIGTPAAGPGEERVGA 360
DB 301 HAERPPGPRRSEGERAKSKARASQVKGDSLPBRGPGAPGAPATGAGEERGVA 360
QY 361 RWRGRQNRKRFTEVLAIVIGFVVCWPFPTTYTLTAVGCSVPRTLEKFFWFGYCNS 420
DB 361 RWRGRQNRKRFTEVLAIVIGFVVCWPFPTTYTLTAVGCSVPRTLEKFFWFGYCNS 420
QY 421 LNPVIYTIENHDFRAFKKILCRGDRKRIV 450
DB 421 LNPVIYTIENHDFRAFKKILCRGDRKRIV 450
RESULT 3
A2AA_MOUSE STANDARD; PRT; 450 AA.
ID A2AA_MOUSE
AC 001338;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
GN ADRA2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92342131; PubMed=1353249;
RA Link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Kobilka B.K.;
RT "Cloning of two mouse genes encoding alpha 2-adrenergic receptor
RT subtypes and identification of a single amino acid in the mouse alpha
RT 2-C10 homolog responsible for an interspecies variation in
RT antagonist binding."
RL Mol. Pharmacol. 42:16-27(1992).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: M99377; AAA37213.1; -.
DR HSSP: P29274; 1MMH.
DR MGD: MGI:87934; Adra2a.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 59 1 (POTENTIAL).
FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 96 2 (POTENTIAL).

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FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 173 4 (POTENTIAL).
FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 374 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 375 399 6 (POTENTIAL).
FT DOMAIN 400 409 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 410 430 7 (POTENTIAL).
FT DOMAIN 431 450 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 188 BY SIMILARITY.
FT LIPID 442 442 PALMITATE (BY SIMILARITY).
FT SITE 113 113 IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
FT SITE 200 200 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT SITE 204 204 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT SITE 204 204 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT SITE 204 204 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
SO SEQUENCE 450 AA; 48865 MW; F07E225393AFA93B CRC64;
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Query Match 92.4%; Score 2199; DB 1; Length 450;
Best Local Similarity 92.2%; Pred. No. 1.3e-94;
Matches 415; Conservative 8; Mismatches 27; Indels 0; Gaps 0;

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QY 1 MGSLQPDAGNASWNGTEAPGGGARATPSLOYTLTLVCLAGLMLLTVFGNVLIIVAVFT 60
Db 1 MGSLQPDAGNSSWNGTEAPGGGTRATPSLOYTLTLVCLAGLMLLTVFGNVLIIVAVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFGKAWCEIYALDVLCTSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFGKAWCEIYALDVLCTSS 120
QY 121 IVHLCAISLDRYWSITQAIENLKRTPRRIKAIITVWVISAVISFPLISIEKKGGGG 180
Db 121 IVHLCAISLDRYWSITQAIENLKRTPRRIKAIITVWVISAVISFPLISIEKKGGGG 180
QY 181 PQPAEPRCEINDQKMYVISSCIGSFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDAVA 240
Db 181 QQPAEPPCKINDQKMYVISSSIGSFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDACS 240
QY 241 APPGCTERRPNGLGPERSAGPGGAEAEPPLTQUNGAPGEPAPAGPRDLDLLESSSSD 300
Db 241 APPGADRRPNGLGPBERGAGPTGAEAEPPLTQUNGAPGEPAPAGPRDLDLLESSSSSE 300
QY 301 HAERPPGRRPRPGRGKKGKARASQVKPDSLPRRPGATGIGTPAAGPGEERVGAAKAS 360
Db 301 HAERPPGRRPRPGRGKKGKTRASQVKPDSLPRRPGAGPGASGSGHGEERGGAAKAS 360
QY 361 RWRGRQNRKRTFTVLAIVIGVFWCWFPEFFFTYTLTAVGCSVPRTLKFEFFWFGYCNS 420
Db 361 RWRGRQNRKRTFTVLAIVIGVFWCWFPEFFFTYTLTAVGCPVPSQLNFPEFFWFGYCNS 420
QY 421 LNPVIYTIENHDFRRAFKKILCRGDKRIV 450
Db 421 LNPVIYTIENHDFRRAFKKILCRGDKRIV 450
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RESULT 4
A2AA_CAVPO STANDARD; PRT: 450 AA.
ID A2AA_CAVPO
AC Q60474;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
GN ADRA2A.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Harley;
RX MEDLINE=96152573; PubMed=8573196;
RA Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.;
RT "Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,
RT and alpha 2C adrenoceptor subtypes. Radioligand binding and
RT functional coupling to a CAMP-responsive reporter gene.";
RL Biochem. Pharmacol. 51:291-300(1996).
CC -|- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U25722; AAA67074.1; -.
DR HSSP: P29274; 1MMH.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 59 1 (POTENTIAL).
FT TRANSMEM 60 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 96 2 (POTENTIAL).
FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 129 3 (POTENTIAL).
FT TRANSMEM 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 173 4 (POTENTIAL).
FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 374 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 375 399 6 (POTENTIAL).
FT TRANSMEM 400 409 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 410 430 7 (POTENTIAL).
FT DOMAIN 431 450 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 187 BY SIMILARITY.
FT LIPID 442 442 PALMITATE (BY SIMILARITY).
FT SITE 113 113 IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
FT SITE 199 199 IMPLICATED IN AGONIST BINDING AND RECEPTOR ACTIVATION (BY SIMILARITY).
FT SITE 203 203 IMPLICATED IN AGONIST BINDING AND RECEPTOR ACTIVATION (BY SIMILARITY).
SO SEQUENCE 450 AA; 48910 MW; E6BBE9A7FEB8DD1 CRC64;
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Query Match 91.9%; Score 2188; DB 1; Length 450;
Best Local Similarity 92.5%; Pred. No. 4.3e-94;
Matches 417; Conservative 8; Mismatches 24; Indels 2; Gaps 2;

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QY 1 MGSLQPDAGNASWNGTEAPGGGARATPSLOYTLTLVCLAGLMLLTVFGNVLIIVAVFT 60
Db 1 MGSLQPDGNSWNGTEGPGGTRATPSLOYTLTLVCLVGLLILTVFGNVLIIVAVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFGKAWCEIYALDVLCTSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFGKAWCEIYALDVLCTSS 120
QY 121 IVHLCAISLDRYWSITQAIENLKRTPRRIKAIITVWVISAVISFPLISIEKKGGGG 180
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Db 121 IVHLCAISLDKRWYSITQAIENLKRTPRIKAIIVTWVISAVISFPLISFE-KAGGGG 179
Qy 181 PQPAERCEINDQKWYVISSICGSFFAPCLIMILVYVRIYQIAKRTRVPPSRGPD-A 239
Db 180 QQPAERCEINDQKWYVISSISGSFFAPCLIMILVYVRIYQIAKRTRVPPSRGPD-A 239
Qy 240 AAPPGGTERPNGLGPERGAGGAEAPLPTQLNGAPGEPAPAGPRDTALDLESSSS 299
Db 240 AAPPGGAEERRPNGLGLERGVPGEAEAPLPTQVNGAPGEPAPAGPRDAEALDLESSSS 299
Qy 300 DHAERPPGRRPERGPRGKGAKASQVKGDSLPKRGPGATGICTPAAGGGEERYGAKA 359
Db 300 EHAERPPGARRPERGLRAKSKARASQVKGDSLPKRAPGAGSGTSGSGPGEERGAKA 359
Qy 360 SRWGRQNRERKFTFLAVVIGVFWCMEPEFFTYTLTAVGCSVPRTLKFFFEWFGYCN 419
Db 360 SRWGRQNRERKFTFLAVVIGVFWCMEPEFFTYTLTAVGCSVPRTLKFFFEWFGYCN 419
Qy 420 SLNPVITYTFNHDFRRAFKKILCRGDRKRIV 450
Db 420 SLNPVITYTFNHDFRRAFKKILCRGDRKRIV 450

RESULT 5
A2AA_RAT STANDARD; PRT; 450 AA.
ID A2AA_RAT
AC P22909;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR)
DE (CA2-47) (Alpha-2D adrenergic receptor).
GN ADRA2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91244823; Pubmed=1645350;
RA Lanier S.M., Downing S., Duzic E., Homcy C.J.;
RT "Isolation of rat genomic clones encoding subtypes of the alpha 2-
RT adrenergic receptor. Identification of a unique receptor subtype.";
RL J. Biol. Chem. 266:10470-10478(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91125329; Pubmed=2177834;
RA Chalberg S.C., Duda T., Rhine J.A., Sharma R.K.;
RT "Molecular cloning, sequencing and expression of an alpha 2-adrenergic
RT receptor complementary DNA from rat brain.";
RL Mol. Cell. Biochem. 97:161-172(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95349560; Pubmed=7623790;
RA Wyslowski K., Duda T., Sharma R.K.;
RT "Structural, genetic and pharmacological identity of the rat alpha
RT 2-adrenergic receptor subtype ca2-47 and its molecular
RT characterization in rat adrenal, adrenocortical carcinoma and bovine
RT retina.";
RL Mol. Cell. Biochem. 144:181-190(1995).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; M62372; AAA42034.1; -.
DR EMBL; U79031; AAC24959.1; -.
DR PIR; B40392; B40392.
DR PIR; JH0190; JH0190.
DR HSSP; P29274; IMMh.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33
FT TRANSMEM 34 59
FT DOMAIN 60 70
FT TRANSMEM 71 96
FT DOMAIN 97 106
FT TRANSMEM 107 129
FT DOMAIN 130 149
FT TRANSMEM 150 173
FT DOMAIN 174 192
FT TRANSMEM 193 217
FT DOMAIN 218 374
FT TRANSMEM 375 399
FT DOMAIN 400 409
FT TRANSMEM 410 430
FT DOMAIN 431 450
FT CARBOHYD 10 10
FT CARBOHYD 14 14
FT DISULFID 106 188
FT LIPID 442 442
FT SITE 113 113
FT SITE 200 200
FT SITE 204 204
FT CONFLICT 147 147
FT CONFLICT 154 158
FT CONFLICT 252 253
FT CONFLICT 264 264
FT CONFLICT 304 305
FT CONFLICT 333 333
FT CONFLICT 445 445
SQ SEQUENCE 450 AA; 48939 MW; AFA078DCA3D612AC CRC64;

Query Match 91.0%; Score 2166; DB 1; Length 450;
Best Local Similarity 90.9%; Pred. No. 4.3e-93;
Matches 409; Conservative 9; Mismatches 32; Indels 0; Gaps 0;

Qy 1 MGSLQPDAGNASWNGTEAPGGARATPYSLQVTLTLVCLAGLMLLTVEGNLVIAVFT 60
Db 1 MGSLQPDAGNSSWNGTEAPGGTRATPYSLQVTLTLVCLAGLMLLTVEGNLVIAVFT 60
Qy 61 SRALKAPQNLFLVSLASADILVATLVIPESLANEVMGYFEGKAWCEIYLADVLCCTS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVIPESLANEVMGYFEGKAWCEIYLADVLCCTS 120
Qy 121 IVHLCAISLDKRWYSITQAIENLKRTPRIKAIIVTWVISAVISFPLISIEKGGGG 180
Db 121 IVHLCAISLDKRWYSITQAIENLKRTPRIKAIIVTWVISAVISFPLISIEKGGAGG 180
Qy 181 PQPAERCEINDQKWYVISSICGSFFAPCLIMILVYVRIYQIAKRTRVPPSRGPD-A 240
Db 181 QQPAERCEINDQKWYVISSISGSFFAPCLIMILVYVRIYQIAKRTRVPPSRGPDACS 240
Qy 241 APPGTERPNGLGPERGAGGAEAPLPTQLNGAPGEPAPAGPRDTALDLESSSSD 300
Db 241 APPGADRRPNGLGPERGAGTAGAEAPLPTQLNGAPGEPAPTRPRDGDALDLESSSE 300
Qy 301 HAERPPGRRPERGPRGKGAKASQVKGDSLPKRGPGATGICTPAAGGGEERYGAKAS 360
Db 301 HAERPPGRRPERGPRGKGAKASQVKGDSLPKRGPGATGICTPAAGGGEERYGAKAS 360
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Db 301 HAERPGGPKPERGPRAKGTKASQVKGDSLPRGPGAGAGSAGSGGEEERAGAKAS 360
QY 361 RMGRQNRKREKFTFLAVVIGVFWCWPFFFTYTLTAVGCSVPRTLKFKFFWFGYCNS 420
Db 361 RMGRQNRKREKFTFLAVVIGVFWCWPFFFTYTLTAVGCPVPYQLFNFFWFGYCNS 420
QY 421 INPVIYTIFFNHFRRAFKKILCRGDKRRIY 450
Db 421 INPVIYTIFFNHFRRAFKKILCRGDKRRIY 450
RESULT 6
A2AA_BOVIN
ID A2AA_BOVIN STANDARD; PRT; 452 AA.
AC Q28838;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Alpha-2a adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR)
GN ADRA2A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9811113; PubMed=9450652;
RA Venkataraman V., Duda T., Sharma R.K.;
RT "The bovine alpha 2D-adrenergic receptor gene: structure, expression
in retina, and pharmacological characterization of the encoded
receptor.";
RL Mol. Cell. Biochem. 177:113-123(1997).
RN [2]
RP SEQUENCE OF 171-210 FROM N.A.
RX MEDLINE=94018366; PubMed=8412494;
RA Blaxall H.S., Heck D.A., Bylund D.B.;
RT "Molecular determinants of the alpha-2D adrenergic receptor subtype.";
RL Life Sci. 53:9-9(1993).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: RETINA, BRAIN AND OLFACTORY LOBE.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U79030; AAC24958.1; -
DR EMBL; S66295; AAB28450.1; -
DR HSSP; P29274; LMMH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
Multi-gene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 59 1 (POTENTIAL).
FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 96 2 (POTENTIAL).
FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 173 4 (POTENTIAL).

FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 376 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 377 401 6 (POTENTIAL).
FT DOMAIN 402 411 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 412 432 7 (POTENTIAL).
FT DOMAIN 433 452 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 188 BY SIMILARITY.
FT LIPID 444 444 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 452 AA; 49252 MW; F10C1DD2860CD6F9 CRC64;
Query Match 89.0%; Score 2120; DB 1; Length 452;
Best Local Similarity 90.9%; Pred. No. 5.5e-91;
Matches 412; Conservative 4; Mismatches 33; Indels 4; Gaps 4;
QY 1 MGSLPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLLTVEGNVLIIVFT 60
Db 1 MGSLPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLLTVEGNVLIIVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPESLANEYGYWFGKAWCEIYALDYLFTSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVIPESLANEYGYWFGKAWCEIYALDYLFTSS 120
QY 121 IVHLCAISLDYWSITQALEYNLKRTPRRIKAIITVWVIVSAVISFPPLISTIEKKGGGG 180
Db 121 IVHLCAISLDYWSITQALEYNLKRTPRRIKAIITVWVIVSAVISFPPLISTIEKKGGGG 180
QY 181 PQPAEPCEINDQKWYVIVSSCIGSEFAPCLIMILVYVRIYQIAKRRTRVPSRGPDAVA 240
Db 181 QPSAEPCEINDQKWYVIVSSSIGSEFAPCLIMILVYVRIYQIAKRRTRVPSRGPDAVA 240
QY 241 AP-PGCTERRPNGLGPERSAGPGGAEEPLPTQUNGAPGEPAPAGPRDTDALDLESSS 298
Db 241 AELPGSAERRPNGLGPERGCVPGVAEVEISLQVUNGAPGEPAPAG-AGADALDLESSS 299
QY 299 SDAERPPGRRPERGPRGKKGKARASQVKGDSLPRRGPGATGIGTPAAGPEERV-GAA 357
Db 300 SEHAERPPGRRSERGPRGKKGKARASQVKGDSLPRRGPGATGIGTPAAGPEERSGGA 359
QY 358 KASRWGRQNRKREKFTFLAVVIGVFWCWPFFFTYTLTAVGCSVPRTLKFKFFWFGYC 417
Db 360 KASRWGRQNRKREKFTFLAVVIGVFWCWPFFFTYTLTAVGCPVPYQLFNFFWFGYC 419
QY 418 NSSLNPIYTIFFNHFRRAFKKILCRGDKRRIY 450
Db 420 NSSLNPIYTIFFNHFRRAFKKILCRGDKRRIY 452
RESULT 7
A2AC_HUMAN
ID A2AC_HUMAN STANDARD; PRT; 462 AA.
AC P18825; P35369; Q9HB49;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-2C-adrenergic receptor (Alpha-2C adrenoceptor) (Subtype C4).
GN ADRA2C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Kidney;
RX MEDLINE=88320430; PubMed=2842764;
RA Regan J.W., Kobilka T.S., Yang-Feng T.L., Caron M.G., Lefkowitz R.J.,
RA Kobilka B.K.;
RT "Cloning and expression of a human kidney cDNA for an alpha
2-adrenergic receptor subtype.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:6301-6305(1988).
RN [2]


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RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=98041882; PubMed=9371698;
RA Schaak S., Dovedjian J.C., Cayla C., Sender Y., Paris H.;
RT "Molecular cloning, sequencing and functional study of the promoter
RL region of the human alpha2C4-adrenergic receptor gene.";
RT Biochem. J. 328:431-438(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Yano K., Takeda M., Sugimoto E., Sagai H.;
RT "Molecular cloning and expression of a novel human alpha2C-adrenergic
RT receptor, alpha2CII, gene.";
RT Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT 322-GLY--PRO-325 DEL.
RX MEDLINE=20390061; PubMed=10801795;
RA Small K.M., Forbes S.L., Rahman F.F., Bridges K.M., Liggett S.B.;
RT "A four amino acid deletion polymorphism in the third intracellular
RT loop of the human alpha 2C-adrenergic receptor confers impaired
RT coupling to multiple effectors.";
RT J. Biol. Chem. 275:23059-23064(2000).
RL
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC
CC -1- POLYMORPHISM: The Del322-325 variant has a significant loss of
CC function. It is approximately 10 times more frequent in African-
CC Americans compared with Caucasians (allele frequencies 0.381
CC versus 0.040).
CC
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; J03853; AAA35513.1; -.
DR EMBL; U72648; AAC78723.1; -.
DR EMBL; D13538; BAA02737.1; -.
DR EMBL; AF280399; AAG28076.1; -.
DR EMBL; AF280400; AAG28077.1; -.
DR PIR; A31237; A31237.
DR HSSP; P29274; 1MMH.
DR Genew; HGNC:283; ADRA2C.
DR MIM; 104250; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Polymorphism; Alternative splicing.
KW DOMAIN 1 51
FT TRANSMEM 52 76
FT DOMAIN 77 88
FT TRANSMEM 89 114
FT DOMAIN 115 124
FT TRANSMEM 125 147
FT DOMAIN 148 168
FT TRANSMEM 169 191
FT DOMAIN 192 207
FT TRANSMEM 208 231
FT DOMAIN 232 379
FT TRANSMEM 380 407
FT DOMAIN 408 420
FT TRANSMEM 421 441
FT DOMAIN 442 462
FT DOMAIN 294 308
FT DOMAIN 294 308
FT ARG-RICH (BASIC).

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FT	CARBOHYD	19	19	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	33	33	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	124	202	BY SIMILARITY.
FT	VARSPLIC	270	300	AGENGHCAPPADVEPPDESSAAERRRRRGA -> EARTGT
FT	VARIANT	322	325	ARRPRPTSRTRAQRPBGCAFGP (IN ISOFORM 2). MISSING.
FT	CONFLICT	239	239	/FTID=VAR_012747. L -> R (IN REF. 1 AND 2).
FT	CONFLICT	329	329	E -> Q (IN REF. 1 AND 2).
FT	CONFLICT	401	401	S -> I (IN REF. 1 AND 2).
FT	CONFLICT	446	446	R -> P (IN REF. 1 AND 2).
SO	SEQUENCE	462 AA;	49522 MW;	EIFE9CA21E7F6EDA CRC64;
Query Match				
Best Local Similarity 49.9%; Score 1188; DB 1; Length 462;				
Matches 255; Conservative 40; Mismatches 101; Indels 86; Gaps 10;				
OY	10 NASWNGTEAPGGGARAT-----PYSLOVTLTVLCAGLMLLTVEGNLVITAVFT	60		
Db	19 NASGAGERSGGVANASGASWGPPRGQISAGAVAGLAAYVGFLIVFTVGNVLVAIVLT	78		
OY	61 SRALKAPQNLFVLSLASADILVATVIPFSLANEVMGYWYGKAWCEIYLADVLECTSS	120		
Db	79 SRALRAPQNLFVLSLASADILVATVLMDFSLANELMAWYFQCVMCGVLYALDVLECTSS	138		
OY	121 IVHLCAISLDRYNSITQAIEYNLKRFPRRIKAIITVWVISAVISFPPLISIEKKGGGG	180		
Db	139 IVHLCAISLDRYMSVTQAVEYNLKRTFRVKATIVAVWLISAVISFPPLVSLEYRQPDGA-	197		
OY	181 PQPAERCEINDOKWYVISSCIGSEFADECLIMILVVRIYQTAKRTRVPSPRRCPDAYA	240		
Db	198 ---AYPGCLNDETWTYLLSSCIGSEFADECLIMGLVARIYRAKLTRTTLSEKRAP---V	251		
OY	241 APPGGETRRPNGLGPERSAGPGGAEAEPLOTQLNGARPGEAPAGPRDTDALDESSSSSD	300		
Db	252 GPDGASPTTENGLCAAAGAGENGHCA-----DPEPDESSA	290		
OY	301 HAERPGRPRREPGRPKGKARASOVKPGDSLPRRPGATGIGTPAAGPGEERYGAAKAS	360		
Db	291 AAE----RRRRGALLRRGRRRAGAEGG----AGADGOG--AGPGAESGALTAS	336		
OY	361 RMRG-----RQNRKRFTVLAIVIGVEVCWF	388		
Db	337 RSPGGGRLSRASSRSVEFFLSRRRRARSSVCRKVAQAREKRTFVLAVMGMVEVLCWF	396		
OY	389 PEFTTYTLTAV---GCSVPRTLFKFEFMGYCNSSLNPVIYTIENHDFRAAFKILCRGD	445		
Db	397 PEEFSYSLYGICREACQVPGLFKFEFWIGYCNSSLNPVIYTFVNQDFRRSFKHILERRR	456		
OY	446 RK 447			
Db	457 RR 458			
RESULT 8				
AZAC_CAVPO	STANDARD;	PRT;	455 AA.	
ID	AZAC_CAVPO			
AC	Q60476;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	Alpha-2C adrenergic receptor (Alpha-2C adrenoceptor).			
OS	Cavia porcellus (Guinea pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.			
OX	NCBI_TaxId=10141;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Harley;			
RX	MEDLINE=96152573; PubMed=8573196;			
RA	Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.;			
RT	"Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,			
	and alpha 2C adrenoceptor subtypes.Radioligand binding and			

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RT functional coupling to a CAMP-responsive reporter gene." ;
RL Biochem. Pharmacol. 51:291-300(1996) .
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U25724; AAA67076.1; .
DR HSSP; P29274; 1MMH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation.
FT DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 48 72 1 (POTENTIAL).
FT FT 73 84 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 85 110 2 (POTENTIAL).
FT DOMAIN 111 120 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 121 143 3 (POTENTIAL).
FT FT 144 164 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 165 187 4 (POTENTIAL).
FT DOMAIN 188 203 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 204 227 5 (POTENTIAL).
FT DOMAIN 228 376 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 377 400 6 (POTENTIAL).
FT DOMAIN 401 413 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 414 434 7 (POTENTIAL).
FT DOMAIN 435 455 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 120 198 BY SIMILARITY.
SQ SEQUENCE 455 AA; 49351 MW; 6B657D247FF8A3F4 CRC64;

Query Match 49.5%; Score 1177.5; DB 1; Length 455;
Best Local Similarity 53.7%; Pred. No. 7.2e-48;
Matches 253; Conservative 47; Mismatches 114; Indels 57; Gaps 11;

QY 4 LQPDAGNASWNGTEAPGGGARA-----TPYSLQVTLTVCLAGLMLLTVEGNLV 54
   | : ||| | ||| | : || : | : | : ||| |
DB 11 LAEGPNAS--GAGEGGGVNASGAVWGPPSPQYSAGAVAGIAVVGFLIVFTVGNLV 68

QY 55 IIAVETSRALKAPQNLFLVSLASADILVATLVPFSLANEVGYWFGKAWCEIYALDV 114
   :||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 69 VIAVLTSRALRAPQNLFLVSLASADILVATLVMFSLANELMAVWYFGQVWCYVLLDV 128

QY 115 LFCSTSSIVHLCAISLDRYWSITQAIENYLNKRTPRRIKAITTVWVISAVISFPPLISIEK 174
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 129 LFCSTSSIVHLCAISLDRYWSITQAVEYNLKRTPRRVKATIVAVWLISAITSPPLVSFYR 188

QY 175 KGGGGGQPAEPRCCEINDQKVVYISSCIGSFAPCLIMILVYVRIQIAKRRTVPSPSR 234
   : | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 189 QPDGA----AYPRCGLNDEWYIILSSCIGSFAPCLIMGLYARIVYRAKLRTLTSEKR 244

QY 235 GPDAVAAPPGGTERPNGLGPERKSAGPGGAELPLPTQLNGAPGEPAAPGPRDTDALDLE 294
   || | | | | : ||| | : | : | : | : | : | : | : | :
DB 245 GP---AGPEGESPTTENGGLGAAAA-----AAGENGHCAPPRAD-VEPD 284

QY 295 ESSSSDHAERPPGPRRPER-----GPRGKGKARASQYKPGDSLPRRGPGATGIGTP 345
   |||:::| | | | | | | | | | | | | | | | | | | | | | :
DB 285 ESSAAERRRRRGALRRGAROREAGVEAPGP-GLGSAAD---PGALSVSRSPGPGGRLSR 340

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QY      346 AAGGEE-----RVGAAKSRMGGRONREKRFTEVLAVIGVEVVCWPEPFETTLTAV 399
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db      341 ASRSVSEFFLSRRRRARRSSVCRKKVAQAAREKRFTFLAVVMGVFLCWEPPEFESSLYGI 400

QY      400 --GCSVPRTLFEKFEFWEGYCNSSLNPVIYTIENHDFRAEFKILCRGDRK 447
       | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      401 CREACQLPTPLFKFFFWGYCNSSLNPVIYTIENQDFRSFKHLFRRRR 451

RESULT 9
A2AC_MOUSE STANDARD; PRT; 458 AA.
ID A2AC_MOUSE AC Q01337;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Alpha-2C adrenergic receptor (Alpha-2C adrenoceptor) (Subtype C4).
GN ADRA2C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92342131; Pubmed=1353249;
RA Link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Kobilka B.K.;
RT "Cloning of two mouse genes encoding alpha 2-adrenergic receptor
RT subtypes and identification of a single amino acid in the mouse alpha
RT 2-C10 homolog responsible for an interspecies variation in
RT antagonist binding."
RL Mol. Pharmacol. 42:16-27(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=93250567; Pubmed=8387367;
RA Chang Y.-H., Chang A.C., Chen W.-M., Chang N.-C.A.;
RT "Molecular characterization of a murine homologue of alpha 2C4
RT adrenoceptor subtype gene."
RL Biochem. Mol. Biol. Int. 29:467-474(1993).
CC -I- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; M99376; AAA37212.1; -.
CC DR EMBL; M97516; AAA37183.1; -.
CC DR HSSP; P29274; IMMH.
CC DR MGD; MG1:87936; Adra2c.
CC DR InterPro: IPR000276; GPCR_Rhodpsn.
CC DR Pfam; PF00001; 7tm_1; 1.
CC DR PRINTS; PR00237; GPCRRHODOPSN.
CC DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation.
KW DOMAIN 1 51 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 52 76 1 (POTENTIAL).
FT DOMAIN 77 88 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 89 114 2 (POTENTIAL).
FT DOMAIN 115 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 147 3 (POTENTIAL).
FT DOMAIN 148 168 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 169 191 4 (POTENTIAL).
FT DOMAIN 192 207 EXTRACELLULAR (POTENTIAL).
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FT  TRANSMEM  208  231  5 (POTENTIAL).
FT  DOMAIN  232  379  CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM  380  403  6 (POTENTIAL).
FT  DOMAIN  404  416  EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM  417  437  7 (POTENTIAL).
FT  DOMAIN  438  458  CYTOPLASMIC (POTENTIAL).
FT  DOMAIN  291  305  ARG-RICH (BASIC).
FT  CARBOHYD  19  19  N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD  33  33  N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  DISULFID  124  202  BY SIMILARITY.
FT  CONFLICT  196  196  G -> V (IN REF. 2).
FT  CONFLICT  296  296  G -> A (IN REF. 2).
FT  CONFLICT  298  298  L -> V (IN REF. 2).
SQ  SEQUENCE  458 AA; 49906 MM; COA8BDF0302BF1FB CRC64;

Query Match 49.38; Score 1175; DB 1; Length 458;
Best Local Similarity 54.18; Pred. No. 9.5e-48;
Matches 252; Conservative 48; Mismatches 104; Indels 62; Gaps 12;

OY  14 NGTEA----PGGARAT-----PYSLOYTLVCLAGLMLLTVEGNVLIATVFT 60
    ||::|| ||||| ||| | | | | | | | | | | | | | | | | | | | | | | |
Db  19 NGS DAGEWGGGAGANASGTDWVPPPGQYSAGAVAGLAAVGFLIVETVGNVLVIATVLT 78

OY  61 SRALKAPONLFLVSLASADILVATLVIPFSLANEVGYWFGKAWCEIYALDVLCTSS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  79 SRALRAPONLFLVSLASADILVATLVMPFSLANELMAVWYFGQVWCQGVYALDVLCTSS 138

OY  121 IVHLCATSLDRWYSITQAIENYLNKRTPRRIKAITTWVISAVISFPPLISTIEKKGGGG 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||:|
Db  139 IVHLCATSLDRWYSVQAVEYNLKRTPRKRKATYAVWVLISAVISFPPLVSFYRRPDGA- 197

OY  181 POBAEPRCEINDOKWVYISSCIGSFAPCLIMILYVRYIOIAKRRTRVPSRRGPDAVA 240
    ||::|| |::| ||::| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  198 ---AYPOCGLNDETWTYIISSCIGSFAPCLIMGLVYARIYRVAKLRTLTSEKRG- -A 251

OY  241 APPGTERRPNGLGPERSAPGGAEAELPTQLNGAPGEPAAGPRDTDALDLESSSSD 300
    | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  252 GPDGASPTTENG LG--KA GENGHCAPP-RTEV-----EP-----DESSAAE 290

OY  301 HAERPPGRRPERGPRGKAKARASQVKPGDSLPRRPGATGIGTPAGPGEERVGAAKAS 360
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  291 RRRRRGALRRGRRREGAEGDGTGSADGPGGLAEOGARTASRSP--GPGGRLSRASSRS 348

OY  361 -----RWGR-----QNRKRTFVLAVIGVFWVCMFPFFFTYTLTAV--GC 401
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  349 VEFPLSRRRRRARSSVCRKVAQAAREKRTFVLAVVWGVFLCWFPEFFFSYSLGICREAC 408

OY  402 SVPRTLKFEFFWFGYCNSLNPIVITYTFNHDFRRAFKKILCRGDRK 447
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  409 QLEPPLKFEFFWIGYCNSLNPIVITYTFNODFRSRFKHILFRRRRR 454

RESULT 10
A2AC_RAT
ID A2AC_RAT STANDARD; PRT; 458 AA.
AC P22086;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Alpha-2C adrenergic receptor (Alpha-2C adrenoceptor) (Subtype C4).
GN ADRA2C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathl; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91126047; PubMed=1704126;
RA Flordellis C.S., Handy D.E., Bresnahan M.R., Zannis V.I., Gavras H.;
RT "Cloning and expression of a rat brain alpha 2B-adrenergic receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:1019-1023(1991).
RN [2]
RP SEQUENCE FROM N.A.

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RX  MEDLINE=91130596; PubMed=1704314;
RA  Voigt M.M., McCune S.K., Kanterman R.Y., Felder C.C.;
RT  "The rat alpha 2-C4 adrenergic receptor gene encodes a novel
RT  pharmacological subtype.";
RL  FEBS Lett. 278:45-50(1991).
RN  [3]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=91244823; PubMed=1645350;
RA  Lanier S.M., Downing S., Duzic E., Homcy C.J.;
RT  "Isolation of rat genomic clones encoding subtypes of the alpha 2-
RT  adrenergic receptor. Identification of a unique receptor subtype.";
RL  J. Biol. Chem. 266:10470-10478(1991).
RN  [4]
RP  SEQUENCE FROM N.A.
RA  Saitoh M., Imai A., Shimomura H.;
RT  "Cloning of rat alpha-2-B-adrenergic receptor gene and expression in
RT  rat submandibular gland.";
RL  Shigaku 80:317-326(1992).
CC  -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC  INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC  PROTEINS.
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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DR  EMBL; M58316; AAA40634.1; -.
DR  EMBL; X57659; CAA40861.1; -.
DR  EMBL; M62371; AAA42033.1; -.
DR  EMBL; D00819; BAA00700.1; -.
DR  PIR; A37869; A37869.
DR  PIR; S13023; S13023.
DR  PIR; A40392; A40392.
DR  HSSP; P29274; 1MMH.
DR  InterPro; IPR000276; GPCR_Rhodopsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCR_RHODOPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW  G-protein coupled receptor; Transmembrane; Glycoprotein;
KW  Multigene family; Phosphorylation.
FT  DOMAIN 1 51 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 52 76 1 (POTENTIAL).
FT  DOMAIN 77 88 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 89 114 2 (POTENTIAL).
FT  DOMAIN 115 124 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 125 147 3 (POTENTIAL).
FT  DOMAIN 148 168 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 169 191 4 (POTENTIAL).
FT  DOMAIN 192 207 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 208 231 5 (POTENTIAL).
FT  DOMAIN 232 379 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 380 403 6 (POTENTIAL).
FT  DOMAIN 404 416 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 417 437 7 (POTENTIAL).
FT  DOMAIN 438 458 CYTOPLASMIC (POTENTIAL).
FT  DOMAIN 291 305 ARG-RICH (BASIC).
FT  CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  DISULFID 124 202 BY SIMILARITY.
FT  CONFLICT 24 24 G -> R (IN REF. 4).
FT  CONFLICT 40 40 G -> A (IN REF. 1).
FT  CONFLICT 69 69 N -> T (IN REF. 1).
FT  CONFLICT 155 155 Q -> E (IN REF. 2).
FT  CONFLICT 245 245 S -> T (IN REF. 1).
FT  CONFLICT 252 252 G -> R (IN REF. 3).
FT  CONFLICT 275 275 A -> R (IN REF. 4).

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FT CONFLICT 298 298 L -> V (IN REF. 3).
SQ SEQUENCE 458 AA; 49864 MW; 6846C2AF963B3BF CRC64;

Query Match
Best Local Similarity 54.1%; Score 1175; DB 1; Length 458;
Matches 252; Conservative 48; Mismatches 104; Indels 62; Gaps 12;

QY 14 NGTEA---PGGARAT-----PYSLOVTLTVCLAGLLMLTVFGNVLIIVFT 60
   ||::| |||||: || | | : | |::| |||||::| |
Db 19 NGSDAGEWSSGGGANASGIDWGPDPGQYSAGAVAGLAAYGVFLIVTVGVNLVIIVALT 78
QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANVMGYWFGKAWCEIYLALDVLFTSS 120
   ||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79 SRALRAPQNLFLVSLASADILVATLVMPFSLANELMAYWFGVWCQVYLALDVLFTSS 138
QY 121 IVHLCAISLDRYWSITQALEYNLKRTPRRRIKAIITVWVISAIVSFPLISIEKKGGGG 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 139 IVHLCAISLDRYWSYVQAVEYNLKRTPRRVKATIVAAVWLISAVISFPPLVSFYRRPDGA- 197
QY 181 PQPAEPRCEINDQKWYVVISSCIGSFEAPCLIMILVYVRIYQIAKRRTRVPPSRGPDAVA 240
   ||::| ||::| ||::| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 198 ---AYPQGLNDETWTYILSSCIGSFEAPCLIMGLVARIYVAKLRTLTSEKRGF--A 251
QY 241 APPGGETRRPNGLGPERASGPGCAEAEPPLTQNLGAPGEPAAPAGPRDTDALDLESSSSD 300
   | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 252 GPDGASPTTENG LG- KAAGENGHCAPP-RTEV-----EP-----DESSAAE 290
QY 301 HAERPPGRRRPERGPRGKAKARASQVKPGDSLPRRPGATGIGTPAAGPEERVGAAKAS 360
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 291 RRRRGALRRGRRREGAEGDTGSADGPGPLAEQAGARTASRSP--GPGGRLSRASSRS 348
QY 361 -----RWGR-----QNRKRTFVLAVVIGVEVWCWPEPFEFTYTLTAV--GC 401
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 349 VEFELSRRRRARSSVCRKKAQAAREKRTFVLAVVMGVFVLCWPEFFFSYSLYGICREAC 408
QY 402 SVPRTLKFEFFWEGYCNSSLNPVIYTTIENHDFRAAFKKILCRGDRK 447
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 409 QLPEPLKFEFFWIGYCNSLNPIYTVFNQDFRRSFKHILERRRR 454

RESULT 11
A2AB_CAVPO STANDARD; PRT; 448 AA.
ID A2AB_CAVPO STANDARD; PRT; 448 AA.
AC Q60475;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
GN ADRA2B.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavilidae; Cavia.
OC NCBI_TaxID=10141;
OX [1]
RN RP SEQUENCE FROM N.A.
RP STRAIN=Hartley;
RX MEDLINE=96152573; PubMed=8573196;
RA Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.;
RT "Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,
RT and alpha 2C adrenoceptor subtypes. Radioligand binding and
RT functional coupling to a CAMP-responsive reporter gene.";
RL Biochem. Pharmacol. 51:291-300(1996).
CC -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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[illegible]

DR EMBL; U07743; AAA17386.1; -.
DR HSSP; P29274; 1MMH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 33 57 1 (POTENTIAL).
FT DOMAIN 58 69 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 70 95 2 (POTENTIAL).
FT DOMAIN 96 105 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 106 128 3 (POTENTIAL).
FT DOMAIN 129 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 172 4 (POTENTIAL).
FT DOMAIN 173 188 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 189 212 5 (POTENTIAL).
FT DOMAIN 213 356 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 357 380 6 (POTENTIAL).
FT DOMAIN 381 393 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 394 413 7 (POTENTIAL).
FT DOMAIN 414 432 CYTOPLASMIC (POTENTIAL).
FT DISULFID 105 183 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 432 AA; 48563 MW; 0A42FAF9849FA8BA CRC64;

Query Match 47.5%; Score 1130.5; DB 1; Length 432;
Best Local Similarity 54.3%; Pred. No. 9.8e-46;
Matches 242; Conservative 48; Mismatches 115; Indels 41; Gaps 11;

QY 10 NASWNGTEAPGGARATPYSLQVTLTVCLAGLLMLTFEGNVLTIAVFTSRALKAPQN 69
DB 18 NASWS---ADSG-----YSLAIAISIALVSLFLFTVGNILVIATVLSRALKAPQN 68
QY 70 LFLVSLASADILVATLVIPFSLANEMGWTFGKAWCEIYALDYLCTSSIVHLCALSL 129
DB 69 LFLVSLATADILVATLVMPFSLANELMGWTFGKWCIGIYALDYLCTSSIVHLCALSL 128
QY 130 DRYWSITQAIENYKRTPRRIKAIITVWISAVISFPPLISIEKKGGGGGPQPAEPCE 189
DB 129 DRYWSVTQAVEYNIKRTPKRVKCIIVYWLISAFISSPPLSID----SNYISSQPQCM 184
QY 190 INDQKWYVISSICGSEFAPCLIMILVYRIYQIAKRTRVPPSRGPDVAAPPGCTERR 249
DB 185 LNDDTWYILSSMASFEAPCLIMILVYIRIYQVAKTRTR--SMGKE--PRPDGVYQT 238
QY 250 PNGLGPERGAGGAE----AEPLPTQINGAPGEPAPAGPRDTALDLESSSSDHAER 304
DB 239 ENGLNKANSPCHGDRENGHCQCPPTPSQRTVTIGQ-----QTDADMDSEFSSEKGH 291
QY 305 PPGRRPERGPRGKARASQVKPGDSLPRKPGATGIGTPAAGPGEERVGAAKASRWRG 364
DB 292 KPORODSQRAKR-PGLKSSISKOSARISRYSNKSVDLFASRRKRRSSIAEKKVS---- 346
QY 365 RQNRKRTFVLAVVIGVFVVCWPEFFFTYTLTAV--GCSVPRTLLEKFFFWFGYCNSL 421
DB 347 -QAREKRTFVLAVVGVVVCWPEFFFTSYSLHAVCRDYCKIPDTLEK-FFWIGYCNSL 404
QY 422 NPVIYTIENHDFRAFKKILCRGDRK 447
DB 405 NPAITYTIENRDFRAFKKILCKSWKK 430

RESULT 14
A2AB_HUMAN
ID A2AB_HUMAN STANDARD; PRT; 450 AA.
AC P18089;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Subtype C2).

GN ADRA2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90311349; Pubmed=2164221;
RA Lomasney J.W., Lorenz W., Allen L.F., King K., Regan J.W.,
RA Yang-Feng T.L., Caron M.G., Lefkowitz R.J.;
RT "Expansion of the alpha 2-adrenergic receptor family: cloning and
RT characterization of a human alpha 2-adrenergic receptor subtype, the
RT gene for which is located on chromosome 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5094-5098(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91042469; Pubmed=2172775;
RA Weinschenk R.L., Zgombick J.M., Macchi M., Adham N., Lichtblau H.,
RA Branchek T.A., Hartig P.R.;
RT "Cloning, expression, and pharmacological characterization of a human
RT alpha 2B-adrenergic receptor.";
RL Mol. Pharmacol. 38:681-688(1990).
RN [3]
RP SEQUENCE FROM N.A.
RA Cayla C., Schaak S., Bouloumie A., Deyedjian J.C., Paris H.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 95-389 FROM N.A.
RX MEDLINE=91054503; Pubmed=2173582;
RA Chang A.C., Ho T.F., Chang N.-C.A.;
RT "In vitro amplification by polymerase chain reaction of a partial
RT gene encoding the third subtype of alpha-2 adrenergic receptor in
RT humans.";
RL Biochem. Biophys. Res. Commun. 172:817-823(1990).
CC -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS. THE RANK ORDER OF POTENCY FOR AGONISTS OF THIS RECEPTOR
CC IS CLONIDINE > NOREPINEPHRINE > EPINEPHRINE = OXYMETAOLINE >
CC DOPAMINE > P-TYRAMINE = PHENYLEPHRINE > SEROTONIN > P-SYNEPHRINE /
CC P-OCTOPAMINE. FOR ANTAGONISTS, THE RANK ORDER IS YOHIMBINE >
CC CHLORPROMAZINE > PENTOLAMINE > MIANSERINE > SPIPERONE > PRAZOSIN
CC > ALPRENOLOL > PROPRANOLOL > PINDOLOL.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; M34041; AAA51666.1; -.
DR EMBL; M38742; AAA62823.1; -.
DR EMBL; AF005900; AAB62558.1; -.
DR PIR; A36158; A36158.
DR PIR; A37223; A37223.
DR HSSP; P29274; 1MMH.
DR Genew; HGNC:282; ADRA2B.
DR MIM; 104260; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family;
KW phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 12 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 13 38 1 (POTENTIAL).
FT DOMAIN 39 49 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 50 75 2 (POTENTIAL).
FT DOMAIN 76 85 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	86	108	3 (POTENTIAL).
FT	DOMAIN	109	130	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	131	153	4 (POTENTIAL).
FT	DOMAIN	154	169	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	170	193	5 (POTENTIAL).
FT	DOMAIN	194	372	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	373	396	6 (POTENTIAL).
FT	DOMAIN	397	405	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	406	429	7 (POTENTIAL).
FT	DOMAIN	430	450	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	294	311	ASP/GLU-RICH (ACIDIC).
FT	DISULFID	85	164	BY SIMILARITY.
FT	LIPID	442	442	PALMITATE (POTENTIAL).
FT	SITE	92	92	IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
FT	SITE	176	176	IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT	SITE	180	180	IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT	CONFLICT	362	363	HV -> QL (IN REF. 3 AND 4).
SO	SEQUENCE	450 AA;	49948 MW;	A476817C8788E1FD CRC64;
Query Match				
Best Local Similarity		47.38;	Score 1125.5;	DB 1; Length 450;
Matches 243; Conservative		53.28;	Pred. No. 1.7e-45;	
		50;	Mismatches 105;	Indels 59; Gaps 14;

[illegible]

RESULT	15
A2AB_MOUSE	
ID	A2AB_MOUSE
AC	P30545;
DT	01-APR-1993 (Rel. 25, Created)
DT	01-APR-1993 (Rel. 25, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
GN	ADRA2B.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
OX	NCBI_TaxID=10090;
RN	[1]

RP SEQUENCE FROM N.A.
RC STRAIN-DBA/2; TISSUE=Liver;
RX MEDLINE-93129625; PubMed=1336396;
RA Chen W.-M., Chang A.C., Shie B.J., Chang Y.-H., Chang N.-C.A.;
RT "Molecular cloning and characterization of a mouse alpha 2C2
RT adrenoceptor subtype gene.";
RL Biochim. Biophys. Acta 1171:219-223(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-92378586; PubMed=1354956;
RA Chruscinski A.J., Link R.E., Daunt D.A., Barsh G.S., Kobilka B.K.;
RT "Cloning and expression of the mouse homolog of the human alpha 2-C2
RT adrenergic receptor.";
RL Biochem. Biophys. Res. Commun. 186:1280-1287(1992).
CC -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).

CC	-	-	-	-
DR	EMBL; M94583; AAA73895.1;	.	.	
DR	EMBL; L00979; AAA37131.1;	ALT_INIT.		
DR	PIR; JH0693; JH0693.			
DR	PIR; S28221; S28221.			
DR	HSSP; P29274; IMMH.			
DR	MGD; MGI:87935; Adra2b.			
DR	InterPro; IPR00276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCR RHODOPSN.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Multigene family;			
KW	Phosphorylation; Lipoprotein; Palmitate.			
FT	DOMAIN	1	17	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	18	42	1 (POTENTIAL).
FT	DOMAIN	43	54	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	55	80	2 (POTENTIAL).
FT	DOMAIN	81	90	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	91	113	3 (POTENTIAL).
FT	DOMAIN	114	135	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	136	158	4 (POTENTIAL).
FT	DOMAIN	159	174	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	175	198	5 (POTENTIAL).
FT	DOMAIN	199	377	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	378	401	6 (POTENTIAL).
FT	DOMAIN	402	410	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	411	434	7 (POTENTIAL).
FT	DOMAIN	435	455	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	90	169	BY SIMILARITY.
FT	LIPID	447	447	PALMITATE (POTENTIAL).
FT	DOMAIN	306	316	ASP/GLU-RICH (ACIDIC).
FT	SITE	97	97	IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
FT	SITE	181	181	IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT	SITE	185	185	IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT	CONFLICT	202	202	V -> L (IN REF. 1).
FT	CONFLICT	229	230	MISSING (IN REF. 2).
SO	SEQUENCE	455 AA;	50615 MW;	A3954AD76DE6263 CRC64;

Query Match	47.08;	Score 1119.5;	DB 1;	Length 455;
Best Local Similarity	53.08;	Pred. No. 3.3e-45;		
Matches 242;	Conservative 49;	Mismatches 107;	Indels 59;	Gaps 14;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 15, 2003, 14:14:47 ; Search time 13.5 Seconds
(without alignments)
1382.544 Million cell updates/sec

Title: US-09-636-259B-4
Perfect score: 2380
Sequence: 1 MGSLOPDAGNASWNGTEAPG.....HDFRRAFKKILCRGDRKRIV 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2375	99.8	450	1 A2AA_HUMAN	P08913 homo sapien
2	2221	93.3	450	1 A2AA_PIG	P18871 sus scrofa
3	2193	92.1	450	1 A2AA_MOUSE	Q01338 mus musculu
4	2182	91.7	450	1 A2AA_CAVPO	Q60474 cavia porce
5	2160	90.8	450	1 A2AA_RAT	P22909 rattus norv
6	2114	88.8	452	1 A2AA_BOVIN	Q28838 bos taurus
7	1182	49.7	462	1 A2AC_HUMAN	P18825 homo sapien
8	1173.5	49.3	448	1 A2AB_CAVPO	Q60475 cavia porce
9	1173	49.3	458	1 A2AC_MOUSE	Q01337 mus musculu
10	1173	49.3	458	1 A2AC_RAT	P22086 rattus norv
11	1171.5	49.2	455	1 A2AC_CAVPO	Q60476 cavia porce
12	1146	48.2	469	1 A2AC_DIDMA	P35405 didelphis m
13	1127.5	47.4	450	1 A2AB_HUMAN	P18089 homo sapien
14	1126.5	47.3	432	1 A2AR_LABOS	Q91081 labrus ossi
15	1121.5	47.1	455	1 A2AB_MOUSE	P30545 mus musculu
16	1100.5	46.2	453	1 A2AB_RAT	P19328 rattus norv
17	1018.5	42.8	436	1 A2AR_CARAU	P32251 carassius a
18	946	39.7	382	1 A2AB_DIDMA	Q77715 didelphis m
19	934	39.2	384	1 A2AB_ELEMA	Q19014 elephas max
20	931	39.1	386	1 A2AB_AMBHO	O18935 amblysomus
21	929	39.0	390	1 A2AB_DUGDU	O77713 dugong dugo
22	928	39.0	388	1 A2AB_ORYAF	O19032 oryctolopus
23	927	38.9	394	1 A2AB_RABIT	O77830 oryctolagus
24	925.5	38.9	389	1 A2AB_PROHA	O19054 procavia ca
25	921.5	38.7	387	1 A2AB_MACPR	O19025 macrosceiid
26	921	38.7	389	1 A2AB_HORSE	O77721 equus cabal
27	920	38.7	392	1 A2AB_BOVIN	O77700 bos taurus
28	916.5	38.5	391	1 A2AB_ERIEU	O19012 erinaceus e
29	896	37.6	384	1 A2AB_ECHTE	O77723 echinops te
30	893.5	37.5	397	1 A2AB_TALEU	O19091 talpa europ
31	693.5	29.1	484	1 OAR1_LOCM1	Q25321 locusta mig
32	692.5	29.1	484	1 OAR2_LOCM1	Q25322 locusta mig
33	681.5	28.6	379	1 GRE2_BALAM	Q93127 balanus amp

34	652	27.4	476	1 GRE1_BALAM	Q93126 balanus amp
35	649	27.3	601	1 OAR_DROME	P22270 drosophila
36	640.5	26.9	477	1 OAR_HELVI	Q25188 heliothis v
37	632.5	26.6	479	1 OAR_BOMMO	Q17232 bombyx mori
38	626.5	26.3	443	1 D2DR_CERAE	P52702 cercopithec
39	624	26.2	444	1 D2DR_BOVIN	P20288 bos taurus
40	624	26.2	463	1 D2DR_FUGRU	P53453 fugu rubrip
41	621.5	26.1	443	1 D2DR_HUMAN	P14416 homo sapien
42	613	25.8	444	1 D2DR_MOUSE	P13953 mus musculu
43	611	25.7	377	1 5H1D_CANFA	P1614 canis fami1
44	608.5	25.6	442	1 D2D1_XENLA	P24628 xenopus lae
45	605	25.4	376	1 5H1D_CAVPO	Q60484 cavia porce

ALIGNMENTS

RESULT 1					
A2AA_HUMAN					
ID	A2AA_HUMAN	STANDARD;	PRT;	450 AA.	
AC	P08913;				
DT	01-NOV-1988 (Rel. 09, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR subtype C10).				
DE	subtye C10).				
GN	ADRA2A OR ADRA2R OR ADRAR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN					
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89308571; PubMed=2568356;				
RA	Fraser C.M., Arakawa S., McCombie W.R., Venter J.C.;				
RT	"Cloning, sequence analysis, and permanent expression of a human				
RT	alpha 2-adrenergic receptor in Chinese hamster ovary cells. Evidence				
RT	for independent pathways of receptor coupling to adenylate cyclase				
RT	attenuation and activation.";				
RL	J. Biol. Chem. 264:11754-11761(1989).				
RN					
RP	[2]				
RC	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RX	TISSUE=Platelet;				
RX	MEDLINE=88042789; PubMed=2823383;				
RA	Kobilka B.K., Matsui H., Kobilka T.S., Yang-Feng T.L., Francke U.,				
RA	Caron M.G., Lefkowitz R.J., Regan J.W.;				
RT	"Cloning, sequencing, and expression of the gene coding for the human				
RT	platelet alpha 2-adrenergic receptor.";				
RL	Science 238:650-656(1987).				
RN					
RP	[3]				
RX	REVISIONS TO 333-365.				
RX	MEDLINE=91009167; PubMed=2170371;				
RA	Guyer C.A., Horstman D.A., Wilson A.L., Clark J.D., Kragoe E.J. Jr.,				
RA	Limbird L.E.;				
RT	"Cloning, sequencing, and expression of the gene encoding the porcine				
RT	alpha 2-adrenergic receptor. Allosteric modulation by Na ⁺ , H ⁺ , and				
RT	amiloride analogs.";				
RL	J. Biol. Chem. 265:17307-17317(1990).				
RN					
RP	[4]				
RP	MUTAGENESIS OF PHE-412.				
RX	MEDLINE=91332079; PubMed=1678390;				
RA	Suryanarayana S., Daunt D.A., von Zastrow M., Kobilka B.K.;				
RT	"A point mutation in the seventh hydrophobic domain of the alpha 2				
RT	adrenergic receptor increases its affinity for a family of beta				
RT	receptor antagonists.";				
RL	J. Biol. Chem. 266:15488-15492(1991).				
RN					
RP	[5]				
RP	MUTAGENESIS OF ASPARTIC ACID AND SERINE RESIDUES.				
RX	MEDLINE=91342598; PubMed=1678850;				
RA	Wang C.-D., Buck M.A., Fraser C.M.;				
RT	"Site-directed mutagenesis of alpha 2a-adrenergic receptors:				
RT	Identification of amino acids involved in ligand binding and receptor				
RT	activation by agonists.";				

RL Mol. Pharmacol. 40:168-179(1991).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS. THE RANK ORDER OF POTENCY FOR AGONISTS OF THIS RECEPTOR
CC IS OXYMETAZOLINE > CLONIDINE > EPINEPHRINE > NOREPINEPHRINE >
CC PHENYLEPHRINE > DOPAMINE > P-SYNEPHRINE > P-TYRAMINE > SEROTONIN -
CC P-OCTOPAMINE. FOR ANTAGONISTS, THE RANK ORDER IS YOHIMBINE >
CC PHENTOLAMINE = MIANSERINE > CHLORPROMAZINE = SPIPERONE = PRAZOSIN
CC > PROPANOLOL > ALPRENOLOL = PINDOLOL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; M23533; AAA51665.1; -.
DR EMBL; M18415; AAA51664.1; -.
DR PIR; A34169; A34169.
DR PIR; A40132; A40132.
DR HSSP; P29274; 1MH.
DR Genew; HGNC:281; ADRA2A.
DR MIM; 104210; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECCEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECCEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33
FT TRANSMEM 34 59
FT DOMAIN 60 70
FT TRANSMEM 71 96
FT DOMAIN 97 106
FT TRANSMEM 107 129
FT DOMAIN 130 149
FT TRANSMEM 150 173
FT DOMAIN 174 192
FT TRANSMEM 193 217
FT DOMAIN 218 374
FT TRANSMEM 375 399
FT DOMAIN 400 406
FT TRANSMEM 407 430
FT DOMAIN 431 450
FT CARBOHYD 10 10
FT CARBOHYD 14 14
FT DISULFID 106 188
FT LIPID 442 442
FT SITE 113 113
FT SITE 200 200
FT SITE 204 204
FT MUTAGEN 79 79
FT MUTAGEN 113 113
FT MUTAGEN 130 130
FT MUTAGEN 200 200
FT MUTAGEN 204 204
FT MUTAGEN 412 412

FT FT ANTAGONIST YOHIMBINE, 3000X INCREASE FOR
FT FT BETA-ANTAGONIST ALPRENOLOL.
FT CONFLICT 104 104 A -> T (IN REF. 2).
FT CONFLICT 157 157 V -> C (IN REF. 2).
FT CONFLICT 333 365 PRGPGATGIGTPAAGGEERVGAAKASRWGR ->
FT RGAGRGRRGSGRRRLQGRGSASGLPRRRAGAGG
FT (IN REF. 1 AND 2).
FT CONFLICT 368 368 R -> L (IN REF. 2).
SQ SEQUENCE 450 AA; 48956 MW; A703CF262F04E8AC CRC64;

Query Match 99.8%; Score 2375; DB 1; Length 450;
Best Local Similarity 99.8%; Pred. No. 5.7e-103;
Matches 449; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSIQPDAGNASWNGTEAPGGGARATPYSLOVTLTLVCLAGLMLLTVPFGVLIIVFT 60
Db 1 MGSIQPDAGNASWNGTEAPGGGARATPYSLOVTLTLVCLAGLMLLTVPFGVLIIVFT 60

QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVGYWFGKAWCEIYALDVLCTSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVGYWFGKAWCEIYALDVLCTSS 120

QY 121 IVHLCAISLDYWSITQAIENLKRTPRIKAITTWVISAVISPPPLISIEKKGGGG 180
Db 121 IVHLCAISLDYWSITQAIENLKRTPRIKAITTWVISAVISPPPLISIEKKGGGG 180

QY 181 POBAEPRCEINDQKWYVSSICGSFAPCLIMLVYVRIOAKRRTRVPPSRGPDAYA 240
Db 181 POBAEPRCEINDQKWYVSSICGSFAPCLIMLVYVRIOAKRRTRVPPSRGPDAYA 240

QY 241 APPGTERRPKGLGPERSGPGGAEAELPTQLNGAPGEPAPAGPRDPAJDLESSSSD 300
Db 241 APPGTERRPNGLGPERSGPGGAEAELPTQLNGAPGEPAPAGPRDPAJDLESSSSD 300

QY 301 HAERPPGPRRPERGPRGCKARASQVKGDSLPRRGPGATGIGTPAAGGEERVGAAKAS 360
Db 301 HAERPPGPRRPERGPRGCKARASQVKGDSLPRRGPGATGIGTPAAGGEERVGAAKAS 360

QY 361 RWRGRQNRKRFTEFLAVVIGVFWCWFPEFFFTYTLTAVGCSVPRTLKFEFFWGYCNS 420
Db 361 RWRGRQNRKRFTEFLAVVIGVFWCWFPEFFFTYTLTAVGCSVPRTLKFEFFWGYCNS 420

QY 421 LNPVIYTFNHFRRAFKKILCRGDRKRIV 450
Db 421 LNPVIYTFNHFRRAFKKILCRGDRKRIV 450

RESULT 2
A2AA_PIG STANDARD; PRT; 450 AA.
ID A2AA_PIG
AC P18871;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
GN ADRA2A OR A2AR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 212-232.
RC TISSUE=Liver;
RX MEDLINE=91009167; PubMed=2170371;
RA Guyer C.A., Horstman D.A., Wilson A.L., Clark J.D., Kragoe E.J. Jr.,
RA Lambird L.E.;
RT "Cloning, sequencing, and expression of the gene encoding the porcine
RT alpha 2-adrenergic receptor. Allosteric modulation by Na+, H+, and
RL J. Biol. Chem. 265:17307-17317(1990).
RN [2]
RP MUTAGENESIS OF CYS-442.
RX MEDLINE=93216775; PubMed=8385131;

RA Kennedy M.E., Limbird L.E.;
RT "Mutations of the alpha 2A-adrenergic receptor that eliminate
RT detectable palmitoylation do not perturb receptor-G-protein
RT coupling.";
RL J. Biol. Chem. 268:8003-8011(1993).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: ALPHA2-ADRENERGIC RECEPTOR SHOWS AN ALLOSTERIC
CC MODULATION BY NA+, H+, AND AMILORIDE ANALOGS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL: J05652; AAA30984.1; -.
DR PIR: A38316; A38316.
DR HSSP: P29274; 1MMH.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33
FT TRANSMEM 34 59
FT DOMAIN 60 70
FT TRANSMEM 71 96
FT DOMAIN 97 106
FT TRANSMEM 107 129
FT DOMAIN 130 149
FT TRANSMEM 150 173
FT DOMAIN 174 192
FT TRANSMEM 193 217
FT DOMAIN 218 374
FT TRANSMEM 375 399
FT DOMAIN 400 409
FT TRANSMEM 410 430
FT DOMAIN 431 450
FT CARBOHYD 10 10
FT CARBOHYD 14 14
FT DISULFID 106 188
FT LIPID 442 442
FT SITE 113 113
FT SITE 200 200
FT SITE 204 204
FT MUTAGEN 442 442
SQ SEQUENCE 450 AA; 48975 MM; 79D7D5847372074E CRC64;

Query Match 93.3%; Score 2221; DB 1; Length 450;
Best Local Similarity 93.8%; Pred. No. 6.7e-96;
Matches 422; Conservative 3; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGSLOPDAGNASWNGTEAPGGGARATPYSLQVTLTLVCLAGLMLTFEGNVLIIVFT 60
Db 1 MGSLOPEAGNASWNGTEAPGGGARATPYSLQVTLTLVCLAGLMLTFEGNVLIIVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVWGWFYFGKAWCEIYALDVLCTSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVWGWFYFGKAWCEIYALDVLCTSS 120
QY 121 IVHLCAISLDRWYSTQAIIEYNLKRTPRIKAIITVWVISAVISFPLISIEKKGGGG 180
Db 121 IVHLCAISLDRWYSTQAIIEYNLKRTPRIKAIITVWVISAVISFPLISIEKKGGGG 180

Db 121 IVHLCAISLDRWYSTQAIIEYNLKRTPRIKAIITVWVISAVISFPLISIEKKAGCGG 180
QY 181 POPAEPRCEINDQKWYVISSCIGSFAPCLIMILVYVRIYQIAKRRTRVPPSRRGPDAAV 240
Db 181 QOPAEPRCEINDQKWYVISSCIGSFAPCLIMILVYVRIYQIAKRRTRVPPSRRGPDAAV 240
QY 241 APPGTERRRPGLGPERSAGPGCAEAPLPTQLNGAPGEPAPAGPRDTALDLESSSSD 300
Db 241 ALPGAERRRPGLGPERGVGVAEAPLPVQLNGAPGEPAPAGPRDADGLDESSSSSE 300
QY 301 HAERPPGRRRPERGPRGKGAKARASQYKPGDSLPRRPGAPGAPATGAGEERGVAKAS 360
Db 301 HAERPPGRRRPERGPRGKGAKARASQYKPGDSLPRRPGAPGAPATGAGEERGVAKAS 360
QY 361 RWRGRQNRERKFTFLAVVIGVFVVCWPFFFTYTLTAVGCVPRTLKFFFWGYCNS 420
Db 361 RWRGRQNRERKFTFLAVVIGVFVVCWPFFFTYTLTAVGCVPRTLKFFFWGYCNS 420
QY 421 LNPVIYTFNHDFRRAFKKILCRGDKRIV 450
Db 421 LNPVIYTFNHDFRRAFKKILCRGDKRIV 450

RESULT 3
A2AA_MOUSE STANDARD; PRT; 450 AA.
ID A2AA_MOUSE
AC Q01338;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
GN ADRA2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92342131; Pubmed-1353249;
RA link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Kobilka B.K.;
RA "Cloning of two mouse genes encoding alpha 2-adrenergic receptor
RT subtypes and identification of a single amino acid in the mouse alpha
RT 2-C10 homolog responsible for an interspecies variation in
RT antagonist binding.";
RL Mol. Pharmacol. 42:16-27(1992).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M99377; AAA37213.1; -.
DR HSSP: P29274; 1MMH.
DR MGD: MGI:87934; Adra2a.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33
FT TRANSMEM 34 59
FT DOMAIN 60 70
FT TRANSMEM 71 96


```
FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 173 4 (POTENTIAL).
FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 374 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 375 399 6 (POTENTIAL).
FT DOMAIN 400 430 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 410 430 7 (POTENTIAL).
FT DOMAIN 431 450 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 188 BY SIMILARITY.
FT LIPID 442 442 PALMITATE (BY SIMILARITY).
FT SITE 113 113 IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
FT SITE 200 200 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT SITE 204 204 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
SQ SEQUENCE 450 AA; 48865 MW; F07E225393AFA93B CRC64;
```

Query Match 92.1%; Score 2193; DB 1; Length 450;
Best Local Similarity 92.0%; Pred. No. 1.3e-94;
Matches 414; Conservative 8; Mismatches 28; Indels 0; Gaps 0;

```
QY 1 MGSLOPDAGNASWNGTEAPGGARATPSLOYTLTLVCLAGLMLLTVEGNVLIIVFT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGSLOPDAGNSSWNGTEAPGGGTRATPSLOYTLTLVCLAGLMLLTVEGNVLIIVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVPFSLANEVMGYWYFGKAWCEIYLALDVLCTSS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SRALKAPQNLFLVSLASADILVATLVPFSLANEVMGYWYFGKAWCEIYLALDVLCTSS 120
QY 121 IVHLCAISLDRYWSITQAI EYNLKRTPRIRKAIITTWVISAVISFPPLISIEKKGGGG 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 IVHLCAISLDRYWSITQAI EYNLKRTPRIRKAIITTWVISAVISFPPLISIEKKGGGG 180
QY 181 PQPAEPRCEINDQWYVISSCIGSEFPAPCLIMLVYVRIYQIAKRTRVPPSRRGPDAVA 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 QQPAEPRCKINDQWYVISSSIGSEFPAPCLIMLVYVRIYQIAKRTRVPPSRRGPDACS 240
QY 241 APPGGETERRPKGIGPERSAGPGGAEPPLPTQNLGAPGEPAPAGPRDLDLLESSSSSD 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 APPGADRRPNGIGBERGAGPTGAEAEPPLPTQNLGAPGEPAPAGPRDLDLLESSSSSE 300
QY 301 HAERPPGRRPERGPRGKAKARASQVKGDSLPRRPGATGIGTPAAGPGEERVGAAKAS 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 HAERPPGRRPRDGRGAKKTRASQVKGDSLPRRPGAGAGPGASGSGHGEERGGAOKAS 360
QY 361 RWRGRQNRKREFTFVLAVVIGVFVVCWPEFFFTYTLTAVGCSVPRTLKFFFWFGYCNS 420
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 RWRGRQNRKREFTFVLAVVIGVFVVCWPEFFFTYTLTAVGCPVPQLENFFFWFGYCNS 420
QY 421 LNPVIYTIENHDFRRAFKKILCRGDKRKRIY 450
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 421 LNPVIYTIENHDFRRAFKKILCRGDKRKRIY 450
```

RESULT 4
A2AA_CAVPO STANDARD; PRT; 450 AA.
ID A2AA_CAVPO
AC 060474;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
GN Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriicognathi; Cavidae; Cavia.
OX NCBI_Taxid=10141;

```
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley;
RA MEDLINE=96152573; PubMed=8573196;
RX Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.;
RT "Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,
RT and alpha 2C adrenoceptor subtypes. Radioligand binding and
RT functional coupling to a CAMP-responsive reporter gene.";
RL Biochem. Pharmacol. 51:291-300(1996).
CC -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U25722; AAA67074.1; -.
CC HSSP; P29274; 1MMH.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCR_RHODOPSN.
CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family; Phosphorylation; Lipoprotein; Palmitate.
KW DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 59 1 (POTENTIAL).
FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 96 2 (POTENTIAL).
FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 173 4 (POTENTIAL).
FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 217 5 (POTENTIAL).
FT DOMAIN 218 374 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 375 399 6 (POTENTIAL).
FT DOMAIN 400 430 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 410 430 7 (POTENTIAL).
FT DOMAIN 431 450 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 187 BY SIMILARITY.
FT LIPID 442 442 PALMITATE (BY SIMILARITY).
FT SITE 113 113 IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
FT SITE 199 199 IMPLICATED IN AGONIST BINDING AND RECEPTOR ACTIVATION (BY SIMILARITY).
FT SITE 203 203 IMPLICATED IN AGONIST BINDING RECEPTOR ACTIVATION (BY SIMILARITY).
SQ SEQUENCE 450 AA; 48910 MW; E6BBE9A7FFB8DD1 CRC64;
```

Query Match 91.7%; Score 2182; DB 1; Length 450;
Best Local Similarity 92.2%; Pred. No. 4.1e-94;
Matches 416; Conservative 8; Mismatches 25; Indels 2; Gaps 2;

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QY 1 MGSLOPDAGNASWNGTEAPGGARATPSLOYTLTLVCLAGLMLLTVEGNVLIIVFT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGSLOPDAGNASWNGTEGCGGTRATPSLOYTLTLVCLVGLLTLTVEGNVLIIVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVPFSLANEVMGYWYFGKAWCEIYLALDVLCTSS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SRALKAPQNLFLVSLASADILVATLVPFSLANEVMGYWYFGKAWCEIYLALDVLCTSS 120
QY 121 IVHLCAISLDRYWSITQAI EYNLKRTPRIRKAIITTWVISAVISFPPLISIEKKGGGG 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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```
Db 121 IVHLCAISLDRYWSITQAIENYLNKRTPRRIKAIIVTWVVISAVISFPPLISFE-KAGGGG 179
QY 181 PGPAPERCEINDQKWYVSSICGSFFAPCLIMILVYVRIYQIAKRRTRVPPSRGPD-A-V 239
Db 180 QGPAPERCEINDQKWYVSSISGSFFAPCLIMILVYVRIYQIAKRRTRVPPSRGPD-AHA 239
QY 240 AAPPGCTERRPKGLGPERSGAPGAEAEPLPTQLNGAGGEPAPAGPRDTDALDLESSSS 299
Db 240 AAPPGGAERRPNGLGLERGVPGGAEAEPLPTQVNGAGGEPAPAGPRDAEALDLESSSS 299
QY 300 DHAERPPGRRPERGPRGKGAKARASQVKGPSDLPKRGPGATGICTPAAGPGGEERVGAKA 359
Db 300 EHAERPPGARRRPERGLRAKSKARASQVKGPSDLPKRAFGAAGSGTSGSGPGEERGGAKA 359
QY 360 SRWGRONREKRTFTVLAVVIGVFWCPEFFTYTLTAVGCSVPRTLKFEFFWEGYCNS 419
Db 360 SRWGRONREKRTFTVLAVVIGVFWCPEFFTYTLTAVGCSVPRTLKFEFFWEGYCNS 419
QY 420 SLNPVIYTIENHDFRRAFKKILCRGDRKRIY 450
Db 420 SLNPVIYTIENHDFRRAFKKILCRGDRKRIY 450

RESULT 5
A2AA_RAT
ID A2AA_RAT STANDARD: PRT: 450 AA.
AC P22909;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR)
DE (CA2-47) (Alpha-2D adrenergic receptor).
GN ADRA2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91244823; PubMed-1645350;
RA Lanier S.M., Downing S., Duzic E., Homcy C.J.;
RT "Isolation of rat genomic clones encoding subtypes of the alpha 2-
RT adrenergic receptor. Identification of a unique receptor subtype.";
RL J. Biol. Chem. 266:10470-10478(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-91125329; PubMed-2177834;
RA Chaberg S.C., Duda T., Rhine J.A., Sharma R.K.;
RT "Molecular cloning, sequencing and expression of an alpha 2-adrenergic
RT receptor complementary DNA from rat brain.";
RL Mol. Cell. Biochem. 97:161-172(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-95349560; PubMed-7623790;
RA Wypijewski K., Duda T., Sharma R.K.;
RT "Structural, genetic and pharmacological identity of the rat alpha
RT 2-adrenergic receptor subtype ca2-47 and its molecular
RT characterization in rat adrenal, adrenocortical carcinoma and bovine
RT retina.";
RL Mol. Cell. Biochem. 144:181-190(1995).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; M62372; AAA42034.1; -.
DR EMBL; U79031; AAC24959.1; -.
DR PIR; B40392; B40392.
DR PIR; JH0190; JH0190.
DR HSSP; P29274; 1MMH.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 33
FT TRANSMEM 34 59
FT DOMAIN 60 70
FT TRANSMEM 71 96
FT DOMAIN 97 106
FT TRANSMEM 107 129
FT DOMAIN 130 149
FT TRANSMEM 150 173
FT DOMAIN 174 192
FT TRANSMEM 193 217
FT DOMAIN 218 374
FT TRANSMEM 375 399
FT DOMAIN 400 409
FT TRANSMEM 410 430
FT DOMAIN 431 450
FT CARBOHYD 10 10
FT CARBOHYD 14 14
FT DISULFID 106 188
FT LIPID 442 442
FT SITE 113 113
FT SITE 200 200
FT SITE 204 204
FT CONFLICT 147 147
FT CONFLICT 154 158
FT CONFLICT 252 253
FT CONFLICT 264 264
FT CONFLICT 304 305
FT CONFLICT 333 333
FT CONFLICT 445 445
SQ SEQUENCE 450 AA; 48939 MW; AFA078DCA3D612AC CRC64;

Query Match 90.8%; Score 2160; DB 1; Length 450;
Best Local Similarity 90.7%; Pred. No. 4.2e-93;
Matches 408; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

QY 1 MGSLOPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLLTVEGNVLIIVFT 60
Db 1 MGSLOPDAGNSSWNGTEAPGGGTRATPYSLQVTLTVCLAGLMLLTVEGNVLIIVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFGKAWCEIYIALDVLCTSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFGKAWCEIYIALDVLCTSS 120
QY 121 IVHLCAISLDRYWSITQAIENYLNKRTPRRIKAIITVWVVISAVISFPPLISIEKKGGGG 180
Db 121 IVHLCAISLDRYWSITQAIENYLNKRTPRRIKAIITVWVVISAVISFPPLISIEKKGAGG 180
QY 181 PGPAPERCEINDQKWYVSSICGSFFAPCLIMILVYVRIYQIAKRRTRVPPSRGPD-AVA 240
Db 181 QGPAPERCKINDQKWYVSSISGSFFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDACS 240
QY 241 APPGCTERRPKGLGPERSGAPGAEAEPLPTQLNGAGGEPAPAGPRDTDALDLESSSSD 300
Db 241 APPGADRRPNGLGPERGAGTAGAEAEPLPTQLNGAGGEPAPTRPRGDALDLESSSSSE 300
QY 301 HAERPPGARRRPERGPRGKGAKARASQVKGPSDLPKRGPGATGICTPAAGPGEERVGAKAS 360
Db 301 HAERPPGARRRPERGPRGKGAKARASQVKGPSDLPKRGPGATGICTPAAGPGEERVGAKAS 360
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Db 301 HAERPQGPCKPERGPRAKGTKASQVKKPGDSLPRRPGGAAGPGASGSGGGEERRAGGAKAS 360

QY 361 RWRGRQNRKRFTEFLAVVIGVEVVCWPFPEFFTYTLTAVGCSVPRTLFRKFFEWGYCNSS 420

Db 361 RWRGRQNRKRFTEFLAVVIGVEVVCWPFPEFFTYTLTAVGCPVPYQLFNFEEFWGYCNSS 420

QY 421 LNPVIYTIENHDFRRAFKKILCRGDKRKIV 450

Db 421 LNPVIYTIENHDFRRAFKKILCRGDKRKIV 450

RESULT 6

A2AA_BOVIN

ID A2AA_BOVIN STANDARD; PRT; 452 AA.

AC Q28838;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR)

DE (Alpha-2D adrenergic receptor).

GN ADRA2A.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98111113; PubMed=9450652;

RA Venkataraman V., Duda T., Sharma R.K.;

RT "The bovine alpha 2D-adrenergic receptor gene: structure, expression in retina, and pharmacological characterization of the encoded receptor.";

RL Mol. Cell. Biochem. 177:113-123(1997).

RN [2]

RP SEQUENCE OF 171-210 FROM N.A.

RX MEDLINE=94018366; PubMed=8412494;

RA Blaxall H.S., Heck D.A., Bylund D.B.;

RT "Molecular determinants of the alpha-2D adrenergic receptor subtype.";

RL Life Sci. 53:9-9(1993).

CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: RETINA, BRAIN AND OLFACTORY LOBE.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

CC EMBL; U79030; AAC24958.1; -.

DR EMBL; S66295; AAB28450.1; -.

DR HSSP; P29274; 1MMH.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation; Lipoprotein; Palmitate.

FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 34 59 1 (POTENTIAL).

FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 71 96 2 (POTENTIAL).

FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 107 129 3 (POTENTIAL).

FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 150 173 4 (POTENTIAL).

FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 193 217 5 (POTENTIAL).

FT DOMAIN 218 376 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 377 401 6 (POTENTIAL).

FT DOMAIN 402 411 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 412 432 7 (POTENTIAL).

FT DOMAIN 433 452 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 106 188 BY SIMILARITY.

FT LIPID 444 444 PALMITATE (BY SIMILARITY).

SQ SEQUENCE 452 AA; 49252 MW; F10C1DD2860CD6F9 CRC64;

Query Match 88.8%; Score 2114; DB 1; Length 452;

Best Local Similarity 90.7%; Pred. No. 5.4e-91;

Matches 411; Conservative 4; Mismatches 34; Indels 4; Gaps 4;

QY 1 MGSLOPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLLTVEGNVLIATVFT 60

Db 1 MGSLOPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLLTVEGNVLIATVFT 60

QY 61 SRALKAPQNLFLVSLASADILVATLVIPESLANEVMGYWFGKAWCEIYLALDVLCTSS 120

Db 61 SRALKAPQNLFLVSLASADILVATLVIPESLANEVMGYWFGKAWCEIYLALDVLCTSS 120

QY 121 IVHLCAISLDRYWSITQAIEXYMLKTRPRIKAIITVWVISAVISFPPLISIEKKGGGG 180

Db 121 IVHLCAISLDRYWSITQAIEXYMLKTRPRIKAIITVWVISAVISFPPLISIEKKGRSG 180

QY 181 PQAPRCEINDQKWYVISSCIGSFFAPCLIMILVYVRIQIAKRRTRVPPSRGPDAYA 240

Db 181 QPSAEPCEINDQKWYVISSSISGFFAPCLIMILVYVRIQIAKRRTRVPPSRGPDATA 240

QY 241 AP-PGCTERRPKGLGPER-SAGPGGAEAEPPLTQNLGAPGEPAPAGPRDTDALDLEESS 298

Db 241 AELPGSAERRPNGLGPERGAVPGVAEVESLQVLNGAPGEPAPAG-AGADALDLEESS 299

QY 299 SDHAERPGRPRPERGPRGKGARASQVKPGDSLPRRPGATGIGTPAAGPGEERY-GAA 357

Db 300 SEHAERPGRSRSESGPRAKGARASQVKPGDSLPRRPGATGLGAPTAGPAEERSGGA 359

QY 358 KASRWGRQNRKRFTEFLAVVIGVEVVCWPFPEFFTYTLTAVGCSVPRTLFRKFFEWFGYC 417

Db 360 KASRWGRQNRKRFTEFLAVVIGVEVVCWPFPEFFTYTLTAVGCPVPYQLFNFEEFWFGYC 419

QY 418 NSSLNPVIYTIENHDFRRAFKKILCRGDKRKIV 450

Db 420 NSSLNPVIYTIENHDFRRAFKKILCRGDKRKIV 452

RESULT 7

A2AC_HUMAN

ID A2AC_HUMAN STANDARD; PRT; 462 AA.

AC P18825; P35369; Q9HB49;

DT 01-NOV-1990 (Rel. 16, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Alpha-2C-adrenergic receptor (Alpha-2C adrenoceptor) (Subtype C4).

GN ADRA2C.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Kidney;

RX MEDLINE=88320430; PubMed=2842764;

RA Regan J.W., Kobilka T.S., Yang-Feng T.L., Caron M.G., Lefkowitz R.J., Kobilka B.K.;

RT "Cloning and expression of a human kidney cDNA for an alpha 2-adrenergic receptor subtype.";

RL Proc. Natl. Acad. Sci. U.S.A. 85:6301-6305(1988).

RN [2]

```

RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=98041882; PubMed=9371698;
RA Schaak S., Devedjian J.C., Cayla C., Sender Y., Paris H.;
RT "Molecular cloning, sequencing and functional study of the promoter
RL region of the human alpha2C4-adrenergic receptor gene.";
RN Biochem. J. 328:431-438(1997).
[3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Yano K., Takeda M., Sugimoto E., Sagai H.;
RT "Molecular cloning and expression of a novel human alpha2C-adrenergic
RL receptor, alpha2CII, gene.";
RN Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT 322-GLY--PRO-325 DEL.
RX MEDLINE=20390061; PubMed=10801795;
RA Small K.M., Forbes S.L., Rahman F.F., Bridges K.M., Liggett S.B.;
RT "A four amino acid deletion polymorphism in the third intracellular
RL loop of the human alpha 2C-adrenergic receptor confers impaired
RT coupling to multiple effectors.";
RN J. Biol. Chem. 275:23059-23064(2000).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- POLYMORPHISM: The Del322-325 variant has a significant loss of
CC function. It is approximately 10 times more frequent in African-
CC Americans compared with Caucasians (allele frequencies 0.381
CC versus 0.040).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, J03853; AAA35513.1; -.
DR EMBL, U72648; AAC78723.1; -.
DR EMBL, D13538; BAA02737.1; -.
DR EMBL, AF280399; AAG28076.1; -.
DR EMBL, AF280400; AAG28077.1; -.
DR PIR, A31237; A31237.
DR HSSP, P29274; 1MMH.
DR GeneW, HGNC:283; ADRA2C.
DR MIM, 104250; -.
DR InterPro, IPR000276; GPCR_Rhodpsn.
DR Pfam, PF00001; 7tm_1; 1.
DR PRINTS, PR00237; GPCRHHODPSN.
DR PROSITE, PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE, PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Polymorphism; Alternative splicing.
FT DOMAIN 1 51
FT TRANSMEM 52 76 1 (POTENTIAL).
FT DOMAIN 77 88 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 89 114 2 (POTENTIAL).
FT DOMAIN 115 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 147 3 (POTENTIAL).
FT DOMAIN 148 168 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 169 191 4 (POTENTIAL).
FT DOMAIN 192 207 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 208 231 5 (POTENTIAL).
FT DOMAIN 232 379 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 380 407 6 (POTENTIAL).
FT DOMAIN 408 420 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 421 441 7 (POTENTIAL).
FT DOMAIN 442 462 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 294 308 ARG-RICH (BASIC).

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FT	CARBOHYD	19	19	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	33	33	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	124	202	BY SIMILARITY.
FT	VARSPIC	270	300	AGENGHCAPPADVEPDESSAAERRRRRGA -> EARTG
FT	VARSPIC	270	300	ARRPPTWSRTTRAQDRPGGAGGP (IN ISOFORM 2).
FT	VARSPIC	270	300	MISSING.
FT	VARSPIC	270	300	FTID=VAR_012747.
FT	CONFLICT	239	239	L -> R (IN REF. 1 AND 2).
FT	CONFLICT	329	329	E -> Q (IN REF. 1 AND 2).
FT	CONFLICT	401	401	S -> I (IN REF. 1 AND 2).
FT	CONFLICT	446	446	R -> P (IN REF. 1 AND 2).
FT	SEQUENCE	462	49522	MM; EIEF9CA21E7F6EDA CRC64;
SO	SEQUENCE	462	49522	MM; EIEF9CA21E7F6EDA CRC64;
Query Match		49.7%;	Score 1182;	DB 1; Length 462;
Best Local Similarity		52.7%;	Pred. No. 3.2e-48;	
Matches 254;	Conservative	40;	Mismatches 102;	Indels 86; Gaps
OY	10	NASWNGTEAPGGGARAT-----PYSLOVTLTLVCLAGLMLLTVEGNLVITAVT	60	
Db	19	NASGAGERGGGVANASGASWGPPrGOYSAGAVAGLAAVGVFLIVTVGNVLVITAVLT	78	
OY	61	SRALKAPQNLFLVSLASADILVATLVIPESLANEVMGWYFGKAWCEIYALDVLCTSS	120	
Db	79	SRALRAPQNLFLVSLASADILVATLVMPSLANELMAYWYFGVWCVYALDVLCTSS	138	
OY	121	IVHLCAISLDRWNSITQAIENLKRPRRIKALITTWVISAVISFPPLISIEKGGGGC	180	
Db	139	IVHLCAISLDRWNSITQAVEYNLKRTPRRYKATIVAVWLISAVISFPPLVSLYRQPDGA-	197	
OY	181	PQPAEPRCEINDQKWYVISSCIGSEFAPCLIMILVYVRITQIAKRRTRVPPSRGRPDAYA	240	
Db	198	---AYPQCGLNDETWIILSSCIGSEFAPCLIMGLVYARIYRVAKLRTLTLEKRAP---V	251	
OY	241	APPGTERRPKGLGPEBSAGPGGAEEAPLPTQLNGAPGEPAPAGPRDLDLESSSD	300	
Db	252	GPDGASPTTENGIGAAAGANGHCA-----PPPA-----DVEPDESSA	290	
OY	301	HAERPPGPRRPERGPRGKGAKARASQVKPDLSLRPGATIGTPAAGPGEERVGAAKAS	360	
Db	291	AAE-----RRRRGALRRGRRRAGAEAG-----AGADGG--AGPGAESGALTAS	336	
OY	361	RWRG-----RQNRREKRTFVLAVVIGVFVVCWF	388	
Db	337	RSPGPGRLSRASSRSVEFELSRRRARRASSVCRRKVAQAREKRETFVLAVMVGVFVLCWF	396	
OY	389	PEFTTYTLTAV---GCSVPRTLKFEFFWEGCNSLNPIVYITIFNHFRRAFKKILRCGD	445	
Db	397	PEFFSYSLYGICREACOVPGPLKFFFWIGICNSSLNPIVYITVFNDPFRRSFKHILFRRR	456	
OY	446	RK 447		
Db	457	RR 458		
RESULT 8				
A2AB_CAVPO				
ID	A2AB_CAVPO	STANDARD;	PRT;	448 AA.
AC	Q60475;			
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, last sequence update)		
DT	16-OCT-2001	(Rel. 40, last annotation update)		
DN	Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).			
GE	ADRA2B.			
OS	Cavia porcellus (Guinea pig).			
OC	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavilidae; Cavia.			
OX	NCBI_TaxID=10141;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	STRAIN=Hartley;			
RA	MEDLINE=96152573; PubMed=8573196;			
RA	Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.;			
RT	"Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,			


```

RT and alpha 2C adrenoceptor subtypes. Radioligand binding and
RT functional coupling to a CAMP-responsive reporter gene.";
RL Biochem. Pharmacol. 51:291-300(1996).
CC -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U25723; AAA67075.1; -.
DR HSSP; P29274; 1MMH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 12 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 13 38 1 (POTENTIAL).
FT DOMAIN 39 49 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 50 75 2 (POTENTIAL).
FT DOMAIN 76 85 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 86 108 3 (POTENTIAL).
FT DOMAIN 109 130 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 131 153 4 (POTENTIAL).
FT DOMAIN 154 168 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 169 192 5 (POTENTIAL).
FT DOMAIN 193 370 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 371 394 6 (POTENTIAL).
FT DOMAIN 395 403 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 404 427 7 (POTENTIAL).
FT DOMAIN 428 448 CYTOPLASMIC (POTENTIAL).
FT DISULFID 85 163 BY SIMILARITY.
FT LIPID 440 440 PALMITATE (POTENTIAL).
FT DOMAIN 294 309 ASP/GLU-RICH (ACIDIC).
FT SITE 92 92 IMPLICATED IN LIGAND BINDING (BY
FT SIMILARITY).
FT SITE 175 175 IMPLICATED IN CATECHOL AGONIST BINDING
FT (BY SIMILARITY).
FT SITE 179 179 IMPLICATED IN CATECHOL AGONIST BINDING
FT (BY SIMILARITY).
SQ SEQUENCE 448 AA; 49597 MW; 8384F8757E404777 CRC64;
Query Match 49.3%; Score 1173.5; DB 1; Length 448;
Best Local Similarity 53.6%; Pred. No. 7.7e-48;
Matches 245; Conservative 47; Mismatches 104; Indels 61; Gaps 11;
QY 27 PYSLQVTLFLVCLAGLMLLTFEGNVLIIVFTSRALKAPQNLFLVSLASADILVATLV 86
Db 6 PYSVQATAIAAVITFLIFTIFGNALVILAVLTSRLPAPQNLFLVSLAADIIVATLI 65
QY 87 IPFSLANEVMGYWYFGAWCEIYALDVLFTCTSSIVHCAISLDYWSITQAIENMKRT 146
Db 66 IPFSLANELLGWYFWRTWCEVYALDVLFTCTSSIVHCAISLDYWAVSRALYNSKRT 125
QY 147 PRRIKAIITVWVWISAVISFPLISIEKKGGGGGQPAEPRCEINDOKWYVVISCTIGSEF 206
Db 126 PRRIKCIITLTVLWLAIVSLPLI---YKGDQGPSRGPQCKINQEAWYILASSIGSFF 181
QY 207 APCLIMILVYVRIYQIAKRRTRVPPSRGRPDAAVAPPGCTERRPKGLGPERSAAGGAA 266
Db 182 APCLIMILVYLRITLIAR-----SHRRGPRAKGGEGEGESKESR---PSPGGADASAKV 233
QY 267 EPLPTQLNG--APGEPAAGPRDTDALDLEESSSDHAERPPGPRRPERGPRGKAKARA 323

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Db      234 PPLASLSTGEANGHPKPTGEKE-----EGETSEDPGARTLPSPWAALPTSQGQKA 287
        || : || : || | | | : : | : | | | | | : | : | : |
QY      324 SQVKP-----GDSL-PRGPG-----ATGIGTPAAGPE 351
        : | : | : | : | : | : | : | : | : | : | : | : |
Db      288 VVLADAEHEEAEHEEEEGDECEPDQAAPGLPASMCSPSLOQPQSRVLA TLRGVLLGRG- 346
        || | | | | | | | | | | | | | | | | | | | | | |
QY      352 ERVGAAKASRWGR--QNREKRFTFLAVVIGVFVCWPFPEFTYTTLAV--GCSVPR 406
        || | | | | | | | | | | | | | | | | | | | | | |
Db      347 --VGAVDGGWMRRRTQTMTREKRFTFLAVVIGFVLCWFPEFTTYSLGAI CPQHCKVPHG 404
        || | | | | | | | | | | | | | | | | | | | | | |
QY      407 LFKRFWFGYCNSSLNPVIYTTTFNDFERRAFKKILCR 443
        || : || | | | | | | | | | | | | | | | | | | | |
Db      405 LFQFFFWIGYCNSSLNPVIYTTTFNDFERRAFRIICR 441

RESULT 9
A2AC_MOUSE STANDARD; PRT; 458 AA.
ID A2AC_MOUSE AC Q01337;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Alpha-2C adrenergic receptor (Alpha-2C adrenoceptor) (Subtype C4).
SN ADRA2C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92342131; PubMed=1353249;
RA Link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Kobilka B.K.;
RT "Cloning of two mouse genes encoding alpha 2-adrenergic receptor
RT subtypes and identification of a single amino acid in the mouse alpha
RT 2-C10 homolog responsible for an interspecies variation in
RT antagonist binding."
RL Mol. Pharmacol. 42:16-27(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=93250567; PubMed=8387367;
RA Chang Y.-H., Chang A.C., Chen W.-M., Chang N.-C.A.;
RT "Molecular characterization of a murine homologue of alpha 2c4
RT adrenoceptor subtype gene."
RL Biochem. Mol. Biol. Int. 29:467-474(1993).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
Cc      EMBL: M99376; AAA37212.1; -.
DR      EMBL: M97516; AAA37183.1; -.
DR      HSSP: P29274; IMMH.
DR      MGD; MG1:87936; Adra2c.
DR      InterPro: IPR000276; GPCR_Rhodpsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PR00237; GPCRRHODOPSN.
DR      PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR      PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein;
KW      Multigene family; Phosphorylation.
FT      DOMAIN 1 51 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 52 76 1 (POTENTIAL).
```


FT	DOMAIN	77	88	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	89	114	2 (POTENTIAL).
FT	DOMAIN	115	124	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	125	147	3 (POTENTIAL).
FT	DOMAIN	148	168	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	169	191	4 (POTENTIAL).
FT	DOMAIN	192	207	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	208	231	5 (POTENTIAL).
FT	DOMAIN	232	379	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	380	403	6 (POTENTIAL).
FT	DOMAIN	404	416	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	417	437	7 (POTENTIAL).
FT	DOMAIN	438	458	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	291	305	ARG-RICH (BASIC).
FT	CARBOHYD	19	19	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	33	33	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	124	202	BY SIMILARITY.
FT	CONFLICT	196	196	G -> V (IN REF. 2).
FT	CONFLICT	296	296	G -> A (IN REF. 2).
FT	CONFLICT	298	298	L -> V (IN REF. 2).
SO	SEQUENCE	458 AA;	49906 MW;	COA8BDF0302BFI7B CRC64;

Query Match	49.38;	Score 1173;	DB 1;	Length 458;
Best Local Similarity	53.58;	Pred. No. 8.2e-48;		
Matches 251; Conservative	46;	Mismatches 104;	Indels 68;	Gaps 11;

QY	14	NGTEA----	PGGARAT-----	PSLOVTLTLVCLAGLMLTLTFGNVLVI	AVFT	60
		::	:		: ::	:
Db	19	NGSDAGEWGSGGGANASG	TDWVPPPGOYSAGAVAGLA	AVGELIVFTVGNVLVI	AVLT	78
QY	61	SRALKAPQNF	FLVSLASADILVATL	IPESLANEVMGYWEGKAWCEI	YALDVL	FTGSS 120
		:		:	:	
Db	79	SRALARQNF	FLVSLASADILVATL	VMFESLANELMAYWFGVY	LALDVL	FTGSS 138
QY	121	IVHLCAISLDR	WYSITQAI	EYNLKRTPRIKAIIT	TVWVISAVISFPPL	ISIEKKGCGG 180
				:	:	
Db	139	IVHLCAISLDR	WYSVTQAVEYNLKRTPR	KATIVAVWLISAVISFPPL	VSFYRR	PDGA- 197
QY	181	POPAEPRCEI	NDOKWYV	ISSCISGFEAPCLIMILVY	VRIOYLAKRRT	RVPSPSRGRPDAYA 240
		:: :	::			::
Db	198	--AYPGG	LNDETWYLSSCISGFEAPCLIMGLVY	ARIYRAKLRTRL	SEKRG	---- 250
QY	241	APPGTERRP	KGLGPERSAGPGAEAPL	PTQLNG--	APGEDAPAGPRDT	DALDLEESS 297
						::
Db	251	-----	AGPDGAS----	PTTENGLKAGAGENG	HCAPRTE-VEP	DESS 287
QY	298	SSDHAERPP	GPDRPERGPRGKGKARASQV	KPGDSLPRRGPGATIGT	PRAGPGE	ERVGA 357
		:::				
Db	288	AAERRRRR	RGALRRGGRREGAEGDIT	GADGPGPGLAEQGA	RTASRSP--	GPGGRLSNAS 345
QY	358	KAS-----	RWGR-----	ONREKRTFVLAV	IGVFWCWFPEFF	TYTLTAV-- 399
Db	346	SRSVEFFLS	RRRRARSSVCRKRVADAREK	RFTFVLAVVMGVFLC	WPFFFFSYSL	YGTICR 405
QY	400	-GCSVPR	TLKEFFFWGYCNS	SLNPVIYTIENHDFRRA	FKTILCRGDRK	447
		:				:
Db	406	EACQLPEPL	KEFFFWIGYCNS	SLNPVIYTVFVNODFR	RSFKHILERRRR	454

RESULT 10		
AZAC_RAT		
ID	AZAC_RAT	STANDARD; PRT; 458 AA.
AC	P22086;	
DT	01-AUG-1991 (Rel. 19, Created)	
DT	01-APR-1993 (Rel. 25, Last sequence update)	
DT	01-NOV-1997 (Rel. 35, Last annotation update)	
DE	Alpha-2C adrenergic receptor (Alpha-2C adrenoceptor) (Subtype C4).	
GN	ADRA2C.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX	NCBI_TaxID=10116;	
RN	[1]	

```

RP SEQUENCE FROM N.A.
RX MEDLINE-91126047; Pubmed-1704126;
RA Flordellis C.S., Handy D.E., Bresnahan M.R., Zannis V.I., Gavras H.;;
RT "Cloning and expression of a rat brain alpha 2B-adrenergic receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:1019-1023(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-91130596; Pubmed-1704314;
RA Voigt M.M., McCune S.K., Kanterman R.Y., Felder C.C.;;
RT "The rat alpha 2-C4 adrenergic receptor gene encodes a novel
  pharmacological subtype.";
RL FEBS Lett. 278:45-50(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-91244823; Pubmed-1645350;
RA Lanier S.M., Downing S., Duzic E., Homcy C.J.;;
RT "Isolation of rat genomic clones encoding subtypes of the alpha 2-
  adrenergic receptor. Identification of a unique receptor subtype.";
RL J. Biol. Chem. 266:10470-10478(1991).
RN [4]
RP SEQUENCE FROM N.A.
RA Saitoh M., Imai A., Shimomura H.;;
RT "Cloning of rat alpha-2-B-adrenergic receptor gene and expression in
  rat submandibular gland.";
RL Shigaku 80:317-326(1992).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
  INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
  PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL; M58316; AAAA0634.1; -.
DR EMBL; X57659; CAA40861.1; -.
DR EMBL; M62371; AAA42033.1; -.
DR EMBL; D00819; BAA00700.1; -.
DR PIR; A37869; A37869.
DR PIR; S13023; S13023.
DR PIR; A40392; A40392.
DR HSSP; P29274; 1MMH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
  Multigene family; Phosphorylation.
FT DOMAIN 1 51 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 52 76 1 (POTENTIAL).
FT DOMAIN 77 88 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 89 114 2 (POTENTIAL).
FT DOMAIN 115 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 147 3 (POTENTIAL).
FT DOMAIN 148 168 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 169 191 4 (POTENTIAL).
FT DOMAIN 192 207 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 208 231 5 (POTENTIAL).
FT DOMAIN 232 379 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 380 403 6 (POTENTIAL).
FT DOMAIN 404 416 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 417 437 7 (POTENTIAL).
FT DOMAIN 438 458 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 291 305 ARG-RICH (BASIC).
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 124 202 BY SIMILARITY.

```

FT	CONFLICT	24	24	G -> R (IN REF. 4).
FT	CONFLICT	40	40	G -> A (IN REF. 1).
FT	CONFLICT	69	69	N -> T (IN REF. 1).
FT	CONFLICT	155	155	Q -> E (IN REF. 2).
FT	CONFLICT	245	245	S -> T (IN REF. 1).
FT	CONFLICT	252	252	G -> R (IN REF. 3).
FT	CONFLICT	275	275	A -> R (IN REF. 4).
FT	CONFLICT	298	298	L -> V (IN REF. 3).
SQ	SEQUENCE	458	AA; 49864	MW; 6846C2AF963B33BF CRC64;

Query Match	49.38;	Score 1173;	DB 1;	Length 458;
Best Local Similarity	53.58;	Pred. No. 8.2e-48;		
Matches 251; Conservative	46;	Mismatches 104;	Indels 68;	Gaps 11;

QY	14	NGIEA----	PGGARAT-----	PSLQVTLTVLVCAGLMLTVEGNVLVI	AVFT	60				
		::	:							
		::	:		: ::	:				
Db	19	NGSDAGEWGS	GGCANASGTDWGP	PPQGISAGAVAGLA	VGVGLIVTVGNVLVI	AVLT 78				
QY	61	SRALKAPQNL	FLVSLASADIL	VATLVIPE	SLANEVMGYE	KAWCEIYLALDVL	ECTSS 120			
		:			:	:				
		:			:	:				
Db	79	SRALRAPQNL	FLVSLASADIL	VATLVI	MPFSLANELMAY	WYFGQVCGVYLALDVL	ECTSS 138			
QY	121	IVHLCAISL	DRWYSITQAI	EYNLKRTP	PRIKAIITVW	WISAVISFPPLISIE	KGGGG 180			
					:	:				
					:	:				
Db	139	IVHLCAISL	DRWYSITQAVE	YNLKRTP	RVKATIVAW	LISAVISFPPLVSFY	RRPDGA- 197			
QY	181	POPAEPRCEI	NDQKVIYISS	CSIGSEFAP	CLIMILVY	VRIOJAKRRT	RVPPSR	RGPDAVA 240		
			:	:	:	:	:			
Db	198	--AYPOCG	LNDETWYTLSS	CSIGSEFAP	CLIMGLVY	ARIYRAK	LKRTLSE	KRG- 250		
QY	241	APPGGTER	RRPKGLPERS	SAGPGGA	EADLP	Q	LONG--	APGEPAPAGPR	DTDALD	LESS 297
Db	251	-----	-----	AGPDGAS---	PTTENG	L	GKAAGENG	CHCAPRTE-	VEPDESS 287	
QY	298	SSDHAERPP	GP	RRPERGPR	GKGKARASQ	YKPGDSL	PRRG	PATGIGT	PAAGPGE	ERYGAA 357
		:::						:		:
Db	288	AAERRRRR	RGALRRGARR	REGAEGD	TGSADGPG	PLAEOGAR	IASRSP-	GP	GRLSRAS 345	
QY	358	KAS-----	RMGR-----	QNRER	FTVLA	VVIGVEV	VCWPF	FFTYT	LTAV-- 399	
								:		:
Db	346	SRSVEFFL	SRRRARRASS	VCRRKA	QAQARE	RFTFVLA	VVMGV	FLCWP	FFFSYS	LYGICR 405
QY	400	-GCSVP	RTL	KEFFFW	GYCNS	SLNPV	YITIFN	HD	FRAA	FKKILCRGDRK 447
			:				:		:	:
Db	406	EACQLPE	PL	KEFFFW	IGYCNS	SLNPV	YITVFN	OD	FR	SFKHILFRRRR 454

```

RESULT 11
A2AC_CAVPO
ID A2AC_CAVPO STANDARD; PRT; 455 AA.
AC 060476;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Alpha-2C adrenergic receptor (Alpha-2C adrenoceptor).
OS Cavia porcellus (Guinea pig).
OC Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley;
RX MEDLINE=96152573; Pubmed=8573196;
RA Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Regan J.W.;
RT "Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,
RT and alpha 2C adrenoceptor subtypes. Radioligand binding and
RT functional coupling to a CAMP-responsive reporter gene.";
RL Biochem. Pharmacol. 51:291-300(1996).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

```

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DR	EMBL; U25724; AAA67076.1; -.
DR	HSSP; P29274; 1MMH.
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRRHODPSN.
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;
KW	Multigene family; Phosphorylation.
FT	DOMAIN 1 47
FT	TRANSMEM 48 72
FT	DOMAIN 73 84
FT	TRANSMEM 85 110
FT	DOMAIN 111 120
FT	TRANSMEM 121 143
FT	DOMAIN 144 164
FT	TRANSMEM 165 187
FT	DOMAIN 188 203
FT	TRANSMEM 204 227
FT	DOMAIN 228 376
FT	TRANSMEM 377 400
FT	DOMAIN 401 413
FT	TRANSMEM 414 434
FT	DOMAIN 435 455
FT	CARBOHYD 17 17
FT	CARBOHYD 29 29
FT	DISULFID 120 198
SQ	SEQUENCE 455 AA; 49351 MW; 6B657D247FF8A3F4 CRC64;

Query Match	49.28;	Score 1171.5;	DB 1;	Length 455;
Best Local Similarity	53.58;	Pred. No. 9.6e-48;		
Matches 252; Conservative	47;	Mismatches 115;	Indels 57;	Gaps 11;

```
QY      4 LÖPDAGNASMNGTEAPGGARA-----TPISLÖVTLTVCLAGLMLLTVEGNVLV 54
        | : ||| | ||| | : ||| | : ||| |
Db     11 LAEGPMAS--GAGEGGGVNASCVAWGPSPQSISAGAVALAUVGFLLVFTVGNVLV 68
QY      55 IIAVTSRALKAPÖNLFLVSLASADILVATLVDPFSLANEVMGYWFEGKAICEITYLADV 114
        |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db     69 VIAVLTSRALRAPÖNFLVLSLASADILVATLVMPFSLANELMAIWMYFGQWCGVYLADV 128
QY      115 LFCTSSIVHLCAISLDRWYSITÖAIEYNLKRTPRIKAIITVWVISAVISPPPLISTEK 174
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     129 LFCTSSIVHLCALSIDRWYSVTÖAVEYNLKRTPRVKATI VAWWLISAITSPPPLVSFYR 188
QY      175 KGGGGPÖPAEPRCETINDÖKWYVISSCIGSEFPACLIMILVYVRİYÖIAKRTRRVPSRR 234
        | : | ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db     189 QPDGA---AYPRCGLNDETWTYILSSCIGSEFPACLIMGVYARIYRVAKULTRLSEKR 244
QY      235 GPDAVAAPPGGTERRPKGLPERSAGPGGAEAEBPLQTÖNGAPGEPAAGPBDTDALDLE 294
        || | ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| |
Db     245 GP---AGPEGESPTTENGLGAAAAA-----AAGENHCABBRAD-VEPD 284
QY      295 ESSSSDHAERPPGPRRDER-----GPRGSKARASÖVKPGDSLPRRGATGIGTP 345
        |||::: | ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| |
Db     285 ESSAERRRRRRGALRRCARGAREAGVEAPGP-GLGSAAAD--PGALSVSRSGPGGRLSR 340
QY      346 AAGPGE-----RVGAAKASRMWRGRÖNREREFTVLAVVIGVFVWCWPFPEFTYTLTAV 399
        | : | | : | : | : | ||||| ||||| ||||| ||||| ||||| ||||| :
Db     341 ASSRSVEFFLSRRRRARRASSVCRRKVAÖAREKRTFVLAVVMGVFLCWPFPEFSYSLYGI 400
QY      400 ---GCSVPRTLKEFFFWGYCNSSLNPVITYTFNHDFRAFKKILCRGDRK 447
        | : | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     401 CREACQLPTPLKFEFFWIGYCNSSLNPVITYTFNODFRRSFKHILFRRRR 451
```


RP SEQUENCE OF 95-389 FROM N.A.
RX MEDLINE=91054503; PubMed=2173582;
RA Chang A.C., Ho T.F., Chang N.-C.A.;
RT "In vitro amplification by polymerase chain reaction of a partial
RT gene encoding the third subtype of alpha-2 adrenergic receptor in
RT humans.";
RL Biochem. Biophys. Res. Commun. 172:817-823(1990).
CC -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS. THE RANK ORDER OF POTENCY FOR AGONISTS OF THIS RECEPTOR
CC IS CLONIDINE > NOREPINEPHRINE > EPINEPHRINE = OXYMETAZOLINE >
CC DOPAMINE > P-TYRAMINE = PHENYLEPHRINE > SEROTONIN > P-SYNEPHRINE /
CC P-OCTOPAMINE. FOR ANTAGONISTS, THE RANK ORDER IS YOHIMBINE >
CC CHLORPROMAZINE > PHENTOLAMINE > MIANSERINE > SPIPERONE > PRAZOSIN
CC > ALPRENOLOL > PROPRANOLOL > PINDOLOL.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; M34041; AAA51666.1; -.
DR EMBL; M38742; AAA62823.1; -.
DR EMBL; AF005900; AAB62558.1; -.
DR PIR; A36158; A36158.
DR PIR; A37223; A37223.
DR HSSP; P29274; 1MMH.
DR Genew; HGNC:282; ADRA2B.
DR MIM; 104260; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 12 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 13 38 1 (POTENTIAL).
FT DOMAIN 39 49 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 50 75 2 (POTENTIAL).
FT DOMAIN 76 85 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 86 108 3 (POTENTIAL).
FT DOMAIN 109 130 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 131 153 4 (POTENTIAL).
FT DOMAIN 154 169 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 170 193 5 (POTENTIAL).
FT DOMAIN 194 372 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 373 396 6 (POTENTIAL).
FT DOMAIN 397 405 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 406 429 7 (POTENTIAL).
FT DOMAIN 430 450 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 294 311 ASP/GLU-RICH (ACIDIC).
FT DISULFD 85 164 BY SIMILARITY.
FT LIPID 442 442 PALMITATE (POTENTIAL).
FT SITE 92 92 IMPLICATED IN LIGAND BINDING (BY
FT SIMILARITY).
FT SITE 176 176 IMPLICATED IN CATECHOL AGONIST BINDING
FT SITE 180 180 (BY SIMILARITY).
FT CONFLICT 362 363 IMPLICATED IN CATECHOL AGONIST BINDING
SQ SEQUENCE 450 AA; 49948 MW; A476817C8788E1FD CRC64; HV -> QL (IN REF. 3 AND 4).
Query Match 47.4%; Score 1127.5; DB 1; Length 450;
Best Local Similarity 53.2%; Pred. No. 9.9e-46;
Matches 243; Conservative 51; Mismatches 104; Indels 59; Gaps 14;

DB 6 PYSVQATTAATAITFLILFTIFGNALVILAVLTSRSLRPQNLFVLSLAADIVATLI 65
QY 87 IPFSLANEWGYWYFGKAWCEIYALDYLCTSSIVHLCALSLDRWYSITQAIENLKRT 146
DB 66 IPFSLANELGYWYFRRTWCEVIALDYLCTSSIVHLCALSLDRWYAVSRALEYNSKRT 125
QY 147 PRRIKAIITWVISAVISFPPLISIEKKGGGGPQP-AEPRCEINDQKWYISSCIGSF 205
DB 126 PRRIKAIITWVLIWIAVVISLPLI---YKDGQGPQPRPQCKLNOEAWYIASSIGSF 181
QY 206 FAPCLIMILVYVRIYQIAKRRTVRVPSRRGPDVAAPGCTERRPKGLPERSAGPGA 265
DB 182 FAPCLIMILVYLRILYIAKR-----SNRRGPRAKGGPGGESKQPR--PDHGALASAK 233
QY 266 AEPLPT-----QLNG---APGEPAPA-GPRDTDALDLES-----SS 298
DB 234 LPALASVASAREVNGHSGSTGEKEGETPEDTGTALPPSWAALLPNSGGQKGEVCGASP 293
QY 299 SDHAERPPGPRRPERGPRGKARASQVKGPD--SLPRGPG-----ATGIGTPAAGPE 351
DB 294 EDEAE-----EEEEEEEECEQAVPVSASACSPLOQPGSRVLATLRGOYLLGRG- 348
QY 352 ERVGAKAKSRWGRON--REKRTFVLAIVIGVFVVCWPEFFFTYTLTAV--GCSVPRT 406
DB 349 --VGAIGQWRRRAHVTRERKRTFVLAIVIGVFVLCWPEFFFSYSLGAICPKCKVPHG 406
QY 407 LKFFFWFGYCNSSLNPVITYTFNHDFRAFKILCR 443
DB 407 LQFFFWIGYCNSSLNPVITYTFNODFRRAFRILCR 443
RESULT 14
A2AR_LABOS
ID A2AR_LABOS STANDARD; PRT; 432 AA.
AC Q91081;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Alpha-2 adrenergic receptor (Alpha-2 adrenoceptor).
OS Labrus ossifagus (Cuckoo wrasse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
OC Labridae; Labrus.
OX NCBI_Taxid=30800;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94035926; PubMed=7693288;
RA Svensson S.P.S., Bailey T.J., Pepperl D.J., Grundstroem N.,
RA Ala-Uotila S., Scheinin M., Karlsson J.O.G., Regan J.W.;
RT "Cloning and expression of a fish alpha 2-adrenoceptor.";
RL Br. J. Pharmacol. 110:54-60(1993).
CC -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U07743; AAA17386.1; -.
DR HSSP; P29274; 1MMH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.

DR	PROSITE, PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.
FT	DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 33 57 1 (POTENTIAL).
FT	DOMAIN 58 69 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 70 95 2 (POTENTIAL).
FT	DOMAIN 96 105 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 106 128 3 (POTENTIAL).
FT	DOMAIN 129 149 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 150 172 4 (POTENTIAL).
FT	DOMAIN 173 188 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 189 212 5 (POTENTIAL).
FT	DOMAIN 213 356 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 357 380 6 (POTENTIAL).
FT	DOMAIN 381 393 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 394 413 7 (POTENTIAL).
FT	DOMAIN 414 432 CYTOPLASMIC (POTENTIAL).
FT	DISULFID 105 183 BY SIMILARITY.
FT	CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE 432 AA; 48563 MW; 0A42FAF9849FA8BA CRC64;

Query Match	47.38;	Score 1126.5;	DB 1;	Length 432;
Best Local Similarity	53.08;	Pred. No. 1.1e-45;		
Matches 240;	Conservative 50;	Mismatches 108;	Indels 55;	Gaps 11;

```

0Y 10 NASWNGTEAPGGGARATPYSLQVTLTLVCLAGLMLTLVGNVLVIIVFTSRALKAPON 69
    |||: | | ||| :: | :| | ||:| | ||| |||
Db 18 NASWS---ADSG-----YSLAAIASIAALVSLFLFTVGNILVIAVLTSRALKAPON 68
    70 LFLVSLASADILVATLVIPESLANEVMGYFGKAWCEIYALDVLCTSSIVHICAISL 129
    |||||:|||||:|||||:||||| | ||||| ||||| |||||
Db 69 LFLVSLATADILVATLVMPFSLANELMGWYFGKWCGIYALDVLCTSSIVHICAISL 128
    130 DRYWSITQAIENYLNKRTPRRIKAITTWVISAVISFPPLISIEKKGGGPQPAEBRCE 189
    |||||:|||||:|||||: | :| | | ||:| | :| :|
Db 129 DRYWSVTQAVEYNLKRTPKRVKCIIVWLISAFISSPPLSID---SNNYISSQOQM 184
    190 INDQKWYVSISSCIGSEFAPCLIMILYVYRIQIAKRRTRPBPSRRGPDVAAPPGTERR 249
    :| | :| :| :| :| | | | | | :| | | | |
Db 185 LNDDTWYLISSSMASFEAPCLIMILYIRIQVAKTRTR-----SMSCHEPR 231
    250 PKGL-----GPERSAGP-----GGAEAEP LPTQLNGAPGEPAAPAGPRDTALDLNESS 297
    | :| | :| :| | :| :| | :| :| :| :| :|
Db 232 PDGVTQTENGLNKANSPCCHGDRENGHCQCPPTPSQRTVITGQ-----QTDADADESF 284
    298 SSDHAERPPGPRRPERGPRGKGKARASQVYKPGDSLPRRGPGATGICTPAAGPGEERYGAA 357
    ||: | :| :| | | :| :| | :| :| :| :|
Db 285 SSEGKGHKRQRODSQRAKR-PGLKSSSISKOSARISRVSXNSVDLFASRKKRRRSSIAEK 343
    358 KASRWRGRONREKRETFVLAVVIGVFWCWPPEFFTYTLTAV--GCSVPRTLKFEFFWF 414
    | | | | | | | | | | | | | | | | | | | | | | | |
Db 344 KVS-----QAREKRFTFVLAVVMGVFWCWPPEFFSYSLHAVCRDYCKIPDTLFR-FEWI 397
    415 GYCNSLSLNPVIYTIENHDFRRAFKITLCRGDRK 447
    ||||| | | | | | | | | | | :|
Db 398 GYCNSLSLNPVIYTIENRDFRRAFOKITLCKSMWK 430

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RESULT 15
A2AB_MOUSE
ID A2AB_MOUSE STANDARD; PRT; 455 AA.
AC P30545;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
GN ADRA2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

```

```

RP      SEQUENCE FROM N.A.
RC      STRAIN=DBA/2; TISSUE=Liver;
RX      MEDLINE=93129625; PubMed=1336396;
RT      Chen W.-M., Chang A.C., Shle B.J., Chang Y.-H., Chang N.-C.A.;
RT      "Molecular cloning and characterization of a mouse alpha 2C2
RT      adrenoceptor subtype gene.";
RL      Blochim. Biophys. Acta 1171:219-223(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92378586; PubMed=1354956;
RA      Chruscinski A.J., Link R.E., Daunt D.A., Barsh G.S., Kobilka B.K.;
RT      "Cloning and expression of the mouse homolog of the human alpha 2-C2
RT      adrenergic receptor.";
RL      Biochem. Biophys. Res. Commun. 186:1280-1287(1992).
CC      -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC      INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC      PROTEINS.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).

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CC	-----
DR	EMBL; M94583; AAAT73895.1; -. EMBL; L00979; AAA37131.1; ALT_INIT. PIR; JH0693; JH0693.
DR	PIR; S28221; S28221.
DR	HSSP; P29274; 1MH.
DR	MGI; 87935; Adra2b.
DR	InterPro; IPR00276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRRHODPSN.
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR	PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
KW	G-protein coupled receptor; Transmembrane; Multigene family; Phosphorylation; Lipoprotein; Palmitate.
KM	
FT	DOMAIN 1 17 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 18 42 1 (POTENTIAL).
FT	DOMAIN 43 54 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 55 80 2 (POTENTIAL).
FT	DOMAIN 81 90 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 91 113 3 (POTENTIAL).
FT	DOMAIN 114 135 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 136 158 4 (POTENTIAL).
FT	DOMAIN 159 174 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 175 198 5 (POTENTIAL).
FT	DOMAIN 199 377 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 378 401 6 (POTENTIAL).
FT	DOMAIN 402 410 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 411 434 7 (POTENTIAL).
FT	DOMAIN 435 455 CYTOPLASMIC (POTENTIAL).
FT	DISULFID 90 169 BY SIMILARITY.
FT	LIPID 447 447 PALMITATE (POTENTIAL).
FT	DOMAIN 306 316 ASP/GLU-RICH (ACIDIC).
FT	SITE 97 97 IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
FT	SITE 181 181 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT	SITE 185 185 IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT	CONFLICT 202 202 V -> L (IN REF. 1).
FT	CONFLICT 229 230 MISSING (IN REF. 2).
SO	SEQUENCE 455 AA; 50615 MW; A3954AD76E0E6263 CRC64;

Query Match	47.1%;	Score 1121.5;	DB 1;	Length 455;
Best Local Similarity	53.08;	Pred. No. 1.9e-45;		
Matches 242;	Conservative	50;	Mismatches 106;	Indels 59;
				Gaps 14;

1000,			

[1]	Matches	242,	Mismatches
		30,	Indels
			35,
			Gaps
			14

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OM protein - protein search, using sw model

Run on: February 15, 2003, 14:30:52 ; Search time 50 Seconds
(without alignments)
1854.424 Million cell updates/sec

Title: US-09-636-259B-3
Perfect score: 2381
Sequence: 1 MGSLQPDAGNASWNGTEAPG.....HDFRAAFKKILCRGDRKRRIY 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvivirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2375	99.7	450	4	Q9BZK1	Q9bzk1 homo sapien
2	1305.5	54.8	388	13	Q90WY4	Q90wy4 brachydanio
3	1180.5	49.6	432	13	Q90WY6	Q90wy6 brachydanio
4	1135	47.7	510	13	Q90WY5	Q90wy5 brachydanio
5	1124	47.2	447	4	Q9BZK0	Q9bzk0 homo sapien
6	1115.5	46.9	448	11	Q925K6	Q925k6 mus musculu
7	1114.5	46.8	448	11	Q925K7	Q925k7 mus musculu
8	1110.5	46.6	453	11	Q925E4	Q925e4 rattus norv
9	967.5	40.6	393	11	Q9JTW2	Q9jtw2 cavia porce
10	941	39.5	392	6	Q95N90	Q95n90 tadarida br
11	940	39.5	390	6	Q9GKZ6	Q9gkz6 trichechus
12	940	39.5	390	6	Q9GLI9	Q9gli9 cynocephalu
13	938.5	39.4	395	6	Q9GLI2	Q9gli2 manis sp. a
14	937.5	39.4	379	6	Q9GLI3	Q9gli3 macropus ru
15	937.5	39.4	391	6	Q8SOA0	Q8sga0 emballonura
16	936.5	39.3	389	6	Q9GKZ5	Q9gkz5 tupaia tana

17	934.5	39.2	393	6	Q9GLI1	Q9gli1 nycticebus
18	932.5	39.2	395	6	Q95N91	Q95n91 tonatia bid
19	932	39.1	390	6	Q95N89	Q95n89 taphozous s
20	931	39.1	388	6	Q9GLI8	Q9gli8 dicerops bic
21	930.5	39.1	383	6	Q9GLI20	Q9gli20 cynopterus
22	930.5	39.1	387	6	Q9GLI7	Q9gli7 felis silve
23	930.5	39.1	389	6	Q9GLI07	Q9gli07 phoca vitul
24	929.5	39.0	393	6	Q95N92	Q95n92 myotis daub
25	927.5	39.0	393	6	Q9GLI5	Q9gli5 macrotus ca
26	926	38.9	392	6	Q9GLI35	Q9gli35 balaenopter
27	925.5	38.9	385	6	Q9GLI14	Q9gli14 micropotamo
28	925.5	38.9	393	6	Q9GLI6	Q9gli6 hippopotamu
29	923.5	38.8	385	6	Q9GKZ7	Q9gkz7 tenrec ecau
30	922.5	38.7	391	6	Q9GLI06	Q9gli06 sus scrofa
31	922	38.7	388	6	Q8SQI1	Q8sqi1 nycteris th
32	921.5	38.7	389	6	Q95N94	Q95n94 hipposidero
33	920.5	38.7	391	6	Q8SQB3	Q8sqb3 antrozous p
34	920	38.6	388	6	Q8SQI93	Q8sqi93 nycteris gr
35	919	38.6	396	6	Q8SQI87	Q8sqi87 rhoqeessa t
36	914.5	38.4	395	6	Q8SQI94	Q8sqi94 noctilio al
37	914	38.4	392	6	Q95N95	Q95n95 megaderma l
38	912	38.3	394	6	Q8SQI1	Q8sqi1 desmodus ro
39	911.5	38.3	389	6	Q8SQI95	Q8sqi95 nyctimene a
40	909.5	38.2	383	6	Q95N93	Q95n93 pteropus ra
41	909	38.2	398	6	Q8SQI92	Q8sqi92 natalus str
42	908.5	38.2	383	6	Q9GLI28	Q9gli28 bradypoma tr
43	902	37.9	365	6	Q8SQI88	Q8sqi88 rhinopoma h
44	900.5	37.8	389	6	Q8SQI89	Q8sqi89 rhinolophus
45	684.5	28.7	419	5	Q77254	Q77254 boophilus m

ALIGNMENTS

RESULT 1	
Q9BZK1	
ID Q9BZK1	PRELIMINARY; PRT; 450 AA.
AC Q9BZK1;	
DT 01-JUN-2001 (TREMBLrel. 17, Created)	
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)	
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE Alpha 2A adrenergic receptor.	
GN ADRA2A.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheraia; Primates; Catarrhini; Homiidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=20556293; PubMed=10948191;	
RA Small K.M., Forbes S.L., Brown K.M., Liggett S.B.;	
RT "An asn to lys polymorphism in the third intracellular loop of the	
RT human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted	
RT Gl coupling.";	
RL J. Biol. Chem. 275:38518-38523(2000).	
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
DR EMBL; AF316894; AAK01634.1; .	
DR HSSP; P29274; IMM.	
DR InterPro; IPR000276; GPCR_Rhodpsn.	
DR Pfam; PF00001; 7tm_1; 1.	
DR PRINTS; PR00237; GPCR_RHODPSN.	
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.	
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.	
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.	
FT VARIANT 251 251 K -> N.	
SQ SEQUENCE 450 AA; 48970 MW; 94E02E227CE5ECFE CRC64;	
Query Match	99.7%; Score 2375; DB 4; Length 450;
Best local Similarity	99.8%; Pred. No. 7.4e-165;
Matches 449; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY 1 MGSLQPDAGNASWNGTEAPGGGARATPYSLQVTLTLVCLAGLLMLTFVGNVLVIIVFT 60	

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|||||
Db 1 MGSLOPDAGNASWNGTEAPGGGARATPYSLOVTLTVCLAGLMLTFVGNVLIIAVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVPFSLANEVMGYWYFGKAWCEIYALDVLCTSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVPFSLANEVMGYWYFGKAWCEIYALDVLCTSS 120
QY 121 IVHLCAISLDRWSTIQAIEYNLKRTPRRIKAIITTWVISAVISFPPLISIEKKGGGG 180
Db 121 IVHLCAISLDRWSTIQAIEYNLKRTPRRIKAIITTWVISAVISFPPLISIEKKGGGG 180
QY 181 POPAEPRCEINDQKWYVISSCIGSFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDAYA 240
Db 181 POPAEPRCEINDQKWYVISSCIGSFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDAYA 240
QY 241 APPGGETERRPNGLPEPSAGPGGAEAEPPLTQNLGAPGEPAPAGPRDTDALDLESSSSD 300
Db 241 APPGGETERRPKGLPERSAGPGGAEAEPPLTQNLGAPGEPAPAGPRDTDALDLESSSSD 300
QY 301 HAERPPGPRRPERGPRGKGKARASQVKPGDSLPRRGPGATGIGTPAAGPGEERVGAAKAS 360
Db 301 HAERPPGPRRPERGPRGKGKARASQVKPGDSLPRRGPGATGIGTPAAGPGEERVGAAKAS 360
QY 361 RWRGRQNRREKRFTEVLAIVIGVVCWPFPEFTYTLTAVGCSVPRTLEKFEFFWFGYCNS 420
Db 361 RWRGRQNRREKRFTEVLAIVIGVVCWPFPEFTYTLTAVGCSVPRTLEKFEFFWFGYCNS 420
QY 421 LNPVITYTFNHFRAFKKILCRGDRKRIV 450
Db 421 LNPVITYTFNHFRAFKKILCRGDRKRIV 450
```

RESULT 2

```
Q90WY4 PRELIMINARY; PRT; 388 AA.
AC Q90WY4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha2A-adrenergic receptor.
GN ADRA2A.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Ruuskanen J., Xhaard H., Marjamaki A., Salaneck E., Salminen T.,
RA Yan Y.L., Postlethwait J.H., Johnson M.S., Larhammar D., Scheinin M.;
RT "Origin of Alpha2-Adrenergic Receptor Subtypes as Revealed by Cloning
RT and Mapping of Three Receptor Subtype Genes in the Zebrafish (Danio
RT rerio).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY048971; AAL07510.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 388 AA; 43996 MW; 431965A04E1986DD CRC64;
```

Query Match 54.8%; Score 1305.5; DB 13; Length 388;
Best Local Similarity 60.5%; Pred. No. 3.3e-87;
Matches 266; Conservative 37; Mismatches 78; Indels 59; Gaps 8;

```
QY 15 GTEAPGGARATPYSLOVTLTVCLAGLMLTFVGNVLIIAVFTSRALKAPQNLFLVS 74
Db 4 GANATNGTNATKEYTLLVALPLSIAVGLLLIIFGNVLIIAVFTSRALKAPQNLFLVS 63
QY 75 LASADILVATLVPFSLANEVMGYWYFGKAWCEIYALDVLCTSSIVHLCAISLDRYWS 134
Db 64 LASADILVATLVPFSLANEVMGYWYFGKAWCEIYALDVLCTASITHLCAISLDRYWS 123
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```
QY 135 ITQATEYNLKRTPRRIKAIITTWVISAVISFPPLISIEKKGGGGQPAPAEPRCEINDQK 194
Db 124 ITQATEYNLKRTPQRIKRIITFWIIAAVISCPPLTMKSEG-----DICDINKEK 175
QY 195 WYVISSCIGSFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDAAVAPPGTERRPNGLG 254
Db 176 WYVISSCIGSFPLPCITIMLVYIRIYQIAKRRTRAP-----G 213
QY 255 PERSAPGGAEAEPPLTQNLGAPGEPAPAGPRDTD---ALDLESSSSDHAERPPGPRRP 311
Db 214 DHRKNEVGKKENDP-HEKLNIGION---AEPDDKDEINGVDMESSSSSDHKVSNPCSLKK 268
QY 312 ERGPRGKGKARASQVKPGDSLPRRGPGATGIGTPAAGPGEERVGAAKASRWRGRQNRREK 371
Db 269 K--SSKGTKLSQIKPGD-----GDKTEACQTTKASRWGRQNRREK 308
QY 372 FTFVLAIVIGVVCWPFPEFTYTLTA-VGCSVPRTLEKFEFFWFGYCNSLNPVITYTFN 430
Db 309 FTFVLAIVIGVVCWPFPEFTYTFATCDCCVPETLEKFEFFWFGYCNSLNPITYTFN 368
QY 431 HDFRAFKKILCRGDRKRIV 450
Db 369 NDFRRSEFKKILCRDRKRIV 388
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RESULT 3

```
Q90WY6 PRELIMINARY; PRT; 432 AA.
AC Q90WY6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha2C-adrenergic receptor.
GN ADRA2C.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Ruuskanen J., Xhaard H., Marjamaki A., Salaneck E., Salminen T.,
RA Yan Y.L., Postlethwait J.H., Johnson M.S., Larhammar D., Scheinin M.;
RT "Origin of Alpha2-Adrenergic Receptor Subtypes as Revealed by Cloning
RT and Mapping of Three Receptor Subtype Genes in the Zebrafish (Danio
RT rerio).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY048969; AAL07508.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 432 AA; 49137 MW; 1A52F0283C663DA7 CRC64;
```

Query Match 49.6%; Score 1180.5; DB 13; Length 432;
Best Local Similarity 56.6%; Pred. No. 4.5e-78;
Matches 243; Conservative 45; Mismatches 112; Indels 29; Gaps 8;

```
QY 20 GGGARATPYSLOVTLTVCLAGLMLTFVGNVLIIAVFTSRALKAPQNLFLVSLASAD 79
Db 22 GNSTNSTSYSPATIIIGLAVSFLILFTIVGNVLVIAVLTSRALKPQNLFLVSLASAD 81
QY 80 IIVATLVPFSLANEVMGYWYFGKAWCEIYALDVLCTSSIVHLCAISLDRWSTIQA 139
Db 82 IIVATLIIPFSLANEVMGYWYFGEWCNTIYALDVLCTSSIVHLCAISLDRWSTIQA 141
QY 140 EYNLKRTPRRIKAIITTWVISAVISFPPLISIEKKGGGGQPAPAEPRCEINDQWYVIS 199
Db 142 EYNLKRTPRRVKGMIYVWVLISAVISFPPLISMDR---NTVDERRPACQLNDHTWYILY 197
QY 200 SCIGSFAPCLIMILVYVRIYQIAKRRTR-VPPSRGPDAAVAPPGTERRPNGLPERS 258
```


Db 418 RAFQKILCK 426

RESULT 4
Q90WY5
ID Q90WY5
PRELIMINARY;
PRT; 510 AA

Query Match	47.78;	Score 1135;	DB 13;	Length 510;
Best Local Similarity	49.28;	Pred. NO. 1.1e-74;		
Matches 246;	Conservative 58;	Mismatches 120;	Indels 76;	Gaps 11

Db 252 PQHKIQNGRDEI ---PGILQNNAKPPI LAVSQVDSVQX.....

Db 487 TIENKDERAEKKILCKNIK 500

RESULT 5
Q9BZK0
ID Q9BZK0 PRELIMINARY; PRT; 447 AA

Query Match	47.28;	Score 1124;	DB 4;	Length 447;
Best Local Similarity	53.28;	Pred. No. 6e-74;		
Matches 243;	Conservative 49;	Mismatches 103;	Indels 62;	Gaps 14

QY 266 AEPLPT-----QJLNG---AFGEFAFN 01NOV2010000000

Db 234 LPALASVASAREVNGHSHKSTGEKEGETPEDTGTALPPSWALPNSGQGQKEGVCGASP 293
QY 299 SDHAERPPGPRRPERGPRGKGKARASQVKPGD--SLPRRPG-----ATGIGTPAAGPGE 351
Db 294 EDEAEE-----EEEEEECEPQAVPVSPASACSPPLQOPQGSRYLATLRGQVLLGRG- 345
QY 352 ERYGAAKASRWGRQ--NREKRTFVLAVVIGVVCWFPPEFTYTLTAV--GCSVPRT 406
Db 346 --VGAIGQGWWRRAQDLTREKRTFVLAVVIGVVCWFPPEFTSYSLGAICPKHCKVPHG 403
QY 407 LKKEFFWFGYCNSSLNPVITYTFNHDFFRAFKILCR 443
Db 404 LFOFFFWIGYCNSSLNPVITYTFNODFFRAFRILCR 440

RESULT 6
ID Q925K6 PRELIMINARY; PRT; 448 AA.
AC Q925K6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Adrenergic receptor alpha 2B.
GN ADRA2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ILS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.,
RT "High-Throughput Sequence Identification of Gene Coding Variants
RT within Alcohol-Related QTLs."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332050; AAK56079.1; -.
DR MGD; MGI:87935; Adra2b.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 448 AA; 49998 MW; B37E5E21B0EC4625 CRC64;

Query Match 46.9%; Score 1115.5; DB 11; Length 448;
Best Local Similarity 52.7%; Pred. No. 2.5e-73;
Matches 241; Conservative 50; Mismatches 105; Indels 61; Gaps 14;
QY 27 PYSLOVTLTVCLAGLMLLTVFGNVLVIAVFTSRALKAPQNLFLVSLASADILVATLV 86
Db 6 PYSVQATAIAIASATFLIFTIFGNALVILAVLTSRSLRAPQNLFLVSLAADIIVATLI 65
QY 87 IPFSLANVMGYWYFGKACWEIYLALDVLFCTSSIVHLCAISLDRYWSITQAIENLKR 146
Db 66 IPFSLANELLGWYFWRAWCEVYLLADVLFCCTSSIVHLCAISLDRYWAVSRALEYNSKRT 125
QY 147 PRRIKAIITVWVISAVISFPPLISIEKKGGGGPOP-AEPRCEINDQKWYVSSCIGSF 205
Db 126 PRRIKCIITVWLIAAVISLPLI---YKGDQRPHPGLPQCELNQEAWYILASSIGSF 181
QY 206 FAPCLIMILVVRVRIQIAKRRTVRPPSRGPDVAVAAPPGTERRPNGLGPERSAAGAE 265
Db 182 FAPCLIMILVLRIVIAKR-----SHCRGLGAKRGSGEGESKKPH---PAAGVPASAK 233
QY 266 AEPLPTQUNG---APGEPAPAGPRDTDALDLESSSSSDHAER---PPG-----PRPERGP 315
Db 234 VPTLVSPSSVGEANGHPKP--PREK-----EEGETPEDPEARALPPNWSALPRSVQDQK 286
QY 316 RKGKARASQVKPGD-----SLPRRPGATGIGTPAAGPEER----- 353
Db 287 KGTSGATAEKGAEDEEEVECEPQTLF--ASPASVFNPPLQOPQTSRVLATLRGQVLLS 344

QY 354 --VGAAKASRWGRQ--NREKRTFVLAVVIGVVCWFPPEFTYTLTAV--GCSVPRT 406
Db 345 KNVGVASGQWWRRTQLSREKRTFVLAVVIGVVCWFPPEFTSYSLGAICPQHCKVPHG 404
QY 407 LKKEFFWFGYCNSSLNPVITYTFNHDFFRAFKILCR 443
Db 405 LFOFFFWIGYCNSSLNPVITYTFNODFFRAFRILCR 441

RESULT 7
ID Q925K7 PRELIMINARY; PRT; 448 AA.
AC Q925K7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Adrenergic receptor alpha 2B.
GN ADRA2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.,
RT "High-Throughput Sequence Identification of Gene Coding Variants
RT within Alcohol-Related QTLs."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332049; AAK56078.1; -.
DR MGD; MGI:87935; Adra2b.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 448 AA; 50018 MW; 1B5ED9456C0B2B73 CRC64;

Query Match 46.8%; Score 1114.5; DB 11; Length 448;
Best Local Similarity 52.7%; Pred. No. 2.9e-73;
Matches 241; Conservative 49; Mismatches 106; Indels 61; Gaps 14;
QY 27 PYSLOVTLTVCLAGLMLLTVFGNVLVIAVFTSRALKAPQNLFLVSLASADILVATLV 86
Db 6 PYSVQATAIAIASATFLIFTIFGNALVILAVLTSRSLRAPQNLFLVSLAADIIVATLI 65
QY 87 IPFSLANVMGYWYFGKACWEIYLALDVLFCTSSIVHLCAISLDRYWSITQAIENLKR 146
Db 66 IPFSLANELLGWYFWRAWCEVYLLADVLFCCTSSIVHLCAISLDRYWAVSRALEYNSKRT 125
QY 147 PRRIKAIITVWVISAVISFPPLISIEKKGGGGPOP-AEPRCEINDQKWYVSSCIGSF 205
Db 126 PRRIKCIITVWLIAAVISLPLI---YKGDQRPHPGLPQCELNQEAWYILASSIGSF 181
QY 206 FAPCLIMILVVRVRIQIAKRRTVRPPSRGPDVAVAAPPGTERRPNGLGPERSAAGAE 265
Db 182 FAPCLIMILVLRIVIAKR-----SHCRGLGAKRGSGEGESKKPH---PAAGVPASAK 233
QY 266 AEPLPTQUNG---APGEPAPAGPRDTDALDLESSSSSDHAER---PPG-----PRPERGP 315
Db 234 VPTLVSPSSVGEANGHPKP--PREK-----EEGETPEDPEARALPPNWSALPRSVQDQK 286
QY 316 RKGKARASQVKPGD-----SLPRRPGATGIGTPAAGPEER----- 353
Db 287 KGTSGATAEKGAEDEEEVECEPQTLF--ASPASVFNPPLQOPQTSRVLATLRGQVLLS 344
QY 354 --VGAAKASRWGRQ--NREKRTFVLAVVIGVVCWFPPEFTYTLTAV--GCSVPRT 406
Db 345 KNVGVASGQWWRRTQLSREKRTFVLAVVIGVVCWFPPEFTSYSLGAICPQHCKVPHG 404
QY 407 LKKEFFWFGYCNSSLNPVITYTFNHDFFRAFKILCR 443

Db 405 LFGFFFWIGYCNSSLNPVITYTFNODFRARFRILCR 441

RESULT 8
Q925E4 PRELIMINARY; PRT; 453 AA.
AC Q925E4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Alpha2B-adrenergic receptor.
GN Rng.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Schaak S., Cussac D., Paris H.;
RT *Cloning and characterization of the rat alpha2B-adrenergic receptor
RT gene promoter.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF366899; AAK53388.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 453 AA; 50369 MW; CBA69CE23EACB511 CRC64;

Query Match 46.6%; Score 1110.5; DB 11; Length 453;
Best Local Similarity 52.5%; Pred. No. 5.8e-73;
Matches 240; Conservative 50; Mismatches 106; Indels 61; Gaps 14;
QY 27 PYSLOVTLVCLAGLMLTLTFGVNLYIAVFTSRALKAPQNLFLVSLASADILVATLV 86
Db 11 PYSVQATAATASAITFLIFTIFGNALVILAVLTSRLRAPQNLFLVSLAADILVATLI 70
QY 87 IPFSLANEVMGWYFGKAWCEIYALDVLECTSSIVHLCAISLDRTWSITQAIENLKR 146
Db 71 IPFSLANELLGWYFWRAWCEVYALDVLECTSSIVHLCAISLDRTWAVSRALRYNSKRT 130
QY 147 PRRIKAIITVWVISAVISFPPLISIEKKGGGQPP-AEPRCEINDQKWVVISGIGSF 205
Db 131 PRRIKCIITLWVLIATAVISLPLI----YKGDQREPERGLPQCELNQEWIYILASSIGSF 186
QY 206 FAPCLIMILVYRITQIAKRTRVPPSRGPDVAAPPGGTERPRLGPERGAGAE 265
Db 187 FAPCLIMILVYRITQIAKRTRVPPSRGPDVAAPPGGTERPRLGPERGAGAE 265
QY 266 AEPLPTQLNG--ADGEPAPAGPRDTALDLESSSSSDHAER---PPG---PRPERGP 315
Db 239 VPTLVSPSSVGEANGHPKP--PREK-----EEGETPEDPEARALPPTWSALPRSGGQK 291
QY 316 RGKGRASQVKKPGD-----SLPRRGPGATGIGTPAAGPGEER----- 353
Db 292 KGTSGATAEGDEDEEVEECEPQTLF--ASPASVCNPLQDPQTSRVLATLRGQVLLG 349
QY 354 --VGAAKASRWGRQ--NREKRTFVLAVVIGVFWCMFPFFFTYTLTAV---GCSVPRT 406
Db 350 KNVGVASGQWWRRTQLSREKRTFVLAVVIGVFWCMFPFFFTSYSIGAICPQHCKVPHG 409
QY 407 LKFFFWGYCNSSLNPVITYTFNHFRRARFKILCR 443
Db 410 LFOFFFWIGYCNSSLNPVITYTFVFNQDFRRAFRILCR 446

RESULT 9
Q9JW2 PRELIMINARY; PRT; 393 AA.
ID Q9JW2
AC Q9JW2;

DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_Taxid=10141;
RN [1]
RP SEQUENCE FROM N.A.

RA Madsen O.;
RT "Molecular evolution of alpha adrenergic receptor 2B."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ271336; CAB66895.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 393
SQ SEQUENCE 393 AA; 42921 MW; 5399B7175A53BD48 CRC64;

Query Match 40.6%; Score 967.5; DB 11; Length 393;
Best Local Similarity 52.2%; Pred. No. 1.2e-62;
Matches 214; Conservative 41; Mismatches 86; Indels 69; Gaps 13;
QY 43 LMLTFVGNVLIIVAVFTSRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGWYFG 102
Db 9 LILFTIFGNALVILAVLTSRLRAPQNLFLVSLAADILVATLIPFSLANELLGWYFW 68
QY 103 KAWCEIYALDVLECTSSIVHLCAISLDRTWSITQAIENLKRTPRRIKAIITVWVISA 162
Db 69 RTWCEVYALDVLECTSSIVHLCAISLDRTWAVSRALRYNSKRTPRRIKCIITLWVLI 128
QY 163 VISFPPLISIEKKGGGQPP-AEPRCEINDQKWVVISGIGSFAPCLIMILVYRITQ 221
Db 129 VISLPLT----YKGDQGPGRGSPQCKINQEWIYILASSIGSFAPCLIMILVYRITL 184
QY 222 IAKRRRTVPPSRGPDVAAPPGGTERPRLGPERGAGAE---PLPTQLNG-- 275
Db 185 IAKR-----SNRGRPRAGKGPQSGQSKESRPL-----PGAPASAKYVPLASPLSTG 232
QY 276 -APGEPAPAGPRDTALDLESSSSSDHAERPPGPRPERGPRGKGRASQVKP----- 328
Db 233 EANGHPKPTGEKE-----EGESSEDPGARTLPSPWALPTSGQGQKKAIVLAPAEAE 286
QY 329 -----GDSL-PRRGP-----ATGIGTPAAGPGEERYGAAKASRW 363
Db 287 EEEEGDECEQAAPGLPASMCSPLQDPQGSRVLATLRGQVLLGRG---VGAVDGQW 343
QY 364 GR--QNREKRTFVLAVVIGVFWCMFPFFFTYTLTAV---GCSVPRTL 408
Db 344 RTQMTREKRTFVLAVVIGVFWCMFPFFFTYSIGAICPQHCKVPHGLF 393

RESULT 10
Q95N90 PRELIMINARY; PRT; 392 AA.
ID Q95N90
AC Q95N90;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Tadarida brasiliensis (Brazilian free-tailed bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Molossidae; Tadarida.
OX NCBI_Taxid=9438;

```
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21267399; PubMed-11353869;
RA Springer M.S., Teeling E.C., Madsen O., Stanhope M.J., de Jong W.W.;
RT "Integrated fossil and molecular data reconstruct bat echolocation.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:6241-6246(2001).
DR EMBL; AC337542; AAK55307.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 392 392
SQ SEQUENCE 392 AA; 42771 MW; 8DA9B78A13C5997E CRC64;

Query Match
Best Local Similarity 39.5%; Score 941; DB 6; Length 392;
Matches 206; Conservative 45; Mismatches 105; Indels 38; Gaps 11;

QY 43 LMLTFGNVLVIIVTSTRALKAPQNLFLVSLASADILVATLVIPFSLANVMGYWFG 102
Db 9 LILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAADILVATLIPFSLANELLGYWYER 68
QY 103 KAWCEIYALDVLICTSSIVHLCAISLDRYWSTQAIENLKRTPRRIKAIITVWVISA 162
Db 69 RMWCEVYALDVLICTSSIVHLCAISLDRYWAVSRALVNSKRTPRRIKCIITVWLIAA 128
QY 163 VISFPPLISIEKKGGGGPQ-P-AEPRCEINDQKWYVISSCIGSFAPCLIMILVYRIYQ 221
Db 129 VISLPPLV---YKGDPPQPRGRPQCKLNOEAWYILASSIGSFAPCLIMILVYRIYV 184
QY 222 IAKRRTVRPPSRGRPDVAAPPGGTERPNGLPERSA-----GPGAEAEPLPT 271
Db 185 IAKR-----SHRRGPRAKKGPEGASRQRLVPGEASAKLPTLASHLVASGEANGHSKPT 239
QY 272 ---QLNGAPGEPA-PAGPRDTDAL-----DLEESSSDHAERPPGPRRPERGRGKKAR 322
Db 240 GEKEKGGTPEDPGNPALPPSWPALPHAGQLKEGVCEASPEEDVGEEEEEEEDQCEPQAL 299
QY 323 ASQVKPGDSLPRRGPGATGTPAAGPG--EERVGAAKASRW---RGRQNRKRTFVLA 377
Db 300 PASPASACSPPLQDPQGSQVLA TLRGQVLLSRGVGAA-GGRWLKRRAQLTREKRTFVLA 358
QY 378 VVIGVEVVCWPFPEFTYTLTAV---GCSVPRITLF 408
Db 359 VVIGVEVLCWPFPEFFSYSLGAICPQCHKVPHGLF 392

RESULT 11
Q9GKZ6 PRELIMINARY; PRT; 390 AA.
AC 09GKZ6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha adrenergic receptor, subtype 2B (Fragment).
GN AAR2B.
OS Trichechus manatus (Caribbean manatee) (West Indian manatee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Sirenia; Trichechidae; Trichechus.
OX NCBI_TaxID=9778;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., Madsen O., Catzefflis F., Stanhope M., de Jong W.W.;
RT "Probing lthe protein sequence support for the 'African clade' of
RT mammals.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ251109; CAC16418.1; -.
DR HSSP; P29274; 1MMH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
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DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1 1
FT NON_TER 390 390
SQ SEQUENCE 390 AA; 42713 MW; 06D90A8D1CE912A3 CRC64;

Query Match
Best Local Similarity 39.5%; Score 940; DB 6; Length 390;
Matches 212; Conservative 37; Mismatches 95; Indels 60; Gaps 14;

QY 43 LMLTFGNVLVIIVTSTRALKAPQNLFLVSLASADILVATLVIPFSLANVMGYWFG 102
Db 9 LILFTIFGNLSVLIVLTSRSLRAPQNLFLVSLAADILVATLIPFSLANELLGYWYFW 68
QY 103 KAWCEIYALDVLICTSSIVHLCAISLDRYWSTQAIENLKRTPRRIKAIITVWVISA 162
Db 69 RTWCEVYALDVLICTSSIVHLCAISLDRYWAVSRALVNSKRTPRRIKCIITVWLIAA 128
QY 163 VISFPPLISIEKKGGGGPQ-P-AEPRCEINDQKWYVISSCIGSFAPCLIMILVYRIYQ 221
Db 129 AISLPPLI---YKGDQGPQPRGRPQCKLNOEAWYILSSSIGSFAPCLIMILVYRIYL 184
QY 222 IAKRRTVRPPSRGRPDVAAPPGGTERPNGL--GPERSAGPGAEAEPLPTQLNG---- 275
Db 185 IAKR-----SHRRGPAGKAPRKGESKQPHSLDSGPSALAN-----LPTLASSLAVA 231
QY 276 --APGEPAAGPRDTDALDLEESSSDHAERPPG-PRRPERGPRK-GKARASQVKPGDS 331
Db 232 GEADGHSMPGKEKER-----ETSEDPGTIPLPSPVLPNSGGQKEGVCGASLEEDADK 286
QY 332 LPRR--GP-----GATGIGTPAAGPGEER-----VGAAKASRWGRQ--N 367
Db 287 EEEEECGPRAVPASPATACSPPLQDPQGSRYLATLRGQVFLRGVGAAGQWRRRAQLT 346
QY 368 REKRFTVLAIVIGVEVVCWPFPEFTYTLTAV---GCSVPRITLF 408
Db 347 REKRFTVLAIVIGVEVLCWPFPEFFSYSLGAICPQCHKVPHGLF 390

RESULT 12
Q9GLI9 PRELIMINARY; PRT; 390 AA.
AC Q9GLI9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Cynocephalus variegatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Dermoptera; Cynocephalidae; Cynocephalus.
OX NCBI_TaxID=9457;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082081; PubMed=11214318;
RA Madsen O., Scally M., Douady C., Kao D., Debry R., Adkins R.,
RA Amrine H., Stanhope M., de Jong W., Springer M.;
RT "Parallel adaptive radiations in two major clades of placental
RT mammals.";
RL Nature 409:610-614(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ251182; CAC16685.1; -.
DR HSSP; P29274; 1MMH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
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Db	606	CAACCGCAGAGTCCACAGGCCCAAGG--GGGGCTGGCCAGGGTGAGTCCACAGCAGCCC	663
QY	738	CGAGCGCAGGCCCAAGGGTCTGGGCCCCGAGCGACGGGGCCCCGGG----GGCGCA	792
Db	664	CGACCCGACCATGGTGGGGCTTGGCCTCAGCCAAACTGGCAGCCCTGGCTCTGTGGCT	723
QY	793	GAGGCCGAACCGCTGCCCAACCACTCAACGGCGCCCTGGCGAGCCCGCGGGCGGG	852
Db	724	TCTGCCAGAGAGGTCAACGGACACTCGAAGTCCACTGGGGAGAAGAGAGGGGGAGACC	783
QY	853	CCGGCGCAGACCGACCGCGCTGGACCTGGAGAGAGAGTCTGTTCGACACAGCCGAGCGG	912
Db	784	CCTGAAGATACTGGGACCCCGGGCTTGGCACCAGTTGGGCTGGCCTTCCCACTCAGGC	843
QY	913	C-----CTCAGGGCCCCGACAGCCGAGCGCG	940
Db	844	CAGGGCCAGAGAGGGGTGTTGTGGGCACTCCAGAGGATGAAGCTGAAGAGAGAGAG	903
QY	941	GTCCCCGGGGCAAGGCCAAGCCCCGAGCGCAGCCAGCTGAAGCCGGGGCAGACGCTGCCGC	1000
Db	904	GAGGAGGAGGAAGAGTGTGAACCCAGGACAGTGCAGTGTCTCCGGCTCAGCTTGACGC	963
QY	1001	GGCGCGGGCGGGGGCGACGGGGATCGGG-----ACGGCGCTGCAGGGC	1045
Db	964	CCCCCGCTGCAGCAGCCACAGGGCTCCCGGGTGTGCGCCACCCCTACGTGGCCAGGTGCTC	1023
QY	1046	CGGGGAGGAGCGCGTGG----GGCTGCCAAGCGCTCGCGCTGGCGCGGGCGGCAGAAC	1101
Db	1024	CTGGGCAGGGGCGGTGGTGTATAGGTGGGCAGTGTGGCGTCCGAAGGGCGCAGCTGACC	1083
QY	1102	CGGAGAAGCGCTTCACTTCGTGCTGGCGCGTGGTGCATCGGAGTGTCTGTGTGTGCTGG	1161
Db	1084	CGGGAAGAGCGCTTCACTTCGTGCTGGCGTGGTGCATTTGGCGCTGTGG	1143
QY	1162	TTCCCTTCTTCTTCACTTACAGCTCAGCGCGCTGG-----GTGCTCCGTGCCA	1212
Db	1144	TTCCCTTCTTCTTCACTTACAGCTCAGCGCGCGCCATCTGCCGGAAGCACTGCAGAGTGGCC	1203
QY	1213	CGCAGCGCTTCAATTTCTTCTGTGCTGGCTACTGCAACAGCTCGTTGAACCCGGTC	1272
Db	1204	CATGGCTCTTCCAGTTCTTCTGTGATCGGCTACTGCAACAGCTCACTGAACCTGT	1263
QY	1273	ATCTACACCACTTCAACCAAGATTTCGCGCGCGCTTCAAGAGATCTCTGTGC	1328
Db	1264	ATCTACACCACTTCAACCAAGACTTCGCGCGTGCCTTCCGAGAGATCTGTGCCG	1319

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Search completed: February 15, 2003, 14:30:30
Job time : 443.817 secs
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[illegible]

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RESULT 15
AAI99906
ID      AAI99906 standard; DNA; 1344 BP.
vv

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AC AA199906;

DT 18-FEB-2002 (first entry)
 YY

Human alpha-2BAR third intracellular loop variant encoding DNA.

OS Homo sapiens.
 XX phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
 KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KW polyanion; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW monomer; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;

05 Homo sapiens.

EH	Key	Location/Qualifiers
FT	CDS	1..1344

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FT /*tag= a
FT /product= "alpha-2BAR"
FT /note= "sequence is de
FT
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sequence is deleted for a 9 nucleotide polymorphic site found at nucleotides 901-909 of the wildtype alpha-2B α protein (AA199905)." /note=

PN W0200179561-A2.

PD 25-OCT-2001.

17-APR-2001; 2001WO-US12575.

17-APR-2000; 2000US-0551744.

19-OCT-2000; 2000US-0692077.

(LIGG/) LIGGETT S B.
(SMAL/) SMALL K M.

Liggett SB, Small KM;

WPI; 2001-611728/70.
P-PSDB; AAM52118.

genotyping an alpa-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -

Claim 5; Page 144-145; 163pp; English.

The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic

receptor gene (I)-(III) by detecting a polymorphic site, comprising:
(a) obtaining a sample having a polynucleotide encoding an alpha-2B, alpha2A or alpha2C or fragment or complement of; and
(b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (II) or a site comprising (A) (ggggcggggcg) or (B) (gggcgcgtgag) at positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the third intracellular loop of the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide polymorphic site found at nucleotides 901-909 of the wildtype gene (AA199905).

Query Match	33.0%;	Score 446;	DB 23;	Length 1344;
Best Local Similarity	63.4%;	Pred. No. 1.6e-61;		
Matches 835; Conservative	0;	Mismatches 405;	Indels 75;	Score 344;

conservative; Mismatches 405; Indels 76; Gaps 7;

QY 78 CCCTTACTCCCTGCAGGTGACCGCTGGTGTCCTGGCCGGCCTCATGCTGCT 137
||| ||||| ||||| | | | | | | | | |
Db 15 CCCCTACTCCGTGCAGGCCACAGCGCCATAGCGGCGGCCCATCACCTTCCATTTCTCTT 74

QY 138 CACCGTGTGCGCAACGCTGTCGTATCATCGCCGHTTCAGAGCCGCCGCTCAAGGC 197
||| | ||||||||| | ||||||| | ||||||| ||
Db 75 TACCATTCTCGGCAACGCTGTGTCATCCTGGCTGTGTGACCAAGCCGCTGCTGCGGC 134

[illegible]

QY 258 CATCCCTTCTCGCTGCCCAACGAGTTCATGGGCTACTGGTACTTCGSCAAGCCTTGTTG 317
|||||
195 CATCCCTTCTCGCTGCCCAACGAGTTCATGGGCTACTGGTACTTCGSCAAGCCTTGTTG 254
|||||

OY	318	CGAGATCTACCTGGGCGCTCGACGTGCTCTTCCTGCACGTCGTCATCGTGCA	CCTGTGGC	377
Dδ	255	CGAGGTGTACCTGGGCGCTCGACGTGCTCTTCTGCACCTGTCCTGTGTCACCTGTGGC		314

QY 378 CATCAGCCCTGGACCGCTACTGTTCCATCACACAGGCCATCGAGTACAACCTGAAGCGCAC 437
|||||
Ddb 315 CATCAGCCCTGGACCGCTACTGGGCGGTGAGCGCGCGCTGGTGATCAACTCCAAGCGCAC 374
|||||

438 GCCGCGCCGATCAAGCCATCATCAACCGTGTGGTCACTCGCCGTCATCTCTT 497
 |||||
 375 CCGCGCCGATCAAGTGCATCATCTCACTGTGTGGCTATGCGCGGCTATCTGCTT 424
 |||||

[illegible][illegible][illegible]

678 CACCCGCTGCCACCAGCCCGGGGTCCGCAGCCTGCGCGCGCCCGGGGGCAC 737
||| ||| | ||| | | | | | | | |

OY 1270 GTCATCTACACCATCTTCAACACGATTTCCGCCGCTTCAAGAGATCTCTGTCGG 1329
|||||
Db 1293 GTCATCTACACGGTCTTCAACACGATTTCCGGATCTTTAAGCACATCTCTTCCGA 1352
OY 1330 GGGACAGCAGACCGGATC 1347
|||
Db 1353 CGGAGGAGAGGGGCTTC 1370

RESULT 14
AAD04761
ID AAD04761 standard; DNA; 1344 BP.

XX AAD04761;
AC
XX
DT 04-JUL-2001 (first entry)

XX Human alpha2B-adrenoceptor (alpha2B-AR) variant gene.
DE
XX
KW Human; cardiast; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
KW norepinephrine; epinephrine; therapy; vascular contraction; variant;
KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
KW acute myocardial infarction; AMI; Prinzmetal's variant; ds.

XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 1..1344
FT /tag= a
FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
FT variant protein"

XX WO200129082-A1.
PN
XX
XX 26-APR-2001.
PD
XX 20-OCT-2000; 2000WO-FI00913.
PF
XX 22-OCT-1999; 99US-0422985.
PR

XX (JUVA-) JUVANTIA PHARMA LTD OY.
PA
XX
PI Snapir A, Heinoonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
PI Scheinin M, Salonen JT, Tuominen T, Lakka TA, Nyssönen K;
PI Salonen R, Kaunonen J, Valkonen V;
PI
XX WPI: 2001-300318/31.
XX DR P-PSDB; AAE00989.
DR
XX
XX
PT New DNA molecule encoding variant specific adrenoceptor protein with
PT deletion of specific amino acids located in the third intracellular
PT loop of the polypeptide, for treating vascular contraction of coronary
PT arteries -
XX
XX Claim 3; page 24-26; 37pp; English.
PS

XX The present sequence is a gene encoding human alpha2B-adrenoceptor
CC (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat
CC element (amino acids 298-309) of 12 glutamates, in an acidic stretch of
CC 18 amino acids (amino acids 294-311), located in the third intracellular
CC loop of the receptor polypeptide. The variant is obtained by deletion of
CC three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR
CC gene is located on chromosome 2. Alpha2-AR mediate many of the
CC physiological effects of the catecholamines, norepinephrine and
CC epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating
CC a mammal suffering from vascular contraction of coronary arteries and a
CC disease involving vascular contraction of coronary arteries which is
CC clinically expressed as coronary heart disease (CHD), unstable chronic
CC angina pectoris which is clinically expressed as Prinzmetal's variant
CC form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
CC gene therapy.
XX

SQ Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;
Query Match 33.0%; Score 446; DB 22; Length 1344;
Best Local Similarity 62.9%; Pred. No. 1.6e-61;
Matches 827; Conservative 0; Mismatches 415; Indels 72; Gaps 6;

OY 78 CCCTTACTCCCTGCAGGTGACGCTGACGCTGTGTGCTGGCCGCTCATGCTGCT 137
|||
Db 15 CCCCTACTCCGTGCAGGCCACAGCGGCATAGCGGGCCCATCACCTTCTCTCTT 74

OY 138 CACCGTGTGGCAACGTGCTGTCATCATCCGCTGTTCACGAGCCGCGCTCAAGC 197
|||
Db 75 TACCATCTTGGCAACGCTGTGTCATCTGTGTGTGACCAAGCCGCTGCGCGC 134

OY 198 GCCCCAAACCTCTTCTGTGTCTGTGCTGCGCCGACATCTGTGTGCGCATCGT 257
|||
Db 135 CCTCAGAACCTGTCTGTGTGTGCTGCGCCGCGGACATCTGTGTGCGCATCT 194

OY 258 CATCCCTTCTCGCTGGCCACAGAGTCATGGGCTACTGTACTTCCGCAAGCTTGTG 317
|||
Db 195 CATCCCTTCTCGCTGGCCACAGAGTCATGGGCTACTGTGTACTTCCGCGCATGTGTG 254

OY 318 CGAGATCTACCTGGCGCTGCAGCTGTCTTGCACGTCGTCCATCGTGCACCTGTGCGC 377
|||
Db 255 CGAGGTACTCTGGCGCTGCAGCTGTCTTGTGCACCTGTCCATCGTGCACCTGTGCGC 314

OY 378 CATCAGCCCTGACCGCTACTGTGTCATCACACAGGCCATCGAGTACAACCTGAAGCGCAC 437
|||
Db 315 CATCAGCCCTGACCGCTACTGTGTCATCACACAGGCCATCGAGTACAACCTGAAGCGCAC 374

OY 438 GCCCGCGGCATCAAGGCCATCATCATCACCGTGTGGGTCACTCTCGCGCTACCTCTT 497
|||
Db 375 CCCCGCGGCATCAAGGTGATCATCTCTACTGTGTGTGCTCATCGCGCGCTACCTCTT 434

OY 498 CCCCGCGCTCATCTCCATCGAGAGAAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGC 557
|||
Db 435 GCCCGCGCTCATCT-----ACAAGGGCGACCAAGGGCGCGCGCGCGCGCGCGCGC 485

OY 558 GCGCTGCGAGATCAACGACCAAGAGTGTGTCATCTCTGTGTCATCTGCTCTCTCTT 617
|||
Db 486 CCACTGCAAGCTCAACGACGAGGCGCTGTGTATCTTGGCTCCAGCATCGGATCTTCTT 545

OY 618 CGCTCCCTGCTCATCATGATCTGTGTCTACGTGCGCATCTTACCAATCGCCAAAGCTTCG 677
|||
Db 546 TGTCTCTGCTCATCATGATCTTGTGTCTTACCTGCGCATCTTACCTGCGCCAAACGACG 605

OY 678 CACCCGCGTGCCACCCA-----GCCCGCGGTGCCGGAACGCCGCTG 718
|||
Db 606 CAACCGCAGAGTCCCAAGGCCAAGGGGGGCTGTGGGCAAGGTGAGTCCAAAGCAAGCCCCG 665

OY 719 CCGCGCGCGCGGGG-----CACCGAGCGCAGGCCCAAGGCTCTGG 760
|||
Db 666 ACCCGACCATGTGTGGGCTTGGCTTCAGCCAAACTGCGCAGCCCTGCTGTGCTTC 725

OY 761 GCCCGAGCGCAGCGCGGGCGCGG-----GGCGCAGAGGCCGAACGCTGCCAC 812
|||
Db 726 TGCCAGAGAGTCAACGACACTCGAAGTCCACTGGGGAGAAGAGAGGAGAGAACCC 785

OY 813 CCAGCTCAACGCGCCCTGTGGCGAGCCCGCGCGCGCGCGCGCGCGCGCGCACAGCGCT 872
|||
Db 786 TGAAGATACGTGGACCCCGGCTTGGCCACCAAGTTGGGCTGCCCTTCCCACTCAGGCCA 845

OY 873 GGACCTGAGAGAGCTGCTTTCGACCAAGCGCGCAGCGCGCGCTCCAGGGCCCGCAGACC 932
|||
Db 846 GGGCCAGAGAGGAGGTGTTTGTGGGCACTCCAGAGAGATGAAGCTGAAGAGAGAGAAGA 905

OY 933 CGAGCGGTCCCGGGGCAAGGCAAGGCCCGAGCGAGCGCAAGTGAAGCCGGGCGACAG 992
|||
Db 906 GAGAGAGAGAGATGTGAACCCAGAGAGTGCAGAGTGTTCGGGCTCAGCTTGCACGCC 965

OY 993 CTTGCCGCGCGCGCGCGCGCGCGAGCGAGCGCGGATCGGACGCGCGCTGCAGGGCGCGGGA 1052
|||
Db 966 CCGGCTGACGACGACAGAGGCTCCCGGCTGTGGCCACCCCTACGTGCGCAGGTGCTCT 1025

AA064890
ID AA064890 standard; DNA; 1382 BP.
XX
AC AA064890;
XX
DT 01-FEB-1995 (first entry)
XX
DE Human derived adrenalina alpha 2CII receptor DNA.
XX
KW adrenalina receptor; alpha CII; screening; detection; pharmacology;
KW drugs; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..2
FT /tag= a
FT /note= "5'-non translated region"
FT CDS 3..1376
FT /tag= b
FT /product= adrenalina alpha CII receptor
FT misc_feature 3..5
FT /tag= b
FT /note= "encodes Met; this codon may or may not be present, but can only be present if nucleotides 6-53 are also present"
FT misc_feature 6..53
FT /tag= c
FT /note= "this sequence may or may not be present"
FT 3'UTR 1377..1382
FT /tag= c
FT /note= "3'-non-translated region"
PN JP06121686-A.
XX
PD 06-MAY-1994.
XX
PF 12-OCT-1992; 92JP-0272744.
XX
PR 12-OCT-1992; 92JP-0272744.
XX
PA (ASAH) ASAH I KASEI KOGYO KK.
XX
DR WPI; 1994-185923/23.
DR P-PSDB; AAR54834.
XX
PT Adrenaline receptor gene encoding alpha 2CII receptor - for
PT screening drugs reactive to the alpha 2CII receptor
XX
PS Claim 1; Page 9-11; 13pp; Japanese.
XX
CC This sequence encodes the amino acid sequence of a polypeptide
CC (AAR54834) that constitutes human derived adrenalina alpha 2CII
CC receptor. this can be used for the study of the pharmacological
CC importance of the gene expression in humans.
XX
SQ Sequence 1382 BP; 165 A; 480 C; 497 G; 240 T; 0 other;

Query Match 38.0%; Score 512.4; DB 15; Length 1382;
Best Local Similarity 64.7%; Pred. No. 6.3e-72;
Matches 866; Conservative 0; Mismatches 421; Indels 51; Gaps 5;

QY 199 CCCC AAAACCTCTTCGTGTCCTTGCCCTGGCCGACATCCTGGTGCCACGCTGTC 258
DB 255 CCAAGAAACCTCTTCGTGTCCTTGCCCTGGCCGACATCCTGGTGCCACGCTGTC 314
QY 259 ATCCCTTTCGCTGGCCAAACGAGGTGATGGGCTACTGTACTTGGCAAGGCTGGTGC 318
DB 315 ATGCCCTTCTCGTTGGCCAAACGAGCTCATGGCCCTACTGTACTTGGGAGGTGGTGC 374
QY 319 GAGATCTACCTGGCCCTCGACGTGCTCTCTGACAGCTGTCATGTCGACCTGTGGCC 378
DB 375 GCGGTGTACCTGGCCCTCGATGTGCTGTTTGCACCTGTCGATGTCGATGTCGTGC 434
QY 379 ATCAGCCTGACCCGCTACTGTGTCATCACAGGCCATCGATACACCTGAAGCCACG 438
DB 435 ATCAGCCTGACCCGCTACTGTGTCGACGAGCCGCTCGATACACCTGAAGCCACA 494
QY 439 CCGCGCCGATCAAGGCCATCATCATCAGCTGTGGTCACTCGCCGTCATCTCCTTC 498
DB 495 CCACGCCGCTCAAGGCCACCATGTCGTCGTCATCTCGCCGTCATCTCCTTC 554
QY 499 CCGCGCTCATCTCCATCGAGAAAGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 558
DB 555 CCGCGCTGTGCTCTGCTTACCGCCAGCCGACGCGGCGGCGGCGGCGGCGGCGGCGG 602
QY 559 CGTGGGATCAACGACGACGAGAGTGTACGTATCTGTCATCTGTCATCGGCTCTTC 618
DB 603 CAGTGGGCTCAACGACGACGAGCCTGTATCATCTGTCCTCTCATCGGCTCTCTTC 662
QY 619 GCTCCCTGCTCATCATGATCTGTCATGTCGTCATGTCGTCATGTCGTCATGTCGTC 678
DB 663 GCGCCCTGCTCATCATGAGGCTGTCATGTCGTCATGTCGTCATGTCGTCATGTCGTC 722
QY 679 ACCCGGTCACACCCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 738
DB 723 ACCGTCACGCTCAGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 782
QY 739 GAGCGCAGGCCCAAGGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 798
DB 783 GA-----AAACGGGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 824
QY 799 GAACCGCTGCCACCCAGCTCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 858
DB 825 -----CACTGCG 880
QY 859 GACACCGACGCGCTGAGCCTGAGAGAGCTGCTTCCGACACGCGCGCGCGCGCGCTCA 918
DB 881 GAGCG 940
QY 919 GGGCGCGCAGACCCGAGCGCGGTCCCGGGGCAAGGCAAGCGCCGAGCGCAGGTG 978
DB 941 GGGCGCGCGCGGTGCGAGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1000
QY 979 AAGCGGCGCAGACCTGCT 1038
DB 1001 GTCCCGCGCGCGCGGTGCGCGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1060
QY 1039 GCAGGCGCGCGGAGAGCGCGGTGGGCGCTGCCAAGCGCTCGCGTGGCGCGCGCGCG 1098
DB 1061 GTCGCGCGG-----GCG 1112
QY 1099 AACCGGAGAAAGCGCTCATCGTTCGTGCGCGCGCTGATCGAGTGTGCTGCTGC 1158
DB 1113 GCGCGGAGAAAGCGCTCATCGTTCGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1172
QY 1159 TGGTCCCTTCTTCTTACCTACACGCTCACGCGCTC-----GGGTGCTCGCTG 1209
DB 1173 TGGTCCCTTCTTCTTACCTACACGCTTGTGCTGCGCGCGCGCGCGCGCGCGCGCG 1232
QY 1210 CCACGACGCTCTTCAATCTTCTTGTGTCGCGCTACTGCAACAGCTCGTTGAACCG 1269
DB 1233 CCGGCGCGCGCTCTTCAAGTCTTCTTGTGATCGGCTACTGCAACAGCTCGCTCAACCG 1292

PF 17-APR-2001; 2001WO-US12575.
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI: 2001-611728/70.
DR P-PSDB: AAM52126.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
PS Claim 103; Page 158; 163pp; English.

xx The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising:
cc (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
cc alpha2A or alpha2C or fragment or complement of; and
cc (b) detecting a polymorphic site comprising nucleotide positions 901-909
cc of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
cc or a site comprising (A) (ggggcgggcg) or (B) (gggcgcgtg) at
cc positions 961-972 of (III). The method may be used for genotyping an
cc alpha2B, alpha2A or alpha2C receptor gene and further used to determine
cc whether an individual is at increased risk of developing a disease
cc associated with alpha2B, alpha2A or alpha2, comprising detecting a
cc polymorphic site which correlate to disease selected from cardiovascular
cc disease, central nervous system disease and combinations of these. In
cc addition, the technique may be used to predict an individual's response
cc to an alpha2B, alpha2A, or alpha2C agonist (e.g. ephedrine,
cc norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
cc combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
cc rauwolfine, idazoxan, tolazoline, phentolamine and combinations of
cc these) by detecting the polymorphic site and correlating the site to a
cc predetermined response (where the response is correlated to adenylyl
cc cyclase, MAP kinase activity, phosphorylation or inositol phosphate
cc levels). The present sequence is that of the human alpha-2CAR variant,
cc the sequence is deleted for a 12 nucleotide polymorphic site at
cc nucleotides 961-972 of the wildtype gene (AI199931).

Sequence 1371 BP; 164 A; 479 C; 491 G; 237 T; 0 other; XX SO

Overall Match 38.28; Score 516; DB 23; Length 1371;

Best Local Similarity	64.98;	Pred. No. 1./e-12;
Matches	860;	Conservative
Mismatches	415;	Indels
Gaps	54;	Gaps
	5;	

[illegible][illegible]

RESULT 13

CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2CAR, the
CC sequence includes a 12 nucleotide polymorphic site at nucleotides
CC 961-972, absent in the alpha-2CAR variant (AAI99933).

XX Sequence 1383 BP; 164 A; 482 C; 500 G; 237 T; 0 other;

Query Match 39.2%; Score 529; DB 23; Length 1383;
Best Local Similarity 65.3%; Pred. No. 1.6e-74;
Matches 875; Conservative 0; Mismatches 420; Indels 44; Gaps 5;

QY 19 GACGGGGCAACGGGAGCTGGAGAGGAGCGCGGGGGGGCGCCCGGGGCAAC 78
Db 73 GAGAGGGGACGGCGGGGGTTCGCAATGCTCGGGGCTTCCTGGGGCGCGCGGGC 132
QY 79 CCTTACTCCCTGAGGTGACGCTGACGCTGTGTGCTGCTGGCGCGCTGCTCATGCTGCTC 138
Db 133 CAGTACTCGGGGGGGCGGGTGGCAGGGGCTGGCTGCGGTGTGGGCTTCCTCATGCTTTC 192
QY 139 ACCGTGTCCGGCAACGTGCTCGTCATCATCGCCGTGTTCACGAGCGCGCGCTCAAGCG 198
Db 193 ACCGTGTGGGGCAACGTGCTGTGTGTGATCGCCGTGTGACAGCGCGGGCGCTGCGCGG 252
QY 199 CCCCAGAACTCTTCTCTGTGTCTGTGGCCTCGCGGACATCCTGTGGGCAACGCTGTC 258
Db 253 CCACAGAACTCTTCTCTGT 312
QY 259 ATCCCTTCTCGCTGGGCAAGGCTCATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 318
Db 313 ATGCCCTTCTCGTGTGGCAAGGCTCATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372
QY 319 GAGATCTACCTGGGCTGACGCTGCTCTTCTGACAGCTGCTCCATGCTGACCTGTGCGCC 378
Db 373 GCGGTGTACCTGGCGCTGATGTGCTGTTTGCACCTCGTCGATCGTGTGTC 432
QY 379 ATCAGCCTGACCGCTACTGTCCATCACAGGCGCATGAGTACAACTGAAGCGCAGC 438
Db 433 ATCAGCCTGACCGCTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 492
QY 439 CCGCGCGCATCAAGGCGCATCATCAACGCTGTGGGTATCTGCGCCGTCATCTCTTC 498
Db 493 CCACGCGCGCTCAAGGCGCATCATCGCGCTGTGGTCTCATCTCGCCGTCATCTCTTC 552
QY 499 CCGCGCGCTCATCTCCATCGAGAAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 558
Db 553 CCGCGCGCTGTCTGCTCTTACCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 559 CGCTGGAGATCAAGCAGACGAGAGTGTATGTCATCTGCTGTGTCATGCGGCTCTCTTC 618
Db 601 CAGTGGCGGCTCAAGCAGAGACCTGTATCATCTCTCTCTCTCTCTCTCTCTCTCTCTTC 660
QY 619 GCTCCCTGCTCATGATGATCTGTGTATGCTGCGCATCTACAGATCGCGCAAGCTGCGC 678
Db 661 GCGCCTGCTCATGATGCGGCTGTATGCGCGCATCTACCGAGTGGCCAAAGCTGCGC 720
QY 679 ACCCGGTGCAACCCAGCGCGGGGTCCGGACGCGCTGCGCGCGCGCGCGCGGGGGGACC 738
Db 721 ACGCGACGCTCAGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 739 GAGCGAGGCGCCAAAGGTGTGTGGCGCCCGAGCGCAGCGCGCGCGCGCGCGCGCGCG 798

Db 781 GAAACGGGCTGCGCGCGCGCGGACAGGCGAGCGAGAACGGGCACTGCGCGC----- 831
QY 799 GAACCGCTGCCACCCAGCTCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 857
Db 832 -----CCCG 883
QY 858 CGACACCGAGCGCTGACCTGAGAGAGAGCTGCTTCCACCAACGCCGAGCGGCTTC 917
Db 884 GCG 943
QY 918 AGGCG 977
Db 944 GCGGTGCGGAGCG 1003
QY 978 GAAGCG 1037
Db 1004 CAGGTCCCG 1063
QY 1038 TGCAGGGCG 1097
Db 1064 TCCTGTGCG 1118
QY 1098 GAACCGCGAGAGCGCTTCAAGTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1157
Db 1119 GCGCGCGAGAGAGCGCTTCAAGTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCG 1178
QY 1158 CTGGTCCCTCTTCTTCACTACCTACAGCGCTCAGCGCGCTC-----GGGTGCTCGT 1208
Db 1179 CTGGTCCCTCTTCTTCACTACCTACAGCGCTCAGCGCGCTCAGCGCGCTCAGG 1238
QY 1209 GCCAGCGACGCTCTTCAATCTTCTTGTGTGCGCTGCTGCTGCTGCTGCTGCTG 1268
Db 1239 GCGCGCGCGCGCTCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1298
QY 1269 GGTCACTTACACCATCTTCAACCAAGATTCGCGCGCGCGCGCGCGCGCGCGCG 1328
Db 1299 GGTCACTTACACCATCTTCAACCAAGATTCGCGCGCGCGCGCGCGCGCGCGCG 1358
QY 1329 GGGGACAGAGAGCGGATC 1347
Db 1359 ACGGAGAGAGAGGCGCTTC 1377

RESULT 12
AAI99933
ID AAI99933 standard; DNA; 1371 BP.

XX AC AAI99933;

DT 18-FEB-2002 (first entry)

XX Human alpha-2CAR variant encoding DNA.

DE Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2CAR; chromosome 4; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 1..1371

FT /tag= a
FT /product= "alpha-2CAR"
FT /note= "sequence is deleted for a 12 nucleotide
polymorphic site at nucleotides 961-972 of the
wildtype sequence (AAI99931)"

XX WO200179561-A2.

XX 25-OCT-2001.

XX

QY 61 GCGCGCGCGCGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCC 120
Db 5061 GCGCGCGCTTCGGGTATTTTATTTTGTAGGTGACGTTGACGTTGGTGTGGT 5120
QY 121 GGCCTGCTCATGCTGCTCACCCTGTTCGGCAAGCTGCTGTCATCATCGCCGTGTCACG 180
Db 5121 GGTGTGTTATGTTGTTATCGTGTTCGGTAACGTTGTTATATCGTCGTGTTACG 5180
QY 181 AGCGCGCGCTCAAGGCGCCCAAAACCTCTTCCTGGTGTCTCTGGCCTCGCCGACATC 240
Db 5181 AGTCGCGCGTTTAAGCGCTTTTAAATTTTGTGGTGTGTTGGTTCCGTCGATAT 5240
QY 241 CTGGTGGCCACGCTCGTCATCCCTTCTCGCTGGCCAAAGAGTCAATGGGCTACTGTAC 300
Db 5241 TTGGTGGTTACGTTGTTATTTTTCGTTGGTTAACGAGTTATGGGTTATTGGTAT 5300
QY 301 TTCGGCAAGGCTTGTTGCGAGATCTACCTGGCGCTCAGCTGCTCTTCGACGTCGCC 360
Db 5301 TTCGGTAAGGTTTGGTGCAGATTTATTTGGCGTTCAGCTGTTTTCGACGCTGTT 5360
QY 361 ATCGTGCACCTGTGCGCCATCAGCCTGACCGCTACTGTCATCACAACAGGCCATCGAG 420
Db 5361 ATCGTGTATTTGTCGTTATTTAGTTGATCGTTATGTTTATATAGTTATCGAG 5420
QY 421 TACAACCTGAAGCGCACGCGCGCCGCATCAAGGCCATCATCACCGTGTGGTCAATC 480
Db 5421 TATATTTGAACGCTACGTCGCGCTCGTATTAAGTTATTTATATATCGTGGGTTAT 5480
QY 481 TCGCGCGTCAATCTCTTCCGCGCTCATCTCCATCGAGAAGAGGCGCGCGCGCGC 540
Db 5481 TCGGTCGTTATTTTTCGTCGTTATTTTATCGAGAAGAGGCGCGCGCGCGGT 5540
QY 541 CCGCAGCGCGCGCGCGCGCTGCGAGATCAACGACCGCGCGCGGTCCGGAACGCCGTCGC 600
Db 5541 TCGTAGTCGGTCGAGTCGCGTTCGAGATTAACGATTAGAAGTGTACGTTATTCGTCG 5600
QY 601 TGCATCGGCTCTTCTTCCGCTCCCTGCTCATCATGATCCTGGTCTACGTGCGCATCTAC 660
Db 5601 TGTATCGGTTTTCGTTTTCGTTTATGATTTTGGTTTACGTTGCGTATTTAT 5660
QY 661 CAGATCGCCAAAGCTCGCACCCGCGTGCACACCGCGCGCGGTCCGGAACGCCGTCGCC 720
Db 5661 TAGATCGTTAAGCGTCGTAATCGCGTGTATTTAGTCTCGGGGTCGGAACGTCGTCG 5720
QY 721 GCGCGCGCGCGCGCACCGCAGCGCCCAAGGGTCTGGCCCCGAGCGCAGCGCGCGGC 780
Db 5721 GCGTCGTCGGGGGTATCGACGCTAGGTTTAAACGTTTGGGTTTCGACGCTAGCGCGGT 5780
QY 781 CCGGGGGCGCAGAGCGCAACCGCTGCCACCACTCAACGCGCGCCCTGGCGAGGCC 840
Db 5781 TCGGGGGCGTAGAGTCGAATCGTTGTTATTTAAGTTTAAAGGCTTTTGGCGAGTTC 5840
QY 841 GCGCGCGCGCGCGCGCAGACCGCGCTGACCTGAGAGAGAGAGCTGCTTCCGAC 900
Db 5841 GCGTCGGTCGGGTGCGCGATATCGACGCGTGTGATTTGAGAGAGAGTTCGTTTTCGAT 5900
QY 901 CACGCCGAGCGCCTCCAGGCGCCGACAGCCGAGCGCGGTCCCGGGGCAAGGCAAG 960
Db 5901 TACGTCGAGCGGTTTAAAGGTTTCGTAAGATTCGAGCGCGGTTTTCGGGTTAAAGTTAAG 5960
QY 961 GCGCGAGCGCAGGTGAAGCGCGCGCAGACCTGCCGCGCGCGCGCGCGCGCGAGC 1020
Db 5961 GTTCGAGCGAGTTAAGTGAAGTCGGGCGATAGTTGTGCGCGCGCGGTTCGGGCGCAGC 6020
QY 1021 GGGATCGGAGCGCGCTGCAGGGCGCGGGGAGAGCGCGCTCGCAAGCGCTCG 1080
Db 6021 GGGATCGGAGCGCTGTTAGGGTTCGAGGTCGGGGAAGAGCGCGCTGTTTAAAGCGTCG 6080
QY 1081 CGCTGGCGCGCGCGCAGAACCGCGAGAGCGCTTACGTTGCTGTGGCGCTGATC 1140
Db 6081 CGTTGGCGCGCGCGGTAGATCGCGAGAACGTTTACGTTGCTGTGCTGATATC 6140
QY 1141 GGAGTGTTCGTGTGCTGTTCCCTCTTCTTACCTACACGCTCACGGCGTCGGG 1200

Db 6141 GGAGTGTTCGTGTGCTGTTGTTTTCGTTTATTAATACGTTACGTCGTCGGG 6200
QY 1201 TGCTCCGTCGACGACGCTCTTCAATCTCTCTGCTCGGCTACTGCAACAGCTCG 1260
Db 6201 TGTTCGTGTACGTAACGTTTTCGTTTAAATTTTTCGTTGTTGTTAATAGTTTCG 6260
QY 1261 TTGAACCGGTCATCTACACCATCTTCAACACGATTTCCGCGCGCTTCAAGAGATC 1320
Db 6261 TTGAATTCGTTATTTATATTTATTTTAAATTCAGATTTTCGTCGCGTTTAAAGAGATT 6320
QY 1321 CTCTGTGGGGGAGCAGGAAGCGGATCGTG 1350
Db 6321 TTTTGTGGGGGAGTAGGAACCGGATCGTG 6350

RESULT 11
AAI99931
ID AAI99931 standard; DNA; 1383 BP.
XX
AC AAI99931;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2CAR encoding DNA.
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2CAR; chromosome 4; ds.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT CDS 1..1386
FT /*tag= a
FT /product= "alpha-2CAR"
FT /note= "sequence includes a 12 nucleotide polymorphic
FT site at nucleotides 961-972 absent in the
FT alpha-2CAR variant (AAI99933)"
XX
PN WO200179561-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001MO-US12575.
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGETT S B.
PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
DR P-PSDB; AAM52124.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
PS Example 15; Page 157; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (999gcyggyccg) or (B) (999gcygctgag) at

QY	181	AGCGCGCGCTCAAGGCGCCCCA	AAACCTCTTCTCGGTGTCCTG	GGCTTCGCGCCGACATC	240
Db	5181	AGTCGCGCGTTTAAAGCGCTTTT	AAAAATTTTTTTTGGTGTCTTT	TGGTTCGGTCGATATT	5240
QY	241	CTGTGGCCACGCTCGTCATCCCT	TTTCTCGCTGGCCAACGAGGTC	ATGGGCTACTGTGTAC	300
Db	5241	TTGGTGGTTACGTTCTGTTATTT	TTTTTTCGTTGGTTAACGAGG	TTATGGGTTATTGGTAT	5300
QY	301	TTGCGCAGGCTTGGTGGAGATCT	ACCTGGCGCTCGACGTGCTCTC	TGACAGTGTCC	360
Db	5301	TTGCGTAAGGTTTGGTGGAGATT	TATTTGGCGCTTCAGCGTGT	TTTTTTTGTACGTGTTT	5360
QY	361	ATCGTCACCTGTGGCCATCAGCCT	GGACCGCTACTGGTCCATCAC	ACAGGCCATCGAG	420
Db	5361	ATCGTGTATTGTGCGTTATTAGT	TTGGATCGTTATTGGTTATT	ATATAGGTTATCGAG	5420
QY	421	TACAACCTGAAGCGCACCGCCCG	CGCGCATCAAGGCCATCATCAC	CGGTGGGTATC	480
Db	5421	TATAATTGGAAGCGTACGTCGCG	TGATTAAGGTTATTATATATC	GTGTGGTTATT	5480
QY	481	TCGGCCGTCATCTCTCCCGCGT	CATCTCCATCGAGAAAGAGGG	CGGCGCGCGCC	540
Db	5481	TCGGTCTGTTATTTTTTTTTT	TCGTGTTATTATTATCGAGAA	AGAGGGCGGCGGGGT	5540
QY	541	CCGCAGCCGGCCGACGCCGCGCT	GCAGATCAACGACAGAACTGGT	TACGTATCTGTCG	600
Db	5541	TCGTAGTCGGTCGAGTCGCGT	TCGAGATTAAAGATTAGAGT	GTGCTATTTCTCG	5600
QY	601	TGCATCGGCTCTTCTCTGCTCC	TGCTCATCATGATCCGTGCTAC	GTGCGCATCTAC	660
Db	5601	TGTATCGGTTTTTTTTTTTT	TCGTTTGTATTATGATTTT	GGTTACGTGCGTATTAT	5660
QY	661	CAGATCGCCAAAGCGTCGACACC	CGCGTGCCACACGACCGCGGG	GTCGAGACCGCTCGCC	720
Db	5661	TAGATCGTTAAGCGTCGATTCC	GTGTTATTAGTCTCGGGGTTC	GACGTCGCTC	5720
QY	721	GCGCGCGCGGGGGCACCCGAG	CGGAGGCCCAAGGCTGGGGCCC	CGAGCGCAGCGGGC	780
Db	5721	GCGTCGTCGGGGGGTATCGAG	CGCTAAGGTTAACGGTTTGG	CTTCAGCGTAAGCGGGT	5780
QY	781	CCGGGGGGCGCAGAGCGCGAAC	CGCGCTGCCACCAAGCTCAAC	GCGCGCCCTGGCGAGCCC	840
Db	5781	TCGGGGCGGTAGAGTGAATCG	TGTTTATTAGTTTAACGCG	CTTTTGGCGAGTTTC	5840
QY	841	GCGCGCGCGCGCGCGCGAC	ACCGACGCGCTGCACTGGAG	GAGAGCTGCTCTTCGAC	900
Db	5841	GCGTCGTCGGGTGCGCGCAT	TATCGACGCGTGGATTGGAG	GAGAGCTGTTTTTCGAT	5900
QY	901	CACGCGCAGCGCGCTCAAGG	CCCCCGACAGCCGAGCGCGGT	CCCCGGGGCAAGCGAAG	960
Db	5901	TACGTCGAGCGGTTTTTAC	GGTTTTCTGATGATTCAGCG	CGGTTTTTCGGGGTAAAGCTAAG	5960
QY	961	GCCCCAGCGCAGCCAGTTAA	AGCCGGGGCGACAAGCTCC	CGCGCGCGGGCGGGGCGAGC	1020
Db	5961	GTTCCGAGCGAGTTAGGTGA	AGTCCGGCGATAGTTGTCC	GCGCGCGCTCGGGGCGAGC	6020
QY	1021	GCGATCGGAGCGCCGCGCT	GCAGGGCCGGGGAGAGCGCT	CGGGGCTGCCAAGCGCTGC	1080
Db	6021	GGGATCGGAGCGTGGGTTG	AGGTCGGGGAGAGAGCGCT	CGGGGTTGTTAAAGCGCTGC	6080
QY	1081	CGCTGGCGCGGGCGCAGA	ACCGCGAGAGCGCTTACGTT	CGTGTGCTGGCCGTGCTATC	1140
Db	6081	CGTTGGCGCGGGCGGTAGA	ATCGCGAGACGTTTACGTT	CGTGTGCTGCTGTTATC	6140
QY	1141	GGAGTGTCTGTGTGTGCT	GTTCCCTTCTTCACTACAT	CAGCTCACAGCGCGCTCGGG	1200
Db	6141	GGAGTGTCTGTGTGTGTT	TTTTTTTTTTTATTATAC	GTTTACGCTTACGCTCGGG	6200
QY	1201	TGCTCCGTGCGCAGCAGC	GCCTCTTCAAAATCTTCT	TCTGTGCTTGGCTACTGCA	ACAGCTCG 1260
Db	6201	TGTTTCGTGTACGTACG	TTTTTTTAAATTTTTTTT	TTTTCGTTATTTGTTAT	TGTTATAGTTCG 6260

[illegible]

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RESULT 10
AAD28362
ID      AAD28362 standard; DNA; 7353 BP.

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AC	AAD28362;
XX	
DT	22-APR-2002 (first entry)

Human chemically treated genomic DNA #3.

KW Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;
 KW adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
 KW behavioural disorder; neurological; psychiatric; cancer; schizophrenia;
 KW Tourette's syndrome; smoking; human immunodeficiency virus dementia;
 KW drug abuse; migraine; ds.

OS Homo sapiens.

PN W0200202809-A2.

PD 10-JAN-2002.

PF 02-JUL-2001; 2001WO-EP07540.

PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.

PA (EPIC-) EPIGENOMICS AG.

P1 Olek A, Piepenbrock C, Berlin K;

DR WPI; 2002-154759/20.

PT Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT gene -

PS Claim 1; Page 32-36; 190pp; English.

The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also relates to oligonucleotides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pretreated DNA is useful for the diagnosis or therapy of behavioural disorders, neurological disorders and cancer, in particular major depressive disorder, Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, drug abuse, alcoholism, personality traits, compulsive gambling, human immunodeficiency virus dementia, migraine, behaviours in schizophrenic and schizoaffective patients, and suicidal behaviour in patients with schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPs). The present sequence is human chemically treated genomic DNA.

Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;

Query Match

Matches 1029; Conservative 0; Mismatches 321; Indels 0.

Matches 1029; conservative 0; Mismatches 321; Indels 0; Gaps 0;

QY 1 ATGGGCTCCCTTCAGCCCGGACCGCGCAACGCAGCTGGAAACGGACCGAGCCCCGGG 60
||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5001 ATGGGTTTTGTAGTCGGACCGCGGTAAACGCAGTTTGAAACGGGATCAGGCGCTCGGG 5060

OY 241 CTGTGGCCACGCTCGTCATCCCTTCTCCTGGCCACAGAGTCATGGGCTACTGTAC 300
11111 111 1111 11 111111 111111 11111 111111
Db 1233 TTGGTGGTTACGTTCTGTTATTTTTTTTTCGTTGCTTAACGAGGTATGGTTATGGTAT 1174
OY 301 TTGGCAGAGCTTGGTGCAGATCTACCTGGCCCTCGACGTCTCTTCTGACGTCGCC 360
11111 1111 111111111111 11 1111 11111111 11 11 111111
Db 1173 TTGGTAAAGTTTGGTGCAGATTTAFTTGGCCCTTCGACGTCTTTTTTTGTACGTCGTT 1114
OY 361 ATGTCACCTTGTGCGCCATCAGACCTTGACCGCTACTGCTCCATCAGAGCCATCGAG 420
111111 1 11111 11 11 111111 11 11 1111 11 11 1111
Db 1113 ATGTTATTTGTGCGTTATTTAGTTTGATCGTTATGCTTTATATATAGGTTATCGAG 1054
OY 421 TACAACCTGAAGCCGACGCGCGCCGATCAAGGCCATCATCATCACCGTGGGTATC 480
11 11 11111111 11 1111 11 1111 11 11 11 11111111 11
Db 1053 TATAATTGAAGCGTACGTCGCGTCGTATTAAGGTTATTTATATATATATATATATAT 994
OY 481 TCGCCGTCATCTCTCCGCGCTCATCTCCATCGAGAGAAGGGCGCGCGCGCGC 540
1111 111 11 11 11 11 11 11 11 1111111111111111111111
Db 993 TCGTCGTTATTTTTTTTTCGTCGTTATTTTATCGAAGAAGGGCGCGCGCGCT 934
OY 541 CCGCAGCCGGCCGAGCCGCGCTGCGAGATCAACGACAGAGTGTACGTATCTGTCG 600
11 11 11 1111 1111 11111111 1111 111111111111 11 11111
Db 933 TCGTAGTCGGTCGAGTCGCGTGGCAGATTAACGATTAGAGTGTACGTTATTTCTGTCG 874
OY 601 TGCATCGGCTCTCTTCTGCTCCCTGCTCATCATGATCTGCTTACGTGCGCATCTAC 660
11 11111 1 11 1111 1 11 111111 1111 11111111 11 11
Db 873 TGTATCGGTTTTTTTTTTCGTTTGTGTTTATGATTTTGTGTTTACGTGCGTATTTAT 814
OY 661 CAGATCGCCACAGCTCGCACCCGCGCTGCCACCCAGCCGCGCGCTCCGAGCCGTCGCC 720
11111 11111111 1 11111 1 11 11 111111 11111 11111 11111
Db 813 TAGATCGTTAAGCTCGTATTCGCGTGTATTTAGTCGTCGGGCTTCGAGCTCGTCGTC 754
OY 721 GCGCCGCGCGGGGCGACCGAGCGCAGGCCAAGGCTTGGGCCCGAGCGAGCGCGGC 780
111 11 111111 1 11111 11 11 111 1111 11111 111111
Db 753 GCGTCGTCGGGGGTATCGAGCGTAAAGGTTTGGTTTCGAGCGTAGCGCGGT 694
OY 781 CCGGGGGGGCGAGAGCCGCAACCGCTGCCACCCAGCTCAACGGCGCCCTGCGAGCCC 840
11111111 11111 1111 11 11 11 111111 111111 111111 1
Db 693 TCGGGGGGGCGTAGAGTCGAATCGTGTATTTAGTTTAAACGGCGTTTTCGCGAGTTC 634
OY 841 GCGCCGCGCGGGCGCGCGCAGACCGCGCTGGAACCTGAGAGAGACTGCTTCCGAC 900
111 111 111 111111 1 111111 1111 11111111 1111 11 111
Db 633 GCGTCGTCGGGTCCGCGCATATCGACCGCTTGATTTGAGAGAGAGTTCGTTTTCGAT 574
OY 901 CACGCGGAGCGGCTCCAGGCGCCCGCAGACCCGAGCGCGGTCCCGCGGCGCAAGCAAG 960
111 111111 1 1111 11 111 11111111 11111 11111 111
Db 573 TACGTCGAGCGGTTTTTAAAGGTTTCGTAGATTCGAGCGCGGTTTTCCGGGTAAGTAAG 514
OY 961 GCGCGAGCGAGCCAGGTGAAGCCGGGCGACAGCCCTGCGCGCGCGCGCGCGGGCGAGC 1020
1 1111111 1111111 111111 11 11 11111111 11111111
Db 513 GTTCGAGCGAGTTAGGTGAAGTCGGGCGATAGTTGTCGGCGCGCGGTGCGGGCGAGC 454
OY 1021 GGGATCGGGAGCGCGGCTGCAAGGGCGCGGGGAGAGAGCGCGTGGGGCTGCCAAGCGCTG 1080
1111111111 11 11 1111 111111111111111111 11 1111111
Db 453 GGGATCGGGAGCGTGGTTGTAAGGGTCCGGGGAGAGCGCGTCCGGGTTGTTAAGCGCTG 394
OY 1081 CGCTGCGCGCGGGCGGAGAACCGCGGAGAGCGCTTCACGTTCTGCTGCGCGCTGCTATC 1140
11 1111111111 1111 1111111111 11 11111111 11 11111 111
Db 393 CGTTGCGCGGGCGGTAGAAATCGCGAAGCGTTTACGTTTCGTTGCTGCTGCTATC 334
OY 1141 GGAGTGTCTGTGTGTGTGCTGCTCCCTTCTTCTTCACTACAGCTCACGCGCTCGGG 1200
11111111111111 11111 11 11 11 11 11 11 1111 111111
Db 333 GGAGTGTCTGTGTGTGTGCTGCTTTTCTTTTATTTATACGTTTACGCTGCTCGGG 274
OY 1201 TGCTCGTGCACGACGCTCTTCAAAATCTTCTTCTGCTTGGCTACTGCAACAGCTCG 1260
11 1111 1111 1111 11 11 1111 11 11 111111 11 11 111
Db 273 TGTTCGTGTACGTACGTTTAAATTTTCTTTGCTCGGTATTTGTAATAGTTCG 214
OY 1261 TTGAACCGGTCATCTACACCATCTTCAACACGATTCGCGCGCTTCAGAGAAGATC 1320
11111 1111 11 11 11 11 11 11111 11 1111 11 1111111
Db 213 TTGAATTCGGTATTTATATATATTTTAAATTACGATTTTCGCGCTTTTAAAGAAGATT 154

OY 1321 CTCTGTGCGGGGACAGGAAGCGGATCGTG 1350
1 1111111111 1111111111111111
Db 153 TTTTGTGCGGGGAGTAGGAAGCGGATCGTG 124
RESULT 9
ABL32072
ID ABL32072 standard; DNA; 7353 BP.
XX
AC ABL32072;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 45.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; anti-naemic; cytosolic; neurotropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Plepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
PS Claim 1; SEQ ID NO 45; 32bp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;
Query Match 62.0%; Score 836.4; DB 24; Length 7353;
Best Local Similarity 76.2%; Pred. No. 1.1e-122;
Matches 1029; Conservative 0; Mismatches 321; Indels 0; Gaps 0;

QY 421 TACACCTGAAGCGCACGCCGCCGCATCAAGCCATCATCATCACCGTGTGGTCAATC 480
Db 681 TATAATTTGAAGCGTACGTCGCCGCTGATTAAGGTTATTTATTTATCGTGGGTTATT 740
QY 481 TCGGCCGTCACTCTCTCCCGCCGCTCATCTCCATCGAAGAAAGGCGCGCGCGCGC 540
Db 741 TCGGTCGTATTTTTCGTCGTTTATTTTATCGAAGAAAGGCGCGCGCGCGCGT 800
QY 541 CCGACGCCGCCGACGCCGCGCTGGAGATCAACGACGAAAGTGATCATCTCGTCG 600
Db 801 TCGTAGTCGCTCGAGTCGCGCTGCGAGATTAAAGATTAGAAAGTGATCATCTCGTCG 860
QY 601 TGCATCGGCTCTCTCTCGCTCCCTGCTCATCATCATCTGCTACGTCGCTCATC 660
Db 861 TGTATCGGTTTTTTTTTCGTTTTTTTGTATTATGATTTTGTTCACGTCGCTATTAT 920
QY 661 CAGATCGCCCAAGCGCTGCGACCGCGCTGCCACCCAGCCCGCGGTCGCGAGCGCGTCC 720
Db 921 TAGATCGTTAAGCGTCGATTCGCGCTGTTATTAGTCGCGGTCGAGCGTCGTCGTC 980
QY 721 GCGCCCGCGGGGGGACCGACCGACGAGGCCCAAGGTCCTGGCCCGCGAGCGACGCGGCG 780
Db 981 GCGTCGTCGGGGGATCGAGCGTAGCGTTAAAGGTTTGGGTTTCGAGCGTAGCGCGGCT 1040
QY 781 CCGGGGGGCGCAGAGGCCCAACCGCTGCCACCCAGCTCAACGCGCGCCCTGGCGAGCCC 840
Db 1041 TCGGGGGGCGTAGAGGTCGAATCGTTGTTATTAGTTTAAACGCGCTTTTGGCGAGTTC 1100
QY 841 GCGCCCGCGCGCGCGCGCACACCGCGCTGGACCTGGAGGAGAGCTGCTTCCGAC 900
Db 1101 GCGTCGCTCGGGTCGCGCGCATATCGACCGCTGGATTGGAGGAGAGCTTCTTTTCGAT 1160
QY 901 CAGCGCGAGCGGCTCCAGGGGCCCCCGCAGACCCGAGCGCGTCCCCGGGGCAAGGCAAG 960
Db 1161 TACGTCGAGCGGTTTAAAGGTTTCGTAGATTTCGAGCGCGGTTTCGGGGTAAAGGTAAG 1220
QY 961 GCCCGAGCGAGCGAGTGAAGCCGCGCGCAGACCTGCCGCGCGCGGGCGCGCGAGC 1020
Db 1221 GTTCGAGCGAGTTAGTGAAGTCGCGCGCATAGTTGTCCGCGCGCGGGTCGGGGCGAGC 1280
QY 1021 GGGATCGGGAGCGCGGCTGCAGGGGCGCGGGGAGGAGCGCGTGGCCAAAGCGTCG 1080
Db 1281 GGGATCGGGAGCGTCGTTGTAGGGTCGGGGGAGGAGCGCGTGGTAAAGCGTCG 1340
QY 1081 CGCTGGCGCGCGCGCAGAACCGCGAGAACGCTTCACGTTCTGCTGGCCGTGTCATC 1140
Db 1341 CGTTGGCGCGCGCGGTAGAATCGCGAGAACGCTTTTACGTTCTGTTGCTGCTGATC 1400
QY 1141 GGAGTGTCTGCTGCTGCTGCTCCCTCTCTCTTACCTACACGCTCACGCGCGTCGGG 1200
Db 1401 GGAGTGTCTGCTGCTGCTGCTTTTTTTTTTTTATTTATACGTTTACGTCGTCGGG 1460
QY 1201 TGCTCGTGCCACGCGACGCTCTTCAAAATCTTCTGCTGCTACTGCAACAGCTCG 1260
Db 1461 TGTTCGTGTTACGTACGTTTAAATTTTTTTTTTGGTTCGTTATGTATAGTTTCG 1520
QY 1261 TTGAACCGCGTCATCTACACCATCTTCAACACAGATTCCGCGCGCTTCAAGAAATC 1320
Db 1521 TTGAATTCGTTATTATATATTTTAAATTACGATTTCGTCGCTTTTAAAGAAATT 1580
QY 1321 CTCTGTGCGGGGACAGGAGCGGATCGTG 1350
Db 1581 TTTTGTGCGGGGATAGGAAGCGGATCGTG 1610

RESULT 8
ABQ47499/c
ID ABQ47499 standard; DNA; 1733 BP.
XX
AC ABQ47499;
XX
DT 12-JUL-2002 (first entry)

XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34090.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PE 01-SEP-2001; 2001WO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
XX
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc.; particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.

XX
SQ Sequence 1733 BP; 685 A; 585 C; 211 G; 252 T; 0 other;

Query Match 62.0%; Score 836.4; DB 24; Length 1733;
Best Local Similarity 76.2%; Pred. No. 1.2e-122;
Matches 1029; Conservative 0; Mismatches 321; Indels 0; Gaps 0;

QY 1 ATGGGCTCCCTGCAGCGCGAGCGGGGCAAGCGAGCTGGAACGCGAGCGCGCGG 60
Db 1473 ATGGGTTTTTTGTAGTCGACGCGGGTAAACGCGAGTTGGAACGCGATCGAGCGTCGGG 1414
QY 61 GCGGCGCGCGCGCCACCCCTTACTCCCTGAGGTGACGCTGACGCTGTGCTGCGCC 120
Db 1413 GCGGCGCTTCGGGTATTTTATTTTGAAGTGACGTTGACGTTGCTGTGCTGTC 1354
QY 121 GGCCTGCTCATGCTGCTCAACCGTGTTCGCAACGTCGTCGTCATCATCGCGCTGCACG 180
Db 1353 GCTTGTATTATGTTTATATCGTTCGGAACGCTTCGTTATATCGTCGTGTTACG 1294
QY 181 AGCCGCGCGCTCAAGCGCGCCCAAAACCTCTCTGCTGCTCTGCGCTCGGCGCACATC 240
Db 1293 AGTCGCGCGTTAAGCGCTTTTAAATTTTTTTTGTGTTTGTGTTGCGTCGATATT 1234

QY	601	TGCATCGGCTCCCTTCTTGCTCCCTGCTCATCATGATCCTGGTCTACGTGCGCATCTAC	660
Db	1753	TACATCGACTCCTCTTCTGCTCCCTACCTCATCATATCTTAATCTACGTACGATCTAC	1694
QY	661	CAGATCGCCAAAGCTCGCACACC CGCGTGCACACCAGCCGCGGGTCCGGACGCGTCCG	720
Db	1693	CAATCGCCAAACGTCCGACCCCGGTACCAACCCCAACCGCGAAATCCGAACGCGTCCG	1634
QY	721	GCGCCGCGGGGGGSCACCGAGCGCAGAGGCCCAAGGCTCTGGGCCCGAGCGCAGCGGGC	780
Db	1633	GCGCCGCGGAAAAACACCGAACGCAAAACCAACGATCTAAACCCCGAACGCAACGGAAC	1574
QY	781	CCGCGGGGCGCAGAGGCCGAACCGCTGCCCCACCAAGCTCAACGGCGCCCTTGGCGAGCCC	840
Db	1573	CCGAAAAACGCAAAAACCGAACCGCTACCCACCAACTCAACGAGCGCCCTTAACGAACCC	1514
QY	841	GCGCCGCGCGCGCGCGCGACACCGACCGCGCTGGACCTGGAGGAGAGTCTGCTTCCGAC	900
Db	1513	GCGCCGACCGAACCGCGCGACACCGACGCGCTAAACCTAAAAAAAACCTGCTTCCGAC	1454
QY	901	CACGCGGAGCGGCTCCAGAGGGCCCCGACAGACCCGACGCGTCCCGCGGCGCAAGGCAAG	960
Db	1453	CACGCGGAGCACTCTCCAAAACCCCGAAACCGGATCCCGAAACAAAACAAA	1394
QY	961	GCCCCGAGCGACCAAGGTGAAGCCCGGGGACAGACGCTGCGCGCGCGCGCGCGGCGACG	1020
Db	1393	ACCCGAACGAAACCAATTAACCCGAACGACACCTACCGCGACGGAACCGAAACGACG	1334
QY	1021	GGGATCGGGGACCGCGGCTGCAGGGCGCGGGGGAGAGAGCGCGTCCGCAAGCGCTCG	1080
Db	1333	AAATTCGAAACGCCGACTACAAAACCGAAAAAACGGCTCGAAACTACCAAAACGTG	1274
QY	1081	CGCTGGCGCGGGCGGCGCAGAACCGCGAAGAGCGCTTCAAGTTCGTGCGCGTGGTCAATC	1140
Db	1273	CGCTAACGCGAACGACAAAACCGCGAAACGCTTCAAGTTCGTACTAACCGTAAATCATC	1214
QY	1141	GGAGTGTTCGTGTGTGCTGCTTCCCTTCTTCTTCACTACACGCTACGCGCGCTCGGG	1200
Db	1213	GAAATATTCGTATATATACTAATTCCTTCTTCTTCACTACACGCTACGACCGCTCGAA	1154
QY	1201	TGCTCCGTCCACGACGCTCTCAAAATCTTCTTGTGTTGGCTACTGCAACAGCTCG	1260
Db	1153	TACTCCGTACCAACGACGCTCTCAAAATCTTCTTCAATTCGACTACTACAACACTCG	1094
QY	1261	TTGAACCCGCGTATCTACACCATCTTCAACACAGATTTCGCGCGCTTCAAGAAGATC	1320
Db	1093	TTAAACCCGATCATCTACACCATCTTCAACACAGATTTCGCGCGCTTCAAAAAAATC	1034
QY	1321	CTCTGTCCGGGGGACAGGAAGCGGATCGT	1349
Db	1033	CTCTATCGAAAAAACAAAAACGAATCGT	1005
RESULT 7			
ABQ47498			
ID	ABQ47498	standard; DNA; 1733 BP.	
XX	ABQ47498;		
AC			
XX			
DT	12-JUL-2002	(first entry)	
XX			
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 34089.		
XX			
KW	Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;		
KW	drug; side effect; cancer; central nervous system; cardiovascular;		
KW	gastrointestinal; respiratory system; single nucleotide polymorphism;		
KW	SNP; cell differentiation; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200218632-A2.		
XX			

PD 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WO-EP10074.
 XX
 PR 01-SEP-2000; 2000DE-1043826.
 PR 05-SEP-2000; 2000DE-1044543.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K, Guettig D;
 XX
 DR WPI; 2002-371829/40.
 XX
 XX Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA -
 XX
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.

xx This invention describes a novel method for determining the degree of
cc methylation of a particular cytosine in a motif 5'-CpG-3', present in a
cc genomic sample of DNA. The sample is treated chemically to convert
cc cytosine (C) but not methylated C, to uracil, then part of the genomic
cc DNA that contains the target C is amplified to form a labeled amplicon.
cc The amplicon is hybridised to two classes, each with at least one
cc member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
cc and the degree of hybridisation to both classes is determined from the
cc label on the amplicon. From the ratio of labels hybridised to the two
cc classes of oligomers, the degree of methylation is calculated. The method
cc is used: (i) for diagnosis and/or prognosis of side effects of
cc therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
cc of the central nervous, cardiovascular, gastrointestinal and respiratory
cc systems etc., particularly by detecting mutations or single nucleotide
cc polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
cc types and for investigating cell differentiation. The method allows the
cc methylation status of many C residues to be determined simultaneously.
cc ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
cc method for determining the degree of cytosine methylation described in
cc the disclosure of the invention.

Sequence 1733 BP: 252 A; 211 C; 585 G; 685 T; 0 other;

Query Match	62.0%;	Score 836.4;	DB 24;	Length 1733;
Best Local Similarity	76.2%;	Pred. No. 1.2e-122;		
Matches 1029; Conservative	0;	Mismatches 321;	Indels 0;	Gaps 0;

OY	1	ATGGGCTCCCTGCAGCCGGACGCCGGCAACCGGAGCTGGAAACGGGACGAGCGCCGGGG	60
Db	261	ATGGGTTTTGTGACTCGGACGCGGGTAACGGAGTTGGAAACGGGATCAGGCGTCGGGG	320
OY	61	GCGGGCGCCGGGGCCACCCTTACTCCCTGCAGGTGACGCTGACGCGTGCTGCTGGCC	120
Db	321	GCGGGCGCTCGGGTATTTTTTATTTTTTGTGAGTGACGTTGACGTTGGTGTGTTGGTC	380
OY	121	GGCCTGCTCATGTGCTCACCGTGTTGGAACGTCGTCATCATCGCCGTGTTACG	180
Db	381	GCTTTGTTATGTGTATTATCGTGTCGGTAACGTCGTTGTTATATCGTCGTTTAGC	440
OY	181	AGCCGCGCGCTCAAGCGCCCCAAAACCTCTTCGTGTTGTCCTGCGCTCGCGGCATC	240
Db	441	AGTCGCGCGTTAAGCGCTTTTAAATTTTTTTTGGTGTGTTTGGTTTCGTCGATATT	500
OY	241	CTGGTGGCCACGCTCGTCAATCCCTTCTCGCTGGCCAACGAGTCA TG GGTACTG GTAC	300
Db	501	TTCGTGTTACGTTCTGTTATTTTTTTTTCGTTGGTTAACGAGTTATGGGTATTGGTAT	560
OY	301	TTCGGCAAGGCTTGGTGGCAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGTCGTC	360
Db	561	TTCGTAAGGTTTGGTGGCAGATTTATTTCGCGCTCGACGTGTTTTTTTGTACGTCGTTT	620
OY	361	ATCGTGACCTGTGCGCCATCAGCCTGGACCGCTACTGTGTCATCACACAGGCATCGAG	420
Db	621	ATCGTGTATTGTGCGCTATTAGTTTGATCGTATTGTGTTATTATATAGGTTATCGAG	680

Db 1693 CAAATCGCCAAACGTCGCACCCGCGGTACCAACCAACGCCGGAATCCGAAGCCGCTGCC 1634

QY 721 GCGCCGCGGGGGGACCCGAGCGCAGCCCAAGGTTGGGCCCCGAGCGCAGCGGGGC 780

Db 1633 GCGCCGCGGAAAAACCGAACGCAACCCAAAGATCTAAACCCGAGCGCAGCGGAAC 1574

QY 781 CCGGGGGCGCAGAGCGCCGAACCGCTGCCACCCAGCTCAACGCGCCCTGGCGAGCCC 840

Db 1573 CCGAAAAACGAAAAACCGAACCGCTACCCACCACTCAACGAGCGCCCTTAACGAAACC 1514

QY 841 GCGCGCGCGGGCGCGCGCAGAACCGAGCGGCTGGAAGAGAGAGCTGCTTCCGAC 900

Db 1513 GCGCGGACCGAACCGCGCGACACCGCGCTAAACCTAAAAAAACTGCTCTCCGAC 1454

QY 901 CACGCGGAGCGGCTCCAGGCCCCGAGACCCGAGCGCGGTCGCCGCGGCAAAAGCAAG 960

Db 1453 CACGCGGAACGACCTCCAAAAACCCGCAAAACCGGATCCCGGAAAAACAAACAA 1394

QY 961 GCGCGAGCGAGCGAGGTGAACCGCGGCGACAGCGCTGCCGCGCGCGCGGGCGGAGC 1020

Db 1393 ACCCGAACGAACCAATATAAACCGAACGACAACTACCGGAGCGCAACCGAAAAAGCAGC 1334

QY 1021 GGGATCGGGAGCGCGGCTGCAGGGCGCGGGGAGAGCGCGCTCGGGCTGCCAAGCGCTGC 1080

Db 1333 AAAATCGAAACGCCGACTACAAAAACGAAAAAAACGCGTGAATACTAACAAAAAGTGC 1274

QY 1081 CGCTGGCGCGGGCGGAGAACCGCGAGAACGCTTACAGTTGCTGCTGGCGGTGTCATC 1140

Db 1273 CGCTAACGCGAACGACAAACCGGAAAAACGCTTACAGTTGCTGCTAACCGTAATCATC 1214

QY 1141 GGAGTGTTCGTGCTGCTGCTGCCCTTCTTCTTACCTACAGCTCAGCGCGCTCGGG 1200

Db 1213 GAAATATTGTAATTAATACTAATTCCTTCTTCTTACCTACAGCTCAGCGCGTCAA 1154

QY 1201 TGCTCGGTGCACGACGCTCTTCAAAATCTTCTTCTGTTGCGCTACTGCAACAGCTCG 1260

Db 1153 TACTCCGTACACGACGCTCTTCAAAATCTTCTTCTAATTCGACTACTACAACTCG 1094

QY 1261 TTGAACCGCGTCACTTACACCATCTTCAACACGATTTCCGCCGCGCTTCAAGAAATC 1320

Db 1093 TTAAACCGGATCACTTACACCATCTTCAACACGATTTCCGCCGCGCTTCAAAAAATC 1034

QY 1321 CTCTGTCGGGGGACGGAAGCGGATCGT 1349

Db 1033 CTCTATCGAAAAAACAAAAACGAATCGT 1005

RESULT 6
AAD28363/c
ID AAD28363 standard; DNA; 7353 BP.
XX
AC AAD28363;
XX
DT 22-APR-2002 (first entry)
XX
DE Human chemically treated genomic DNA #4.
XX
KW Human; cytosstatic; antidepressant; neuroleptic; nootropic; antiaddictive;
KW adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
KW behavioural disorder; neurological; psychiatric; cancer; schizophrenia;
KW Tourette's syndrome; smoking; human immunodeficiency virus dementia;
KW drug abuse; migraine; ds.
XX
OS Homo sapiens.
XX
PN WO200202809-A2.
XX
PD 10-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07540.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.

XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-154759/20.
XX
PT Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT gene -
XX
PS Claim 1; Page 36-40; 190pp; English.
XX
CC The invention relates to nucleic acids comprising a segment of chemically
CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC useful for detecting cytosine methylations. The pretreated DNA is useful
CC for the diagnosis or therapy of behavioural disorders, neurological
CC disorders and cancer, in particular major depressive disorder, Tourette's
CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC drug abuse, alcoholism, personality traits, compulsive gambling, human
CC immunodeficiency virus dementia, migraine, behaviours in schizophrenic
CC and schizoaffective patients, and suicidal behaviour in patients with
CC schizophrenia. The nucleic acid is useful for detecting the methylation
CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC (SNPs). The present sequence is human chemically treated genomic DNA.
XX
SQ Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;

Query Match 67.8%; Score 915.4; DB 24; Length 7353;
Best Local Similarity 79.9%; Pred. No. 4.5e-135;
Matches 1078; Conservative 0; Mismatches 271; Indels 0; Gaps 0;

QY 1 ATGGGCTCCCTGCAGCCGCGGCAACGCGAGCTGGAACGGAGCCGAGCGCGGG 60

Db 2353 ATAACTCCCTTACAACCGAACGCGAACACGCGACTAAACGAACCGAAGCGGAAA 2294

QY 61 GCGCGCGCGCGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGCTGCTGCC 120

Db 2293 AACGAGCGCCGGAACCAACCCCTTACTCCCTACAATAACGCTAACGCTAATATACCTAAC 2234

QY 121 GGCCTGCTCATGCTGCTCAACCGTGTTCGGCAACGTGCTGTCATCATGCCGTTCACG 180

Db 2233 GACCTACTCATACTACTACCGGTATTCGACACAGTACTGTCATCATGCCGTATTCACG 2174

QY 181 AGCGCGCGGCTCAAGGCGGCCCAAAACCTTTCCTGCTGCTGCTGCTGCCGACATC 240

Db 2173 AACCGCGGCTCAAAACGCGCCCAAAACCTTCTTAATATCTTAACCTCGACCGACATC 2114

QY 241 CTGGTGGCCACGCTCGTCATCCCTTCTCGCTGGCCACGAGGTATGGCTACTGTGAC 300

Db 2113 CTAAATAACGACGCTCGTCATCCCTTCTCGCTAACCAACGAATCATAACTACTAATAC 2054

QY 301 TTCGGCAAGGCTTGGTGGAGATCTACCTGGCGCTGACGCTGCTCTTGACAGTCGTC 360

Db 2053 TTCGACAAACTTAATACGAATCTTACCTAACGCTGACGCTACTCTTACACGTCGTC 1994

QY 361 ATCTGACACCTGTGGCCATCAGCGTGGACCGCTACTGTCTCATACACAGGCGCATGAG 420

Db 1993 ATCTGACACCTATAGCCATCAACCTTAACCGCTACTAATTCATCACAAACCATCGAA 1934

QY 421 TACAACCTGAAGCGACGCGCGCGCATCAAGGCCATCATCATCAGCTGTGGTCATC 480

Db 1933 TACAACCTAAAAACGACGCGCGCGCATCAAAACCATCATCATCACCCTATTAATCATC 1874

QY 481 TCGCGCTCATCTCTTCCCGCGCTCATCTCCATCGAGAGAAGGGCGCGCGCGCGC 540

Db 1873 TCGACGTCATCTCTTCCCGCGCTCATCTCCATCGAAAAAAGAACGACGACGAC 1814

QY 541 CCGCAGCGCGCGAGCGCGCTGCGAGATCAACGACAGAAAGTGTAGCTCATCTGTCG 600

Db 1813 CCGCAGCGCGAGACCGCGCTACGAAATCAACGACCAAAATATATAGTCACTCTGTCG 1754

Db	981	GCGCGCGCGAAAAACACCGAAGCGCAAAACCAACGATCTAAACCCCGGAACGCAAGCGCGAAC	1040
QY	781	CCGGGGGGCGCAGAGGCCGAACCGCTGCCACCCAGCTCAACGGCGCCCTGCGGAGCCC	840
Db	1041	CCGAAAAACGCAAAAAACCGAACCGCTACCCACCAACTCAACGACGCGCCCTTAACGAACCC	1100
QY	841	GCGCGCGCGGGCGCGCGACACCGACGCGCTGGACTTGAGGAGAGAGCTCGTCTTCCGAC	900
Db	1101	GCGCGGACCGAACC CGCGCGACACCGACGCGCTAAACCTAAAAAAAACCTCGTCTCCGAC	1160
QY	901	CACGCGGAGCGGCTCCAGGGCCCCCGACAGACCCGAGCGGTCCTCCCGGGGCAAAAGGCAAG	960
Db	1161	CACGCGGACGACCTCCCAAAACCCCGCAAAACCCGAGACGCGATCCCGGAACCAAAACAA	1220
QY	961	GCCCCGAGCGACCCAGGTGAAGCCGGGGCGACAGCCTGCCCCGGCGCGGGCGCGCGAGC	1020
Db	1221	ACCCGAAACGAACCAATAAAAACCGAAGCACAACCTACCGCGAGCGGAACCGAAAAACGACG	1280
QY	1021	GGGATCGGGAGCGCGCGCTGCAGGGCCGGGGGAGAGCGCGTCGGGGCTGCCAAGCGCTCG	1080
Db	1281	AAAATCGAAACGCGGACTACAAAAACGAAAAAAAACGCGTCGAAACTACCAAAACGTCG	1340
QY	1081	CGCTGGCGCGGGCGCGAGAACCGCGAGAACGCTTCACGTTGCTGCGCCGTGCTATC	1140
Db	1341	CGCTAACGCGAAGCAAAAAACCGGAAAAACGCTTCACGTTGCTACTAACCGTAAATCATC	1400
QY	1141	GGAGTGTTCGTGCTGCTGCTGTTCCCTTCTTCAACCTACACGCTACGCGCGCGTGGG	1200
Db	1401	GAAATATTCGTAATATTAATAATTCCTTCTTCAACCTACACGCTACGACCGCTCGAA	1460
QY	1201	TGCTCCGTCGCACGACGCTCTTCAAAATCTTCTTGCTGCTCGCTACTGCAACAGCTCG	1260
Db	1461	TACTCCGTACCAAGCAGCGCTCTTCAAAATCTTCTTCAATTCGACTACTACAACAACCTCG	1520
QY	1261	TTGAACCCCGTCATCTACACCATCTTCAACACAGATTCGCGCGCGCTTCAAGAAGATC	1320
Db	1521	TTAAACCCGATCATCTACACCATCTTCAACACAGATTCGCGCGCGCTTCAAAAAAATC	1580
QY	1321	CTCTGTCGGGGGAGACAGGAAGCGGATCGT	1349
Db	1581	CTCTATCGAAAAACAAAAACGAATCGT	1609

ABL32073/c	standard;	DNA;	7353	BP.
ID	ABL32073			
XX				
AC	ABL32073;			
XX				
DT	26-MAR-2002	(first entry)		
XX				
DE	Human	immune system associated gene	SEQ ID NO: 46.	
XX				
KW	Human;	immune system disease;	cytosine methylation;	antiasthmatic;
KW	antiartherosclerotic;	antianaemic;	cytostatic;	nootropic;
KW	neuroprotective;	anti-HIV;	anticonvulsant;	ophthalmological;
KW	antirheumatic;	antiarthritic;	antidiabetic;	antipsoriatic;
KW	antiinflammatory;	cancer;	eye disease;	arteriosclerosis;
KW	acute myeloid leukaemia;	Alzheimer's disease;	AIDS;	epilepsy;
KW	neurofibromatosis;	rheumatoid arthritis;	bowel disease;	
KW	gene;	ds.		
XX				
OS	Homo sapiens.			
XX				
PN	WO200200928-A2.			
XX				
PD	03-JAN-2002.			
XX				
PF	02-JUL-2001;	2001WO-EP07537.		
XX				
PR	30-JUN-2000;	2000DE-1032529.		
PR	01-SEP-2000;	2000DE-1043826.		
XX				

PA (EPiG-) EPIGENOMICS AG.
XX
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX
DR WPI, 2002-130909/17.
XX
XX Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
XX
PS Claim 1; SEQ ID NO 46; 32pp + Sequence Listing; German.
XX
XX The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
XX
XX Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;
SQ

Query Match	67.8%;	Score 915.4;	DB 24;	Length 7353;
Best Local Similarity	79.9%;	Pred. No. 4.5e-135;		
Matches 1078;	Conservative	0;	Mismatches 271;	Indels 0;
				Gaps 0;
QY 1	ATGGCTTCCTGTGAGCCGGAGCGGGGCAACGCGAGCTGGAACGGGACCGAGCGCGGGG	60		
Db 2353	ATAAAGTCCCTTACAAACCGAAGCGGCAACAGCGAACTAAACGAAACCGAAACCGCGAAA	2294		
QY 61	GGCGGCGCGCGGGCCACCCCTTACTCCCTGAGGTGACGCTGAGCTGTGCTGGCC	120		
Db 2293	AACGACGCGCGGAAACCAACCCCTTACTCCCTACAAATTAACGCTAACGCTAATATACCTAAC	2234		
QY 121	GGCTGCTCATGCTGCTACCGTGTGCGCAACGCTGCTGCTCATCATCGCGGTTCACG	180		
Db 2233	GACCTACTCATCTACTACTACCGTATTCGACAAACGTAAGTACTGCTCATCATCGCGGTATTCACG	2174		
QY 181	AGCGCGCGCTCAAGGCGCGCCCAAAACCTCTTCCTGCTGTCTGTGCGCTGCGCGACATC	240		
Db 2173	AACCGCGCGCTCAAAACCGCGCCCAAAACCTCTTCCTAATATCTTAACCTCGACCGACATC	2114		
QY 241	CTGTGCGCAACGCTGCTCATCCCTTCTGCTGCGCAACGAGGTATGGCTACTGTGAC	300		
Db 2113	CTAATTAACCAACGCTGCTCATCCCTTCTGCTTAACCAACGAAATCATTAACCTAATATAC	2054		
QY 301	TTCGCGCAAGGCTTGGTGAGATCTACCTGGCGCTGACGCTGCTCTTCTGCAAGTGTCC	360		
Db 2053	TTCGCAAAACTTAATACGAATCTACCTAACGCTGACGTAAGTCTTCTACACGCTGCTCC	1994		
QY 361	ATCGTGAACCTGTGCGCATCAGCCTGAGCCGCTACTGCTCATCAGACGACCATCGAG	420		
Db 1993	ATCGTGAACCTTAATACGATCAACCTAAACCGCTACTAATCATCAGACCAACCATCGAA	1934		
QY 421	TACAACCTGAAGCGCACGCGCGCGCATCAAGGCCATCATCATCACCCTGTGGTCAATC	480		
Db 1933	TACAACCTGAAGCGCACGCGCGCGCATCAAGGCCATCATCATCACCCTGTAAATCAATC	1874		
QY 481	TGCGCGCTCATCTCTTCCCGCGCTCATCTCCATCGAGAAGAAGGGCGCGCGCGGC	540		
Db 1873	TGCGCGCTCATCTCTTCCCGCGCTCATCTCCATCGAAGGAGGAGGAGGAGGAGGAGGAGG	1814		
QY 541	CCGACGCGCGCGGAGCGCGCTGAGATCAAGCAGACGAGAAGTGTGATGCTCATCTGCTG	600		
Db 1813	CCGACGCGCGGAGCGCGCTGAGATCAAGCAGACGAGAAGTGTGATGCTCATCTGCTGCTG	1754		
QY 601	TGCATCGGCTCTTCTTCCCTGCTGCTCATCATGATGATCTGCTCATGCTGCGCATCTAC	660		
Db 1753	TACATCGACTCTTCTTCCCTGCTGCTCATCATCATTAATCTAATCTACGTCATCTAC	1694		
QY 661	CAGATCGCAAGGCTGCAACCGCGCTGCAACCGCGCGGCTCGGAGCGCGCTGCGC	720		

Db 573 CACGCCGAACGACCTCCAAAACCCCGCAAAACCCGAACGGGATCCCGGAAAACAAAACAA 514

QY 961 GCCCGAGCGAGCCAGGTGAAGCCGGGCGACAGCCTGCCGGCGGCGGGCGGGCGAGC 1020

Db 513 ACCCGAACGAACCAATTAACCGAAGCAGCAACCTACCGCAGCGGAACCGAAACGACG 454

QY 1021 GGGATCGGAGCGCCGGCTGAGGGCCGGGAGAGAGCGCTGGGGCTGCCAAGCGCTCG 1080

Db 453 AAAATCGAAACGCGGACTACAAAACCGAAAAAACGGCTGGAACCTACCAAAACGTCG 394

QY 1081 CGCTGGCGCGGGCGGAGAACCGCGAGAAAGCGCTTCAAGTTCGTGCTGGCCGTGTCATC 1140

Db 393 CGCTAACGCGGACGACAAACCGGAAAAACGCTTCAAGTTCGTGCTGCTAACCGTAATC 334

QY 1141 GGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200

Db 333 GAAATATTCGTAATATTAATTTCCCTTCTTCTTCACTACACGCTCACGACGCTCGAA 274

QY 1201 TGCTCCGTGCGACGACGCTCTCAAAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260

Db 273 TACTCCGTACACGACGCTCTTCAAAATCTTCTTCAATTCGACTACTACAACTACG 214

QY 1261 TTGAACCCGGTCACTACACCATCTTCAACACGATTTCCGCGCGCTTCAAGAAATC 1320

Db 213 TTAACCCGATCATCTACACCATCTTCAACACGATTTCCGCGCGCTTCAAAAAATC 154

QY 1321 CTCTGTCGGGGGACAGGAGCGGATCGT 1349

Db 153 CTCTATCGAAAAAACAAACGAATCGT 125

RESULT 4

ABQ47501

ID ABQ47501 standard; DNA; 1733 BP.

XX

AC ABQ47501;

XX

DT 12-JUL-2002 (first entry)

XX

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34092.

XX

KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

KW drug; side effect; cancer; central nervous system; cardiovascular;

KW gastrointestinal; respiratory system; single nucleotide polymorphism;

KW SNP; cell differentiation; ds.

XX

OS Homo sapiens.

XX

PN WO200218632-A2.

XX

PD 07-MAR-2002.

XX

PF 01-SEP-2001; 2001WO-EP10074.

XX

PR 01-SEP-2000; 2000DE-1043826.

PR 05-SEP-2000; 2000DE-1044543.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX

DR WPI; 2002-371829/40.

XX

PT Determining the degree of cytosine methylation in genomic DNA, useful

PT for diagnosis and prognosis, comprises selective hybridization of

PT amplicons from chemically treated DNA -

XX

PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX

CC This invention describes a novel method for determining the degree of

CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a

CC genomic sample of DNA. The sample is treated chemically to convert

CC cytosine (C) but not methylated C, to uracil, then part of the genomic

CC DNA that contains the target C is amplified to form a labeled amplicon.

CC The amplicon is hybridised to two classes, each with at least one

CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers

CC and the degree of hybridisation to both classes is determined from the

CC label on the amplicon. From the ratio of labels hybridised to the two

CC classes of oligomers, the degree of methylation is calculated. The method

CC is used: (i) for diagnosis and/or prognosis of side effects of

CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders

CC of the central nervous, cardiovascular, gastrointestinal and respiratory

CC systems etc., particularly by detecting mutations or single nucleotide

CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue

CC types and for investigating cell differentiation. The method allows the

CC methylation status of many C residues to be determined simultaneously.

CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the

CC method for determining the degree of cytosine methylation described in

CC the disclosure of the invention.

XX

SQ Sequence 1733 BP; 626 A; 625 C; 211 G; 271 T; 0 other;

Query Match 67.8%; Score 915.4; DB 24; Length 1733;

Best Local Similarity 79.9%; Pred. No. 5e-135;

Matches 1078; Conservative 0; Mismatches 271; Indels 0; Gaps 0;

QY 1 ATGGCTCCCTGACCGCGAGCGGGCAACGCGAGCTGGAACGGAGCGAGCGCGGG 60

Db 261 ATAACTCCCTTACAACCGAAGCGCAACAACGGAACCTAAACGAAACCGAGCGCGAA 320

QY 61 GCGCGCGCGCGCGCACCCCTTACTCCCTGACAGGTGACGCTGACGCTGCTGCTG 120

Db 321 AAGGACGCGCGGAAACACCCCTTACTCCCTTACAATAACGCTAACGCTAATATACCTAAC 380

QY 121 GGCTGCTCATGCTGCTACCGCTGTTGGCAACGCTGCTGCTCATCATCGCCGTGTTACG 180

Db 381 GACCTACTCATACTACTACCGCTAATTCGACAACGCTACTGCTCATCATCGCCGTATTTCACG 440

QY 181 AGCCGCGCGCTCAAGGCGCGCCCAAAACCTTCTCTGCTGCTCTGCGCTCGCGGACATC 240

Db 441 AACCGCGCGCTCAAAACGCGCCCAAAACCTTCTCTAATATCTTAACCTCGACCGACATC 500

QY 241 CTGGTGGCCACGCTGCTATCCCTTCTCGCTGGCCCAAGGTGATGGGCTACTGCTGCTAC 300

Db 501 CTAAATAACCAACGCTGCTATCCCTTCTCGCTAACCAAGAAATCATTAACCTAATAC 560

QY 301 TTGCGCAAGGCTTGGTGGAGATCTACCTGGCGCTGCAAGCTGCTCTTTCGACGCTGCTC 360

Db 561 TTGACAAAACTTAATACGAATCTACCTAACGCTGACGCTACTCTTCTACAGCTGCTCC 620

QY 361 ATCGTGACCTGTGCGCATACCTTGACCGGCTACTGTTCCATCACACAGGCCATCGAG 420

Db 621 ATCGTACACCTATACGCGCATCAACCTTAACCGGCTAATCCATCACACAAACCATCGAA 680

QY 421 TACAACCTGAAGCGCACGCGCGCGCGCATCAAGGCCATCATCATCACCGCTGTGGTCAATC 480

Db 681 TACAACCTAAAACGACGCGCGCGCGCATCAAAACCATCATCATCACCGCTAATAATCATC 740

QY 481 TCGGCGCTCATCTCTTCCCGCGGCTCATCTCCATCGAAGAAGAGGGCGCGCGCGGCGG 540

Db 741 TCGACCGTCACTCTCTTCCCGCGGCTCATCTCCATCGAAGAAAGAGAGAGAGAGAGAGAG 800

QY 541 CCGCAGCGCGCGGAGCGCGGCTGCGAGATCAACGACCAAGAAGTGTACGTATCTGTCG 600

Db 801 CCGCAACCGGACGAGCGCGGCTAGGAATCAACGACCAAAATAATATACGTATCTGTCG 860

QY 601 TGCAATGCGCTCTTCTTCCGCTCCCTGCGCTCATCATGATCCTGCTGCTACGCTGCTAC 660

Db 861 TACATGCACTCTTCTTCCGCTCCCTACCTCATCATTAATCTTAATCTACGATCTAC 920

QY 661 CAGATGCGCAAGCGTGCACCCGCGTGCACCCAGCCGCGGGTCCGGAGCGCGCTGCGC 720

Db 921 CAAATGCGCAAGCGTGCACCCGCGTACCAACCAACCGCGGAATTCGAACGCGCTGCGC 980

QY 721 GCGCGCGCGGGGACCGAGCGCAGGCGCAAGGCTCTGGGCCCGAGCGGAGCGCGGCG 780

ID	ABQ47500 standard; DNA; 1733 BP.	ABQ47500/c
Db	1081	CGCTGGCGGGGGCGGACGAACCGGAGAAAGCGCTTCACGTTGCTGCGCCGTGTCATC 1140
Qy	1141	GGAGTGTTCGTGGTGTCGTGGTTCCCCCTTCTTTCACCTACACGCTCACGGCGTCGGG 1200
Db	1141	GGAGTGTTCGTGGTGTCGTGGTTCCCCCTTCTTTCACCTACACGCTCACGGCGTCGGG 1200
Qy	1201	TGCTCCGTGCGCACGACGCTCTTCAAAATCTTCTTGCTTCGGCTACTGCAACAGCTCG 1260
Db	1201	TGCTCCGTGCGCACGACGCTCTTCAAAATCTTCTTGCTTCGGCTACTGCAACAGCTCG 1260
Qy	1261	TTGAACCCGGTCACTACACCATCTTCAACACAGATTTCCGCCGCGCTTCAAGAAAGATC 1320
Db	1261	TTGAACCCGGTCACTACACCATCTTCAACACAGATTTCCGCCGCGCTTCAAGAAAGATC 1320
Qy	1321	CTCTGTGCGGGGGACAGGAAGCGGATCGTG 1350
Db	1321	CTCTGTGCGGGGGACAGGAAGCGGATCGTG 1350

RESULT 3
 ABQ47500/C
 ID ABQ47500 standard; DNA; 1733 BP.
 XX
 AC ABQ47500;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34091.
 XX
 KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200218632-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WO-EP10074.
 XX
 PR 01-SEP-2000; 2000DE-1043826.
 PR 05-SEP-2000; 2000DE-1044543.
 XX
 PA (EPiG-) EPIGENOMICS AG.
 XX
 PI Olek A, Plepenbrock C, Berlin K, Guetlig D;
 XX
 DR WPI; 2002-371829/40.
 XX
 PT Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA -
 XX
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 CC and the degree of hybridisation to both classes is determined from the
 CC label on the amplicon. From the ratio of labels hybridised to the two
 CC classes of oligomers, the degree of methylation is calculated. The method
 CC is used: (i) for diagnosis and/or prognosis of side effects of
 CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations or single nucleotide
 CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
 CC types and for investigating cell differentiation. The method allows the

CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 1733 BP; 271 A; 211 C; 625 G; 626 T; 0 other;

Query Match	67.8%;	Score 915.4;	DB 24;	Length 1733;
Best Local Similarity	79.98;	Pred. No. 5e-135;		
Matches 1078; Conservative	0;	Mismatches 271;	Indels 0;	Gaps 0;

QY	1	ATGGGCTCCCTGCAGCCGCGGGGCAACGCGAGCTGCAACGGGACCGAGGCGCCGGG	60
Db	1473	ATTAACCTCCCTACAACCGAAGCGGAACAACGCGAACTAAACGAAACCGCGGAAA	1414
QY	61	GGCGGCGCCCGGGCCACCCCTTAATCTCCCTGCAGGTGACGTGACGCTGTGTGCTGGCC	120
Db	1413	AACGACGCGCCGAACCAACCCCTTAATCTCCCTACAAATTAACGCTAATATATACCTAAC	1354

Qy 121 GCGCTCATGCTGTACCGTGTGGCAACGTGCTGCATCATCGCCGTTCACG 180
| | | | | | | | | | | | | | | | | | | | | |
Db 1353 GACTACTCATACTACTACCCTATTGCACAACGTACTCGTCATCATCGCCGTA TTCACG 1294

QY 181 AGCCGCGCTCAAGGCGGCCAAACCTCTCCTGTGTCTTGCCCTGGCCGACATC 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1293 AACCGCGCTCAAAAACGCCCAAACCTTCTTCCTAATAATCTCTAACCTGCAGCCGACATC 1234

QY 241 CTGCTGGCCACGCCTCGTCATCCCTTCTCGCTGGCCAAGGTCA TGGCTACTGTAC 300
 || - ||||||| ||||||| ||||||| ||| |||| |
Db 1233 CTAATAACCAAGCTGTCATCCTTTCTCGCTAACCAAGAAATCATAACTACTAATAC 1174

QY 301 TTCGCAAGGCTTGGTGCGATCTACCTGGCGCTCGACGTGCTTCTGCAAGTCGTC 360
 1173 TTCGACAAACTTAATACGAATCTACCTAACGCTCGACGTACTCTTCTACACGTCGTC 1114

QY 361 ATCGTCACCTGTGCGCCATCAGCCTGGACCCTACTGTGCATTCACACAGGCCATCGAG 420
 ||||| ||||| | ||||| ||| ||||| ||||| ||||| |||||
Db 1113 ATCGTACACCTTATAGCCATCAACTAAACCGCTACTAATCATTCACACAACCATCGAA 1054

QY 421 TACACCTGAAGCGCACGCGCGCCGCATCAAGGCATCATCAACCGTGTGGTCATC 480
||||||| | | ||||||| ||||||| | ||||||| | |||||
Db 1053 TACACCTAAAAAGCACGCGCGCGCATCAAAACCATCATCAACCGTATAATCATC 994

DY 481 TCGGCGTCATCTCCTTCCGGCGGTATCTCATCGAGAGAAGGGCGGGCGGGGC 540
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 993 TCACCGTCATCTCTTTCCGGCGGTATCTCCATCGAAAAAAAACGAGAGAGAGAC 934

[illegible]

601 TGCATGGGCTCCTTCTTGGCTCCCTGGCTCATCATGATCCTGGTCTACGTTGGCATCTAC 660
 873 TATCATGGGCTCCTCCTCTCTCCCTCCCTCCCTCATATCATATATCTCTAATCTACGGTACCGCATCTAC 814

661 CAGATGCCCAAGCGTGCACCCGCGTGCCACCAGCCGCGGCGTCCGGACGCCGTCGCC 720

721 GCGCCGCCGGGGGCGACCGAGCGAGCCCAAGGTCCTGGGCCCGAGCGCAGCGGGC 780

781 CCGGGGGCGCAGAGGCCGACCGCTGCCACCCAGCTCAACGGGGCCCTGGGAGCCC 840

841 GCGCCGCCCCGGCCGCCACACCAGCGCTGGACCTGAGAGAGACTGTCTTCCGAC 900
||||| ||| |

901 CACGCCGAGCGGCCCTCCAGAGGGCCCCGACGACCCGAGCGCGGTCCCCGGGGCAAGGCAAG 960

DT 18-FEB-2002 (first entry)
XX Human alpha-2AAR encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2AAR;
KW GenBank Accession AF281308; chromosome 10; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1353
FT /*tag= a
FT /product= "alpha-2AAR"
XX
PN WO200179561-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US12575.
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
DR P-PSDB; AAM52122.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
PS Example 7; Page 151; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIV)
CC or a site comprising (A) (999c999cgcg) or (B) (999c99ct9ag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR gene
CC (GenBank Accession AF281308).
XX
SQ Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;

Query Match 99.9%; Score 1348.4; DB 23; Length 1350;
Best Local Similarity 99.9%; Pred. No. 8.3e-203;
Matches 1349; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCTCCTGACGCCGACGGGGGCAACGCGAGCTGGAACGGGACCGAGCGCGCGGGG 60

Db 1 ATGGGCTCCTGACGCCGACGGGGGCAACGCGAGCTGGAACGGGACCGAGCGCGGGG 60
QY 61 GCGCGCGCGCGCGCGCACCCCTTACTCCCTGACAGGTGACGCTGACGCTGCTGCTGGCC 120
Db 61 GCGCGCGCGCGCGCGCACCCCTTACTCCCTGACAGGTGACGCTGACGCTGCTGCTGGCC 120
QY 121 GGCCTGCTCAGTGTGCTCACCCTGTGTTGGCAAGCTGCTGCTCATCATCGCCGTGTTACG 180
Db 121 GGCCTGCTCATGTGCTCACCCTGTGTTGGCAAGCTGCTGCTCATCATCGCCGTGTTACG 180
QY 181 AGCCGCGGCTCAAGCG 240
Db 181 AGCCGCGGCTCAAGCG 240
QY 241 CTGGTGGCCACGCTCGTCATCCCTTTCTCGCTGGCCCAACGAGGTGATGGGCTACTGCTAC 300
Db 241 CTGGTGGCCACGCTCGTCATCCCTTTCTCGCTGGCCCAACGAGGTGATGGGCTACTGCTAC 300
QY 301 TTCGGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGACGCTGCTTCTGACAGTCTGCC 360
Db 301 TTCGGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGACGCTGCTTCTGACAGTCTGCC 360
QY 361 ATCGTGACACCTGTGCGCCATCAGCCTGGACCGCTACTGTGTCATCAACAGGCCATCGAG 420
Db 361 ATCGTGACACCTGTGCGCCATCAGCCTGGACCGCTACTGTGTCATCAACAGGCCATCGAG 420
QY 421 TACAACCTGAAGCGCGCACCG 480
Db 421 TACAACCTGAAGCGCGCACCG 480
QY 481 TCGGCGGTATCTCTCTTCCCGCGGCTCATCTCCATCGAGAGAAGGGCGGGCGGGCGGG 540
Db 481 TCGGCGGTATCTCTCTTCCCGCGGCTCATCTCCATCGAGAGAAGGGCGGGCGGGCGGG 540
QY 541 CCGCAGCG 600
Db 541 CCGCAGCG 600
QY 601 TGCATCGGCTCTCTTCTGCTCCCTGCTCATCATGATCCTGCTTACGTGCGCATCTAC 660
Db 601 TGCATCGGCTCTCTTCTGCTCCCTGCTCATCATGATCCTGCTTACGTGCGCATCTAC 660
QY 661 CAGATCGCAAGCGTGCACCGCGCGTGCACCCAGCCGCGGGTCCGGACGCCGTGCGC 720
Db 661 CAGATCGCAAGCGTGCACCGCGCGTGCACCCAGCCGCGGGTCCGGACGCCGTGCGC 720
QY 721 GCGCGCGCGCGCGCGCACCGGCGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 721 GCGCGCGCGCGCGCGCACCGGCGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 781 CCGGGGGCGCGAGAGCGCGGAACCGCTGCCACCCAGCTCAACGGCGCGCGCGCGCGCGCG 840
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QY 841 GCG 900
Db 841 GCG 900
QY 901 CACGCGAGCGCGCTCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
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QY 961 GCCCGAGCGACCGAGTGAAGCG 1020
Db 961 GCCCGAGCGACCGAGTGAAGCG 1020
QY 1021 GGGATCGGGACCGCGCGCTGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
Db 1021 GGGATCGGGACCGCGCGCTGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
QY 1081 CGCTGGCGCGCGCGCGCGAGAACCGCGGAGAAAGCGCTTACGTTGCTGCGCGGTGCTATC 1140
Db 1081 CGCTGGCGCGCGCGCGCGAGAACCGCGGAGAAAGCGCTTACGTTGCTGCGCGGTGCTATC 1140

PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
DR P-PSDB; AAM52123.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
PS Disclosure; Page 152; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcggtgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC rauwolfscine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR variant
CC gene.
XX
SQ Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;
Query Match 100.0%; Score 1350; DB 23; Length 1350;
Best Local Similarity 100.0%; Pred. No. 4.7e-203;
Matches 1350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 361 ATCGTGACCTGTGCGCCATCAGCCTTGAGCCGCTACTGTGCATCACAAGGCCATCGAG 420
QY 421 TACAACCTGAAGCGCACGCCGCGCCGATCAAGGCCATCATCACCGTGTGGTCAATC 480
DB 421 TACAACCTGAAGCGCACGCCGCGCCGATCAAGGCCATCATCACCGTGTGGTCAATC 480
QY 481 TCGGCGGTATCTCTCTTCCCGCGGCTCATCTCCATCGAAGAAAGGGCGGCGCGGC 540
DB 481 TCGGCGGTATCTCTCTTCCCGCGGCTCATCTCCATCGAAGAAAGGGCGGCGCGGC 540
QY 541 CCGCAGCCGCGGAGCCGCGCTGCGAGATCAACGACCAGAGTGGTACGTATCTCTCG 600
DB 541 CCGCAGCCGCGGAGCCGCGCTGCGAGATCAACGACCAGAGTGGTACGTATCTCTCG 600
QY 601 TGCATCGGCTCTCTTCTGCTCCCTGCTCATCATGATCTCTGTCTACGTGGCATCTAC 660
DB 601 TGCATCGGCTCTCTTCTGCTCCCTGCTCATCATGATCTCTGTCTACGTGGCATCTAC 660
QY 661 CAGATCGCAAGCGTCCGACCCCGGTCACCCAGCCGCGGGGTCCGAGCCGTCGCC 720
DB 661 CAGATCGCAAGCGTCCGACCCCGGTCACCCAGCCGCGGGGTCCGAGCCGTCGCC 720
QY 721 GCGCGCGCGGGGGCACCGAGCGAGGCCCAAGGCTGTGGCCCCGAGCGAGCGGGC 780
DB 721 GCGCGCGCGGGGGCACCGAGCGAGGCCCAAGGCTGTGGCCCCGAGCGAGCGGGC 780
QY 781 CCGGGGGCGCAGAGCGCCGAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAGCCC 840
DB 781 CCGGGGGCGCAGAGCGCCGAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAGCCC 840
QY 841 GCGCGCGCGGGCGCGGACACCGACCGCGCTGGACCTGAGAGAGAGCTCTCTCCGAC 900
DB 841 GCGCGCGCGGGCGCGGACACCGACCGCGCTGGACCTGAGAGAGAGCTCTCTCCGAC 900
QY 901 CACGCCGAGCGGCTCCAGGGCGCCGACAGCCGAGCGCGTCCCCGGGCAAGGCAAG 960
DB 901 CACGCCGAGCGGCTCCAGGGCGCCGACAGCCGAGCGCGTCCCCGGGCAAGGCAAG 960
QY 961 GCCCGAGGAGCCAGGTGAAGCGGGGCGACAGCCTGCCGCGGGCGGGCGGGCGGACG 1020
DB 961 GCCCGAGGAGCCAGGTGAAGCGGGGCGACAGCCTGCCGCGGGCGGGCGGGCGGACG 1020
QY 1021 GGGATCGGAGCGCCGCTGCAGGGCGCGGGGAGAGAGCGCTCGGGGCTGCCAAGCGTCG 1080
DB 1021 GGGATCGGAGCGCCGCTGCAGGGCGCGGGGAGAGAGCGCTCGGGGCTGCCAAGCGTCG 1080
QY 1081 CGCTGGCGCGGGCGGCGAGAACCCGCGAGAACGCTTACGTTCTGTGGCGCTGTCATC 1140
DB 1081 CGCTGGCGCGGGCGGCGAGAACCCGCGAGAACGCTTACGTTCTGTGGCGCTGTCATC 1140
QY 1141 GGAGTGTCTGT 1200
DB 1141 GGAGTGTCTGT 1200
QY 1201 TGCTCCGTGCCACGACGCTTCAAAATTTCTTCTGTGTGTGTGTGTGTGTGTGTGTGT 1260
DB 1201 TGCTCCGTGCCACGACGCTTCAAAATTTCTTCTGTGTGTGTGTGTGTGTGTGTGTGT 1260
QY 1261 TTGAACCCGGTCACTACACCACTTCAACCAAGATTTCCGCGCGCTTCAAGAGATC 1320
DB 1261 TTGAACCCGGTCACTACACCACTTCAACCAAGATTTCCGCGCGCTTCAAGAGATC 1320
QY 1321 CTCTGTGGGGGGGACAGGAAGCGGATCGTG 1350
DB 1321 CTCTGTGGGGGGGACAGGAAGCGGATCGTG 1350
RESULT 2
AAI99917
ID AAI99917 standard; DNA; 1350 BP.
XX
AC AAI99917;
XX

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 11:01:28 ; Search time 387.567 Seconds
(without alignments)
7844.310 Million cell updates/sec

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Perfect score: 1350
Sequence: 1 atggctccctgcagccgga.....gggacaggaagcgatcgtg 1350

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1350	100.0	1350	23	AAI99918	Human alpha-2AAR v
2	1348.4	99.9	1350	23	AAI99917	Human alpha-2AAR e
3	915.4	67.8	1733	24	ABQ47500	Oligonucleotide fo
4	915.4	67.8	1733	24	ABQ47501	Oligonucleotide fo
5	915.4	67.8	7353	24	ABL32073	Human immune syste
6	915.4	67.8	7353	24	AAD28363	Human chemically t
7	836.4	62.0	1733	24	ABQ47498	Oligonucleotide fo
8	836.4	62.0	1733	24	ABQ47499	Oligonucleotide fo
9	836.4	62.0	7353	24	ABL32072	Human immune syste

10	836.4	62.0	7353	24	AAD28362	Human chemically t
11	529	39.2	1383	23	AAI99931	Human alpha-2CAR e
12	516	38.2	1371	23	AAI99933	Human alpha-2CAR v
13	512.4	38.0	1382	15	AAQ64890	Human derived adre
14	446	33.0	1344	22	AAD04761	Human alpha2B-adre
15	446	33.0	1344	23	AAI99906	Human alpha-2BAR t
16	444.6	32.9	1353	22	AAD04762	Human alpha2B-adre
17	443	32.8	1353	23	AAI99905	Human alpha-2BAR t
18	423.8	31.4	2064	12	AAQ14151	Human alpha 2 beta
19	423.8	31.4	2064	18	AAT59499	Human alpha-2b adr
20	327.2	24.2	4850	24	AAD28395	Human chemically t
21	259	19.2	1431	18	AAT85635	Balanus amphitrite
22	258.2	19.1	6904	24	ABL32075	Human immune syste
23	258.2	19.1	6904	24	ABL32075	Human chemically t
24	228.6	16.9	4850	24	AAD28394	Human chemically t
25	225	16.7	1140	18	AAT88392	Corn barnacle G-pr
26	202	15.0	1845	21	AAZ98400	Canine betal-adren
27	202	15.0	1845	24	ABK40732	Dog betal-adrenoc
28	188.6	14.0	4401	21	AAZ98404	Rhesus monkey beta
29	188.6	14.0	4401	24	ABK40736	Monkey betal-adren
30	187	13.9	1637	22	AAF61182	Human betal-adreno
31	187	13.9	1637	22	AAF61183	Human betal-adreno
32	187	13.9	1637	22	AAF61184	Human betal-adreno
33	187	13.9	1637	22	AAF61185	Human betal-adreno
34	187	13.9	1637	22	AAF61186	Human betal-adreno
35	187	13.9	1637	22	AAF61187	Human betal-adreno
36	187	13.9	1637	22	AAF61188	Human betal-adreno
37	187	13.9	1637	22	AAF61189	Human betal-adreno
38	187	13.9	1723	21	AAA38338	Human beta-adrener
39	187	13.9	1723	21	AAZ98399	Human betal-adreno
40	187	13.9	1723	24	ABK92208	Prostate cancer-as
41	187	13.9	1723	24	ABK40731	Human betal-adreno
42	179.4	13.3	1525	21	AAZ98405	Mouse betal-adreno
43	179.4	13.3	1525	24	ABK40737	Mouse betal-adreno
44	177.4	13.1	44242	23	ABL19930	Drosophila melanog
45	177	13.1	1038	23	ABL19931	Drosophila melanog

ALIGNMENTS

RESULT 1	
AAI99918	
ID	AAI99918 standard; DNA; 1350 BP.
XX	
AC	AAI99918;
XX	
DT	18-FEB-2002 (first entry)
XX	
DE	Human alpha-2AAR variant encoding DNA.
XX	
KW	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW	polymorphic site; allelic variant; cardiovascular disease;
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW	phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.
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OS	Homo sapiens.
XX	
FH	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	1..1353
FT	/*tag= a
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FT	replace(753,C)
FT	/*tag= b
XX	
PN	WO200179561-A2.
XX	
PD	25-OCT-2001.
XX	
PF	17-APR-2001; 2001WO-US12575.
XX	
PR	17-APR-2000; 2000US-0551744.
PR	10-AUG-2000; 2000US-0636259.

REFERENCE 3 (bases 1 to 966)

AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source

1. .966
location/Qualifiers

/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone="152E12"

/clone_1b="G"

BASE COUNT 197 a 283 c 303 g 175 t 8 others

ORIGIN

Query Match

15.98; Score 214.6; DB 17; Length 966;

Best Local Similarity 75.5%; Pred. No. 2.6e-29;

Matches 265; Conservative 1; Mismatches 85; Indels 0; Gaps 0;

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OY 82 TACTCCCTGCAGGTGACGCTGACGCTGGTGTGCTGGCCGCTGCTCATGCTCACC 141
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 608 TACTCCTTAGGGGACCGCGGCATCGCCGCGCTGCTTAGCTTCATCTCTACAG 667

OY 142 GTGTCGGCAACGTGCTCGTCATCATCGCCGCTGTCACGAGCCGCGCTCAAGCGCCC 201
   ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 668 GTGTCGGGAACATCTGTGTGTGTGTCGCGGTGTGACGAGCCGCGCTCAGAGCGCCG 727

OY 202 CAAAACCTCTTCCTGTGTCTTGCCCTCGGCCGACATCCTGTGGCCACGCTGTCATC 261
   || ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 728 CAGAACCTCTTCCTGTGTGTGTGTCGACCGCGGACATCCTGTGCGCACCTGTGATG 787

OY 262 CCTTTCGCTGGCCACGAGTCATGGGCTACTGTGTACTTCGGCAAGGCTTGTGCGAG 321
   || ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 788 CCTTTCGCTGGCCACGAGTCATGGGCTACTGTGTATTCGGCAGAGTCTGTGCGGG 847

OY 322 ATCTACCTGGCGCTGACGCTGCTTCTGACGTCGTCCATCGTGACACCTGTGCGCATC 381
   || ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 848 ATTATCTGGCTCTGGATGTTTATCTGACACCTCGTCGATCGTCCATCTGTGCGCAATA 907

OY 382 AGCTGACCGCTACTGTGTCATCACACAGGCCATCGAGTACAACCTGAAG 432
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Db 908 AGCTGGACCGCTACTGTGTGTGTGACGAGCGGCTCCAGTACAACCTGAAR 958
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Search completed: February 15, 2003, 18:03:06
Job time : 2700.44 secs

Directionally cloned using the following adaptors:

5'-TCGACCCACGCGTCGG-3' and
5'-GACTAGTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

BASE COUNT 130 a 343 c 278 g 184 t
ORIGIN

Query Match 18.9%; Score 255.2; DB 14; Length 935;
Best Local Similarity 96.6%; Pred. No. 1.1e-36;
Matches 282; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

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Db 394 ATGGGCTCCCTGCAGACCGGAGCGGGGCAACGCGAGCTGGAACGGGACCGAGCGCGGG 453
OY 61 GCGGGCGCGCGGCAACCCCTTACTCCCTGCAGGTGACGCTGACGCTGCTGCTGCC 120
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Db 454 GCGGGCGCGCGGCAACCCCTTACTCCCTGCAGGTGACGCTGACGCTGCTGCTGCC 513
OY 121 GGCCTGCTCATGCTGCTCACCCTGTTCGGCAACGCTGCTGCTCATATCGCCGTTCACG 180
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Db 514 GGCCTGCTCATGCTGCTCACCCTGTTCGGCAACGCTGCTGCTCATATCGCCGTTCACG 573
OY 181 AGCCGGCGGCTCAAGGCGGCGGCAAAACCTCTTCTGCTGCTGCTGCC-TCGGCGGACAT 239
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Db 574 AGCCGGCGGCTCAAGGCGGCGGCAAAACCTCTTCTGCTGCTGCTGCC 633
OY 240 CCTGTGGCCACGCTGCTCATCCC-TTTCCTGCTGGCCCAACGAGGTATGGG 290
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Db 634 CCTGTGGCCACGCTGCTCATCCC-TTTCCTGCTGGCCCAACGAGGCTTGG 685

RESULT 14
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LOCUS
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Or1 end of clone
012P03 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL236849.1 GI:7895984
VERSION
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 896)
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 896)
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 896)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source Location/Qualifiers
1. 896
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="012P03"
/clone_1b="G"
/note="Genoscope sequence ID : C08G012CH02SP1-end :
PUC-Or1"

BASE COUNT 163 a 276 c 295 g 157 t 5 others
ORIGIN

Query Match 16.8%; Score 226.4; DB 17; Length 896;
Best Local Similarity 75.1%; Pred. No. 1.9e-31;
Matches 281; Conservative 1; Mismatches 92; Indels 0; Gaps 0;

OY 82 TACTCCCTGCAGGTGACGCTGACGCTGCTGCTGCTGCGCCCTGCTCATGCTCACC 141
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Db 498 TACTCCTTAGGGCCACCGCCGGCATCGCCGCTGCTCAGCTTCTCATCTGTTACG 557
OY 142 GTGTTCGGCAACGTGCTCATCATCGCCGTGTTACAGAGCCGCGGCTCAAGCGCCC 201
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Db 558 GTGTTCGGGAACATCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 617
OY 202 CAAACCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 261
|||||
Db 618 CAGAACCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 677
OY 262 CCTTCTCGCTGGCCAAAGAGTATGAGGCTACTGCTACTGCTACTGCTACTGCTACTGCT 321
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Db 678 CCTTCTCGCTGGCCAAAGAGTATGAGGCTACTGCTACTGCTACTGCTACTGCTACTGCT 737
OY 322 ATCTACCTGGCGCTGCAGCTGCTCTTCTGCAGCTGCTCATGCTGACCTGCGCCATC 381
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Db 738 ATTTATCTGGCTCTGATGTTTATTTCTGCACCTGCTGATCGTCCATCTGCGCAATA 797
OY 382 AGCTTGACCCGCTACTGCTCATCACAGAGCCATCGAGTACAACTGAAGCGCAGCGG 441
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Db 798 AGCTTGACCCGCTACTGCTGCTCATCGCAGAGCGGCTCCAGTACAACTGAAGAGACCCCT 857
OY 442 CGCCGCATCAAGG 455
Db 858 CAGCGCGTMAAGGCG 871

RESULT 15
CNS02NV2 966 bp DNA linear GSS 14-MAY-2000
LOCUS
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
152E12 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL205895.1 GI:7864714
VERSION
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 966)
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 966)
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished


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Db      58  TCGGGGACAGAGCGGAT 38
|||||
RESULT 10
AL530418
LOCUS      AL530418
DEFINITION AL530418 LTI_NFL001_NBC4 Homo sapiens cDNA clone CSDD007YE02 5
prime, mRNA sequence.
ACCESSION AL530418
VERSION    AL530418
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 867)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="CSDD007YE02"
            /clone_lib="LTI_NFL001_NBC4"
            /sex="male"
            /tissue_type="neuroblastoma cells"
            /lab_host="DH10B"
            /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
            was primed with a NotI-oligo(dT) primer. Five prime end
            enriched, double-stranded cDNA was digested with Not I and
            cloned into the Not I and Eco RV sites of the pCMVSPORT 6
            vector. Library was normalized. Library was constructed
            by Life Technologies. Contact : Feng Liang Life
            Technologies, a division of Invitrogen 9800 Medical Center
            Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
            8371 Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com"

BASE COUNT 98 a 315 c 286 g 143 t 25 others
ORIGIN
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```
Query Match      23.5%; Score 317.6; DB 9; Length 867;
Best Local Similarity 76.8%; Pred. No. 5.4e-48;
Matches 407; Conservative 8; Mismatches 102; Indels 13; Gaps 2;
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OY      105  GCTGTGCTGCTGGCGGCTGCTCATGCTGCACCGTGTGGCAAGTGTCTCAT 164
||||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      351  GCTGGCTKCCGTTGTGGGCTTCTCATGCTTTCACCGTGTGGCAAGTGTGCT 410

OY      165  CATCGCGGTTCACGAGCGCGGCTCAAGGCGCCCAAAACCTCTTCTGCTCTCT 224
||||| | | | | | | | | | | | | | | | | | | | | | | | | |
DB      411  GATCGCGTTCGACCAAGCGGCGCT-GCGCCCCACAAACCTTCTTCTGTCGCT 469

OY      225  GGCTTGGCGGACATCTGTGGCCACGCTGTCATCCCTTCTCTGCTGGCAAGAGT 284
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB      470  TGCCTTGGCCGACATCCTGTGGCCACGCTGTCATGCCCTTCTCTGTCGCAAGAGT 529

OY      285  CATGGCTACTGTGACTTGGCAAGGCTTGTGAGATCTACCTGGCGCTGAGAGTCT 344
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB      530  CATGGCTACTGTGACTTGGGCAAGGTGTGTGGGCGCTGTACCTGGCGCTGATGTCT 589

OY      345  CTTCTGACAGTGTGTCATGTCACCTGTGCGCATGAGCCTTGACCGCTACTGTCCAT 404
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      590  GTTTTGACACTGTGATCGTCGATCTGTGTGCCAACAGCCTTGACCGCTACTGKCGGT 649

OY      405  CACACAGGCCATGAGTACAACTGAAGCGCAGCGCGCGGCATCAAGGCCATCATCAT 464
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      650  GACGAGGCGCGTGAAGTACAACTGAAGCGCACACGCGCGGTCAAGGCCACCATCTCT 709
```

```
OY      465  CACCGTGTGGTATCTGCGCCGTCATCTCTCCCGCCGCTCATCTCATCGAAGAA 524
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      710  GGCGTTGTGCTCAWCTGGCGGCTGATCTCTCCCGCCGCTGCTCTGCTACCGCCA 769

OY      525  GGGCGGCGGCGGCGCGCCGAGCCGCGCGCTGCGAGATCAACGACGAGAAGTG 584
| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      770  GCCCGACGGCG-----CCGCTACCCCGAGTGCSSCTCAACGACGAGACCCG 817

OY      585  GTACGTATCTGCTGTCGATCGGCTCTCTTCTGCTCCCTGCTCATCA 634
||||| | | | | | | | | | | | | | | | | | | | | | | | |
DB      818  GTACATCTCTCTCTCGATCGGCTCCCTCTTCCGCCCTGCTCAACA 867
```

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RESULT 11
BQ887729
LOCUS      BQ887729
DEFINITION AGENCOURT_876435 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313133
5', mRNA sequence.
ACCESSION BQ887729
VERSION    BQ887729
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 988)
AUTHORS   NIH-MGC http://mgc.ncl.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cga@bs-r@mail.nih.gov
            Tissue Procurement: Susan L. Sullivan, PhD.
            cDNA Library Preparation: Resgen, Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.lnl.gov
            plate: LLM13739 row: m column: 06
            High quality sequence start: 8
            High quality sequence stop: 509.
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FEATURES
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            /clone_lib="NIH_MGC_129"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: olfactory epithelium; Vector:
            pCMV-SPORT6.1.ccd; Site_1: EcoRV; Site_2: NotI; Cloned
            unidirectionally. Primer: Oligo dT. Average insert size
            2.2 kb. Constructed by Resgen, Invitrogen Corp. Note: this
            is a NIH_MGC Library."
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BASE COUNT 158 a 349 c 300 g 181 t
ORIGIN
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Query Match      23.5%; Score 317.4; DB 14; Length 988;
Best Local Similarity 74.4%; Pred. No. 5.9e-48;
Matches 432; Conservative 0; Mismatches 136; Indels 13; Gaps 2;
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OY      169  GCCGTGTTACGAGCGCGGCTCAAGCGCCCAAAACCTTCTCTGCTGTGCTG 228
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DB      19   GCTGTGTGACACGCGGACACTGCGGCGCCCGCAGAACCTTCTCTGCTG 78

OY      229  TCGGCGG-ACATCTGTGTGGCACGCTGTCATCCCTTCTGCTGGCCACGAGTCTAT 287
|| || | ||||| ||||| ||||| || ||||| || ||||| || ||||| || |||||
DB      79   TCAGCTACACATCTGTGTGGCCACACTGTCATGCCCTTCTCTGCGCAATGAGCTCAT 138

OY      288  GGGCTACTGTGTTGCGAAGGCTGTGCGAGATCTACTGCGGCTGAGCGTCTCTT 347
|| ||||| ||||| ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB      139  GGCTACTGTGTTGCGGCAAGTGTGTGTGTATACCTGCGCACTGAGCGTCTCTT 198
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[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
SOURCE	ORGANISM	human.		
		Homo sapiens		
		Eumaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
		1 (bases 1 to 358)		
		Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T., Jackson,Y. and Bowers,Y.		
		Endocrine Pancreas Consortium		
		Unpublished (2000)		
		Other_ESTs: ig69h02.xl		
		Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue		
		Endocrine Pancreas Consortium		
		Harvard University, Howard Hughes Medical Institute		
		Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138		
		Tel: 617-495-1812		
		Fax: 617-495-8557		
		Email: dmelton@biohp.harvard.edu		
		Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:		
		Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue		
		(hinoue@im.wustl.edu)		
		Possible reversed clone: similarity on wrong strand		
		Seq primer: -40RP from G1bco		
		High quality sequence stop: 342.		
		Location/Qualifiers		
		1. 358		
		/organism="Homo sapiens"		
		/db_xref="taxon:9606"		
		/clone_lib="HR85 islet"		
		/tissue_type="Purified pancreatic islet"		
		/lab_host="DH10B"		
		/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size -1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."		
		BASE COUNT		
		76 a 114 c 115 g 53 t		
		ORIGIN		
		Query Match		
		Best Local Similarity 99.7%; Pred. No. 2.3e-48;		
		Matches 320; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
		Score 319.4; DB 13; Length 358;		
		Query 1026 CGGGACGCCGGCTGCAGGGCCGGGGAGGAGCGCGTCGGGCTGCCAAGCGTCGGCGCTG 1085		
		Db 358 CGGGACGCCGGCTGCAGGGCCGGGGAGGAGCGCGTCGGGCTGCCAAGCGTCGGCGCTG 299		
		Query 1086 GCGCGGGCGGAGAACCGCGAGAGCGCTTCACGTTCTGCTGGCCGTGGTTCATCGGAGT 1145		
		Db 298 GCGCGGGCGGAGAACCGCGAGAGCGCTTCACGTTCTGCTGGCCGTGGTTCATCGGAGT 239		
		Query 1146 GTTCGTGCTGTGCTGTTCCCTTCTTCTTACCTACACGCTCACGGCCGCGGGTCTC 1205		
		Db 238 GTTCGTGCTGTGCTGTTCCCTTCTTCTTACCTACACGCTCACGGCCGCGGGTCTC 179		
		Query 1206 CGTCCACGACGCGCTTCAAAATTCTTCTGTTGCGGCTACTGCAACAGCTCGTTGAA 1265		
		Db 178 CGTCCACGACGCGCTTCAAAATTCTTCTGTTGCGGCTACTGCAACAGCTCGTTGAA 119		
		Query 1266 CCGGTCATCTACACCATCTTCAACACGATTTCCGCCGCGCCTTCAAGAGATCCTCTG 1325		
		Db 118 CCGGTCATCTACACCATCTTCAACACGATTTCCGCCGCGCCTTCAAGAGATCCTCTG 59		
		Query 1326 TCGGGGGGAGACAGGAAGCGGAT 1346		

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Db 121 CGTCGGCTGCGCGCGCGGCGGACAGAACCCGAGAGCGCTTCAAGTTCGTGCTGCGCCGTGG 180
QY 1136 TCATCGGAGTGTCTGTTGTTGTTGTTCCCTTCTTCTTCACTACACGCTCAGCGCG 1195
Db 181 TCATCGGAGTGTCTGTTGTTGTTGTTCCCTTCTTCTTCACTACACGCTCAGCGCG 240
QY 1196 TCGGGTGTCCGTCGCCACGACGCTCTTCAAAATTCTTCTGTTGCTGCGCTACTGCAACA 1255
Db 241 TCGGGTGTCCGTCGCCACGACGCTCTTCAAAATTCTTCTGTTGCTGCGCTACTGCAACA 300
QY 1256 GCTCGTTGAACCCGCTCATCTACACCATCTTCAACACGAGATTCCGCGCGCTTCAAGA 1315
Db 301 GCTCGTTGAACCCGCTCATCTACACCATCTTCAACACGAGATTTCGCGCGCTTCAAGA 360
QY 1316 AGATCCTCTGTCGGGGGAGACAGACGGATCGTG 1350
Db 361 AGATCCTCTGTCGGGGGAGACAGACGGATCGTG 395

RESULT 7
AL544609 1077 bp mRNA linear EST 16-FEB-2001
LOCUS AL544609 LTI_NFL006_PL2 Homo sapiens CDNA clone CS0DI021YC24 5
DEFINITION prime, mRNA sequence.
ACCESSION AL544609
VERSION AL544609.1 GI:12877089
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1077)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..1077
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI021YC24"
/clone_1lb="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 124 a 397 c 385 g 168 t 3 others
ORIGIN

Query Match 27.0%; Score 364.8; DB 9; Length 1077;
Best Local Similarity 75.1%; Pred. No. 1.5e-56;
Matches 500; Conservative 0; Mismatches 152; Indels 14; Gaps 3;
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Db 480 CGGGCGCT-GCGCGCCACAGAACCTCTTCCCTGTTGTCGCTGCGCTCGCCGACATCCTG 538
QY 244 GTGGCCACGCTGTCATCCCTTCTCGCTGCGCCAAAGAGTCAAGGCTACTGTACTTTC 303
Db 539 GTGGCCACGCTGTCATGCCCTTCTCGTTGCGCCAAAGAGTCAAGGCTACTGTACTTTC 598
QY 304 GGCAGAGCTTGTGGAGATCTACCTGGCGCTCGACGTGCTCTTTCGACAGTCCATC 363
Db 599 GGGCAGGTGTGGTGGCGGTGTACCTGGCGCTCGATGTGCTGTTTGCACCTCGTGATC 658
QY 364 GTGCACCTGTGGCCATCAGCCTTGACCCGCTACTGTGTCATCACAGGCCATCGAGTAC 423
Db 659 GTGCATCTGTGTGCCATCAGCCTTGACCCGCTACTGTGTTGAGCAGGCCGTCGAGTAC 718
QY 424 AACCTGAAGCGCAGCGCGCGCGCATCAAGGCCATCATCATCACCGT-GTGGGTCACTC 482
Db 719 AACCTGAAGCGCAGCAGCGCGCGCATCAAGGCCACCATCGTGGCGCTCATCTC 778
QY 483 GCGCGTCATCTCTCCCGCGCTCATCTCCATCGAGAAGAGCGCGCGCGCGCC 542
Db 779 GCGCGTCATCTCTCTCCCGCGCTGTGTCCTCTACCGCAGCCGACGCGG----- 831
QY 543 GCAGCCGCGCAGCGCGCTGCGAGATCAAGCAGACGAGTGTGATCTCTGTCGTG 602
Db 832 -----CCGCGTACCCGAGTGCAGCGCTCAAGCAGACGACCTGTGATCTCTCTCTG 886
QY 603 CATCGGCTCTTCTTCCGCTCCCTGCGCTCATCATGATCCTGTGTACTGCGCATCTACCA 662
Db 887 CATCGGCTCTTCTTCCGCGCGCTGCGCTCATCATGAGCCCTGTGTACTGCGCATCTACCG 946
QY 663 GATCGCCAAAGCTGCGACCCGCGGTGCCACCCAGCCGCGGGGTCCGAGACGCCGTGCCC 722
Db 947 AGTGCCAAAGCTGCGCAGCGCGCAGCTCAGCAGAGAGCGCGCCCGCGTGGCCCGACGG 1006
QY 723 GCCGCC 728
Db 1007 TCGGTC 1012

RESULT 8
GGAA2AAR 855 bp DNA linear GSS 14-SEP-2001
LOCUS GGAA2AAR
DEFINITION chicken alpha2 adrenergic receptor gene fragment probably subtype
a, genomic survey sequence.
ACCESSION AL606540
VERSION AL606540.1 GI:15591915
KEYWORDS GSS; Alpha2 adrenergic receptor gene.
SOURCE chicken.
ORGANISM Gallus gallus
REFERENCE 1 (bases 1 to 855)
AUTHORS Hunter, C. and Elgar, G.
TITLE Alpha2 adrenergic receptor gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 855)
AUTHORS Hunter, C.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hmp.mrc.ac.uk

FEATURES
source
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/organism="Gallus gallus"
/db_xref="taxon:9031"

BASE COUNT 201 a 248 c 245 g 161 t
ORIGIN

Query Match 23.8%; Score 321; DB 17; Length 855;
Best Local Similarity 64.6%; Pred. No. 1.3e-48;
Matches 614; Conservative 0; Mismatches 235; Indels 102; Gaps 5;
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TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@email.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1671 row: m column: 11
High quality sequence stop: 716.
FEATURES
source
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/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTNN-3', size-selected for average insert size 2.2 kb and normalized to ROP 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 149 a 303 c 290 g 151 t
ORIGIN
Query Match 30.4%; Score 410.6; DB 13; Length 893;
Best Local Similarity 86.0%; Pred. No. 7.3e-65;
Matches 586; Conservative 0; Mismatches 74; Indels 21; Gaps 11;
QY 1 ATGGGCTCCCTGCGAGCCGGGCGGCAACGCGAGCTGAACGGGACCGCGCGGG 60
Db 213 ATGGGCTCCCTGCGAGCCGGGCGGCAACGCGAGCTGAACGGGACCGCGCGGG 272
QY 61 GCGGGCGCGCGGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGGCTGGCC 120
Db 273 GCGGGCGCGCGGGCCACCCCTTACTCCCTGCAGGTGACGCTGGTGGCTGGCC 332
QY 121 GGCCTGCTCATGCTGCTACCGTGTGGCAACGCTGCTCATCATCGCCGCTGTCACG 180
Db 333 GGCCTGCTCATGCTGCTACCGTGTGGCAACGCTGCTCATCATCGCCGCTGTCACG 392
QY 181 AGCCGCGCGCTCAAGCGCGCCCAAAACCTCTTCTGCTGTCTCTGG--CCTCGGCGGACA 238
Db 393 AGCCGCGCGCTCAAGCGCGCCCAAAAGACTCTTCTGCTGTCTCTGACCTCGACGAAAT 452
QY 239 TCCGTGTGGCCACGCTCGT-CATCCCTTTTCTGCTGGCCCAAGAGGTGCTAGGCTACTGG 297
Db 453 TCCGTGTGGCCACGCTCGTACATCCCTTTCTGCTGGCCCAAGAGGTGCTAGGCTACTGG 512
QY 298 TACTTCGGCAA-GGCTTGTGGG-AGATCTACCTGGCGCTCGACGTGCTTTCGACGT 355
Db 513 TACTTCGGCAAAGGGCTTGGTGGCAAGATCTACCTGGCGCTCGACGTGCTTTCGACGT 572
QY 356 -CGTCCATCTGTCACCTGTGGCCCATCAGCCTGGACCCGCTACTGCTCATCACACAGGCC 414
Db 573 ACCTCCATCTGTCACCTGTGGCCCATCAGCCTGGACCCGCTACTGCTCATCACACAGGCC 632
QY 415 ATCGAGTACAACCTGAAGCGCACGCGCGCGCATCAAGGCCATCATCATCACCGTGTGG 474
Db 633 ATCGAGTACAACCTGAAGCGCACGCGCGCGCATCAAGGCCATCATCATCACCGTGTGG 692
QY 475 GTC-ATCTCGCGCGTCACTCTCTCCG-----CCGCTCATCTCCATCGAGAAGAAG 526
Db 693 GTCAATCTCGCGCGTCACTCTCTCCGCGCGGCTTCATCTCCACTCGAGAACAAGGGG 752

QY 527 GCGGGCGCGCGGGCCC-GCAGCCCGCCGAGCCGGCTCGGAGATCAACGA--CCAGAAGT 583
Db 753 CGGAGAGAGCGGGCCCCAGGAAGCGGGCCGAGCCCGCGGAGAGATCAGCAGCAGAAAG 812
QY 584 GGTACGTATCTCGTGTG--CATCGGCTCTTCTTCGCTCCCTGCCTCATCATGATCC 640
Db 813 GTACGTAATTGTGAGATCGTGAATGATACTTTGTTCGCTCCCTGTCATCAGAGTCC 872
QY 641 TGGTCTACGTGCGCATCTACC 661
Db 873 TGG-CAACGCGGCATATACC 892
RESULT 6
BI838282 740 bp mRNA linear EST 04-OCT-2001
LOCUS 603083213F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222475 5',
DEFINITION mRNA sequence.
ACCESSION BI838282
VERSION BI838282
KEYWORDS BI838282.1 GI:15949832
SOURCE EST.
ORGANISM human.
REFERENCE 1 (bases 1 to 740)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@email.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1559 row: 1 column: 04
High quality sequence stop: 740.
FEATURES
source
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/db_xref="taxon:9606"
/clone="IMAGE:5222475"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT 115 a 240 c 235 g 150 t
ORIGIN
Query Match 29.3%; Score 395; DB 13; Length 740;
Best Local Similarity 100.0%; Pred. No. 4.8e-62;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 956 GCAAGGCCGAGAGCCAGGTGAAGCCGGCGGACAGCCTGCCGGCGCGGGCGGGG 1015
Db 1 GCAAGGCCGAGAGCCAGGTGAAGCCGGCGGACAGCCTGCCGGCGCGGGCGGGG 60
QY 1016 CGACGGGATCGGAGACCGCGGCTGCAGGGCGGGGAGAGAGCGGCTCGGGCTGCCAAG 1075
Db 61 CGACGGGATCGGAGACCGCGGCTGCAGGGCGGGGAGAGAGCGGCTCGGGCTGCCAAG 120
QY 1076 CGTCGCGCTGGCGCGGGCGAGAACCGGAGAAAGCGTTACGTTGCTGGCCGTGG 1135

Db 446 AGTCGGCGCTCAAAAGCTCCCCAAACCTCTTCTTGTTGCCCTGGCCTCAGCGGACATC 387

QY 241 CTGGTGGCCACGCTCGTCATCCCTTTCTGCTGGCCACGAGGTGATGGCTACTGTAC 300

Db 386 CTGGTGGCCACGCTGGTCAATCCCTTTCTTTGGCCACGAGGTATGGGTACTGTAC 327

QY 301 TTGGGCAAGGCTGGTGGCGAGATCTACCTGGCGCTCGACGTGCTCTTGCACGCTGCC 360

Db 326 TTGGTAAAGGTGGTGGTGTGAGATCTATTGGCTCTCGACGTGCTCTTTGCACGCTGCC 267

QY 361 ATGTGCACCTGTGGCCCATCAGCCCTGAGCCGCTACTGTGTCATCAGACAGGCCATGAG 420

Db 266 ATAGTGACACCTGTGGCCCATCAGCCCTGAGCCGCTACTGTGTCATCAGCAGGCCATGAG 207

QY 421 TACAACCTGAAGCCGACGCGCGCGCATCAAGGCCATCATCATCACCCTGTGGTCATC 480

Db 206 TACAACCTGAAGCCGACGCGCGCGCATCAAGGCCATCATCATCACCCTGTGGTCATC 147

QY 481 TCGGCCGTCACTCTCCCGCGCTCATCTCCATCGAGAGAAGCGCGCGCGCGCG 540

Db 146 TCGGCTGTCACTCTCTCCCGCGCTCATCTCCATAGAGAGAAGCGCGCGCGCGCG 87

QY 541 CCGCAGCCGCGCGCGCGCGCTGCGAGATCAACGACGACGAGAGTGCTCATCTCTCG 600

Db 86 CAGCAGCCGCGCGCGCGCGAGCTGCAAGATCAACGACGACGAGAGTGCTCATCTCTCG 27

QY 601 TGCATCGGCTCTCTCTCTGCTCCCT 625

Db 26 TCCATCGGCTCTCTCTCTGCGGCTT 2

RESULT 4

LOCUS BQ129312/c 453 bp mRNA linear EST 29-APR-2002

DEFINITION 1j34d05.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:6136736 5' similar to SW:A2AA_HUMAN P08913

ALPHA-2A ADRENERGIC RECEPTOR ; mRNA sequence.

BQ129312

ACCESSION BQ129312.1 GI:20203223

VERSION BQ129312.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 453)

AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Rittler,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R., Williams,T., Jackson,Y. and Bowers,Y.

TITLE Endocrine Pancreas Consortium

JOURNAL Unpublished (2000)

COMMENT Other_ESTs: 1j34d05.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center This clone is available royalty-free through LNL; please contact the IMAGE consortium (info@image.lnl.gov) for further information

Possible reversed clone: similarity on wrong strand

Seq primer: -40RP from Gibco.

FEATURES

source

1..453

location/Qualifiers

organism="Homo sapiens"

db_xref="taxon:9606"

clone="IMAGE:6136736"

/clone_1lb="Melton Normalized Human Islet 4 N4-HIS 1"

/sex="Both"

/tissue_type="Islets of Langerhans"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

BASE COUNT 41 a 189 c 164 g 59 t

ORIGIN

Query Match 33.4%; Score 451.4; DB 14; Length 453;

Best Local Similarity 99.8%; Pred. No. 2.7e-72;

Matches 452; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 718 GCCCGCCGCGGGGGGCGACCGAGCGGCGCCCAAGGCTGTGGCCCCCGAGCGCGG 777

Db 453 GCCCGCCGCGGGGGGCGACCGAGCGGCGCCCAAGGCTGTGGCCCCCGAGCGCGG 394

QY 778 GGGCGGGGGGGCGCAGAGCCGAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAG 837

Db 393 GGGCGGGGGGGCGCAGAGCCGAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAG 334

QY 838 CCGCGCCGCGCGCGCGCGCGGCGACACCGCGCTGGACCTGGAGAGAGCTGCTTCC 897

Db 333 CCGCGCCGCGCGCGCGCGCGGCGACACCGCGCTGGACCTGGAGAGAGCTGCTTCC 274

QY 898 GACCAAGCCGAGCGGCTTCCAGGGGGCGCCGACCCGAGCGCGGTCCCGGGGCAAGGC 957

Db 273 GACCAAGCCGAGCGGCTTCCAGGGGGCGCCGACCCGAGCGCGGTCCCGGGGCAAGGC 214

QY 958 AAGCCCCGAGCGACCGTGAAGCCCGGGCGACACCTCGCGCGCGCGGGCGGCGG 1017

Db 213 AAGCCCCGAGCGACCGTGAAGCCCGGGCGACACCTCGCGCGCGCGGGCGGCGG 154

QY 1018 ACGGGATCGGAGCGCGGCTGCAGAGGGCGGGGAGAGCGCGTGGGCTGCCAAGCG 1077

Db 153 ACGGGATCGGAGCGCGGCTGCAGAGGGCGGGGAGAGCGCGTGGGCTGCCAAGCGG 94

QY 1078 TCGCGCTGGCGCGGGGCGAGAACCGGAGAGGCTTCACGTCTGCTGGCGCTGTC 1137

Db 93 TCGCGCTGGCGCGGGGCGGAGAACCGGAGAGGCTTCACGTCTGCTGGCGCTGTC 34

QY 1138 ATCGAGTGTCTGCTGCTGCTGCTTCCCTTC 1170

Db 33 ATCGAGTGTCTGCTGCTGCTGCTTCCCTTC 1

RESULT 5

LOCUS BI459381 893 bp mRNA linear EST 21-AUG-2001

DEFINITION 603200147F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5266354 5', mRNA sequence.

ACCESSION BI459381

VERSION BI459381.1 GI:15250037

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 893)

AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.

Query Match	36.28;	Score 488.8;	DB 14;	Length 492;
Best Local Similarity	99.6%;	Pred. No. 4.4e-79;		
Matches 490;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY 679	ACCCGCGTCCACCCAGCCGCCGGGGTCCGACCCCGTCCGCCGCCGCCGGGGGGCACC	738		
Db 492	ACCCGCGTCCACCCAGCCGCCGGGGTCCGACCCCGTCCGCCGCCGCCGGGGGGCACC	433		
QY 739	GAGCGCAGGCCCAAGGGTCTGGGCCCCGAGCGCAGCGCGGGCCCGGGGGCGCAGAGCC	798		
Db 432	GAGCGCAGGCCCAAGGGTCTGGGGCCCCGAGCGCAGCGCGGGCCCGGGGGCGCAGAGCC	373		
QY 799	GAACCGCTGCCACCCAGCTCAACGGCGCCCTCTGGCGAGCCCGCGCCGGCGCGCGC	858		
Db 372	GAACCGCTGCCACCCAGCTCAACGGCGCCCTCTGGCGAGCCCGCGCCGGCGCGCGC	313		
QY 859	GACACCGCAGCGCTTGACCTGGAGGAGAGCTCGTCTTCCGACCAAGCCGAGCGGCTCCA	918		
Db 312	GACACCGCAGCGCTTGAGACCTGGAGGAGAGCTCGTCTTCCGACCAAGCCGAGCGGCTCCA	253		
QY 919	GGGCCCCCGCAGACCCGAGCGCGGTCCCCGGGGCAAGGCAAGGCCCGAGCGAGCCAGGTG	978		
Db 252	GGGCCCCCGCAGACCCGAGCGCGGTCCCCGGGGCAAGGCAAGGCCCGAGCGAGCCAGGTG	193		
QY 979	AAGCCGGGCGACAGCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT	1038		
Db 192	AAGCCGGGCGACAGCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT	133		
QY 1039	GCAGGCGCGGGGAGAGCGCGCTCGGGGCTGCCAAGCGCTCGCGCTGGCGCGGGCGCGCAG	1098		
Db 132	GCAGGCGCGGGGAGAGCGCGCTCGGGGCTGCCAAGCGCTCGCGCTGGCGCGGGCGCGCAG	73		
QY 1099	AACCGCGAGAACCGCTTCAAGTCTGCTGCGCCGCTGCTCATCGGAGTGTCTGCTGTGTC	1158		
Db 72	AACCGCGAGAACCGCTTCAAGTCTGCTGCTGCGCCGCTGCTCATCGGAGTGTCTGCTGTGA	13		
QY 1159	TGTTTCCCCCTTC 1170			
Db 12	TGTTTCCCCCTTC 1			
RESULT 3				
LOCUS	BB643669/c			
DEFINITION	BB643669 RIKEN full-length enriched, adult male corpora quadrigemina Mus musculus cDNA clone B230352011 5', mRNA sequence.			
ACCESSION	BB643669			
VERSION	BB643669.1			
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE				
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasakia,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y.			
	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)			
	Unpublished (2001)			
TITLE	Contact: Yoshihide Hayashizaki			
JOURNAL	Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute			
COMMENT	The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan			
	Tel: 81-45-503-9222			
	Fax: 81-45-503-9216			
	Email: genome-res@sc.riken.go.jp,			
	URL:http://genome.gsc.riken.go.jp/			
	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh			

, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura,
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,
Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanka, I., Aizawa,
K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES
source
Location/Qualifiers
1. 691
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="B230352011"
/clone_lib="RIKEN full-length enriched, adult male corpora
quadrigemina"
/sex="male"
/tissue_type="corpora quadrigemina"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAATCCAGACGCTTTTGTTCCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

BASE COUNT 158 a 182 c 233 g 118 t
ORIGIN

Query Match 35.5%; Score 479; DB 10; Length 691;
Best Local Similarity 87.5%; Pred. No. 2.8e-77;
Matches 547; Conservative 0; Mismatches 75; Indels 3; Gaps 2;

Dy 1 ATGGGCTCCCTGCAGCCGAGCGGGCAACGCGAGCTGGAACGGAGCCGAGCGCGGG 60
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Db 623 ATGGGCTCCCTGCAGCCGAATGCGGCACAGC-AGCTGGAACGGAGCCAGCGCGGAG 565

Dy 61 GGCGGGCGCGGGGCCAACCCCTTACTCCCTGCAGGTGAAGCTGACGCTGTGTGCGCTGGCC 120
 | | || ||||| ||||| ||||| ||||| |||||
Db 564 G-CGGCACCCAGCCCGCCCTTACTCCCTGCAGGTGACACTGACGCTGTGCTGGCTGGCT 507

Dy 121 GGCTGCTCATGTGCTCACCCTGTGCGCAACGCTGCTCATCATCGCCGCTGTTACAG 180
 ||||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 506 GGCCTGCTCATGTGTTACACAGTATTGGCAACGCTGTGTTATTATCGCGGTGTTACAC 447

Dy 181 AGCCGCGCGCTCAAGCGCGCCCAAAACCTCTTCTGTGTGTTCTTGCGCTGGCGGCACATC 240
 || ||||||| || ||||||| ||||| ||||| || |||||

Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 445.

FEATURES

source
1. 561
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 63 a 215 c 210 g 73 t
ORIGIN

Query Match 41.4%; Score 559.4; DB 14; Length 561;
Best Local Similarity 99.8%; Pred. No. 7e-92;
Matches 560; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 610 TCCTTCTTCGCTCCCTGCCTCATCATGATCCTGTCTACGTGCGCATCTACAGATCGCC 669
DB 561 TCCTTCTTCGCTCCCTGCCTCATCATGATCCTGTCTACGTGCGCATCTACAGATCGCC 502
OY 670 AAGCGTCGACCCGCGGTGCCACCAACCGCGGGGTCCGACGCCGTGCGCGCGCCCG 729
DB 501 AAGCGTCGACCCGCGGTGCCACCAACCGCGGGGTCCGACGCCGTGCGCGCGCCCG 442
OY 730 GGGGGCAGCAGCGCAGCGCCCAAGGGTCTGGCCCCCAGCGCAGCGCGGGCGGGGGCC 789
DB 441 GGGGGCAGCAGCGCAGCGCCCAAGGGTCTGGCCCCCAGCGCAGCGCGGGCGGGGGCC 382
OY 790 GCAGAGGCGGAACCGCTGCCACCAAGCTCAACGGCGGCCCTGGCGAGCCCGCGCGCC 849
DB 381 GCAGAGGCGGAACCGCTGCCACCAAGCTCAACGGCGGCCCTGGCGAGCCCGCGCGCC 322
OY 850 GGGCGCGCGACACCGACGCGCTGGACCTGGAGAGAGCTGCTTCCGACACGCCGAG 909
DB 321 GGGCGCGCGACACCGACGCGCTGGACCTGGAGAGAGCTGCTTCCGACACGCCGAG 262
OY 910 CGGCTTCAGGGCCCCCGCAGACCGCGGTCCCGGGGCAAGGCAAGGCCCGAGCG 969
DB 261 CGGCTTCAGGGCCCCCGCAGACCGAGCGCGGTCCCGGGGCAAGGCAAGGCCCGAGCG 202
OY 970 AGCCAGGTGAAGCCGGCGACAGCCTCGCGCGCGGGCGGGGGCGACGGGATCGGG 1029
DB 201 AGCCAGGTGAAGCCGGCGCGACAGCCTCGCGCGCGGGCGGGGGCGACGGGATCGGG 142
OY 1030 ACGCCGCTGCAGGGCGCGGGGGAGAGCGCGTGGGGCTGCCAAGGCGTGGCGTGGCG 1089
DB 141 ACGCCGCTGCAGGGCGCGGGGGAGAGCGCGTGGGGCTGCCAAGGCGTGGCGTGGCG 82
OY 1090 GGGCGGCAAGACCGCGAGAGCGCTTCACGTTGCTGGCCGTTGTCATCGAGTGTTC 1149

DB 81 GGGCGGACAGACCGCGAGACGGCTTCACGTTGCTGCGCCCGTGCATCGAGTGTTC 22
OY 1150 GTGGTGTGCTGTGTTCCCTTC 1170
DB 21 GTGGTGTGCTGTGTTCCCTTC 1

RESULT 2

BM967243/c 492 bp mRNA linear EST 29-APR-2002
LOCUS
DEFINITION
BM967243 1j32c09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:6136336 5' similar to SW:A2AA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 492)
Melton,D., Brown,J., Kenty,G., Permult,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestell,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: 1j32c09.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 445.
location/Qualifiers
1. 492
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6136336"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

FEATURES

source

BASE COUNT 44 a 202 c 182 g 64 t
ORIGIN

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 12:34:42 ; Search time 2684.44 Seconds
(without alignments)
8144.696 Million cell updates/sec

Title: US-09-636-259B-2
Perfect score: 1350
Sequence: 1 atgggctccctgcagcgga.....gggacaggaagcgatcgtg 1350

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estopl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inh:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result				Query		SUMMARIES	
No.	Score	Match	Length	DB	ID	Description	

C 1	559.4	41.4	561	14	BM967248	BM967248 i j32d04.y	
C 2	488.8	36.2	492	14	BM967243	BM967243 i j32c09.y	
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5	410.6	30.4	893	13	BI459381	BI459381 603200147	
6	395	29.3	740	13	BI838282	BI838282 603083213	

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8	321	23.8	855	17	GGAA2AAR	AL605540 Chicken a	
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10	317.6	23.5	867	9	AL530418	AL530418 AL530418	
11	317.4	23.5	988	14	BQ887729	BQ887729 AGENCOURT	
12	272.6	20.2	297	14	BQ302172	BQ302172 QV0-BT026	
13	255.2	18.9	935	14	BQ923710	BQ923710 AGENCOURT	
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17	197	14.6	805	17	CNS03CEL	AL237702 Tetraodon	
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19	187.4	13.9	777	17	LREA2AAR	AL605561 Lamprey a	
20	185.6	13.7	801	17	GGAA2CAR	AL605541 Chicken a	
21	179.4	13.3	1010	17	CNS04CMQ	AL284651 Tetraodon	
22	177.2	13.1	702	13	BI836679	BI836679 603089610	
23	175.8	13.0	921	17	CCLA2BAR	AL605559 Herring a	
24	175	13.0	975	17	CNS039RV	AL234292 Tetraodon	
25	173.4	12.8	691	17	HIPA2AAR	AL605565 Sea Horse	
26	173	12.8	697	17	RESA2AAR	AL605551 Frog alph	
27	172.6	12.8	774	17	AGAA2C2AR	AL605580 Toothcarp	
28	172.2	12.8	882	17	HIPA2C2AR	AL605568 Sea Horse	
C 29	171.8	12.7	2146	11	AK018378	AK018378 Mus muscu	
30	169.6	12.6	872	17	ECAA2BAR	AL605560 Horse alp	
31	166.8	12.4	890	17	CNS02WK9	AL605576 Sturgeon	
32	166.2	12.3	693	17	ARUA2BAR	AL605574 Sea Horse	
33	164.8	12.2	535	13	BM647571	BM647571 170006873	
34	164	12.1	723	17	AGAA2A2AR	AL605581 Toothcarp	
35	163.4	12.1	829	9	AL549866	AL549866 AL549866	
36	161.4	12.0	705	17	HGRA2AAR	AL605570 Shark alp	
37	160.6	11.9	753	17	SCAA2CAR	AL605564 Ostrich a	
38	160	11.9	788	17	DREA2CAR	AL605584 Zebrafish	
39	159.4	11.8	788	17	DREA2CAR	AL605553 Gar alpha	
40	158.6	11.7	699	17	LOSA2AAR	AL605569 Sea Horse	
41	154.4	11.4	981	17	HIPA2BAR	AL573897 AL573897	
C 42	151.4	11.2	872	9	AL573897	AL244403 Tetraodon	
43	151	11.2	860	17	CNS03HKO	AL605557 Herring a	
44	150.4	11.1	780	17	CCLA2CAR	AL550664 AL550664	
45	148	11.0	984	9	AL550664		

ALIGNMENTS

RESULT 1
BM967248/c 561 bp mRNA linear EST 29-APR-2002
LOCUS i j32d04.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
DEFINITION cDNA clone IMAGE:6136374 5' similar to SW:AZAA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.

ACCESSION BM967248
VERSION BM967248.1 GI:19561047

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 561)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T.
, Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other_ESTS: i j32d04.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812

Db 909 CTTCTGCGGTATCACCAGAGAGCGGGCTACGCTGTCTCTCCCTCCGTTGCTCTTCTA 968
QY 618 CGTCCCTGCTCATCATGATCCTGCTTACGTGGCATCTACCAGATCGC-----CAA 671
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Db 969 CTTGCCATGGCGGTCAATCGTGTATGTACTGCGCGTGTACGTGTGCGGCGAC 1028
QY 672 GCGTGCACCCGCGTGGCCACCCAGCCGCGGGTCCGACGCCGTGCGCGCGCGCGG 731
| ||| | | | | | | | | | | | | | |
Db 1029 CACGGCAGCCTCGAGGAGGCGTCAAGCGGAGGAGCAAGGCTCCGAGTGTGCT 1088
QY 732 GGGCACCGAGCGCAGGCCCAAGGGTCTGGCCCCGAGCGCAGCGGGCCCGGGGGCGC 791
| ||| | | | | | | | ||| ||| | | |||
Db 1089 GCGCATCCACTGTGCGGGCGGGCCACGGGCGCGGAGGGGGCGCATGCGCAGCGC 1148
QY 792 AGAGCCGAACCGCTGCCCCAACCAGCTCAACGGCGCCCCCTGGCGAGCCCCGCGC 844
| ||| | | | | | | | ||| | | | | | |
Db 1149 CAAGGGCACACCTTCCGAGCTCGCTCTCCGTGCGCCTGCTCAAGTTCTCCC 1201

Search completed: February 13, 2003, 07:47:40
Job time : 94.1176 secs

QY	18	GGAGCGGGGGCAACGGAGCTGGAACTGGGACGGGACCGGAGCGCGCGGGGGGGCGCGCCCGGGCCAC	77
Db	387	GGAGCGGGGGAGCGCGGGCGCGCGCGCGGACGTGAATGGACGGCGGCGCTCGGGGACT	446
QY	78	CCCTTACTCCCTGCAGGTGACGCTGACGCTGCTGTGCTGCGCGGCTGCTCATGCTGCT	137
Db	447	GGTGGTGAGCGCGCAGGGCGGTGGGCGTGGCGCTCTTCCTGGCAGCC--TTCATCCTTAT	503
QY	138	CACCGTGTTCGGCAACGTGCTCTCATCATCGCCGTGTTACAGAGCCCGCGCTCAAGGC	197
Db	504	GGCGGTGGCAGGTAACTGCTGTTCATCCTCTCAGTGGCCCTGCAACCGCCACCTGCAGAC	563
QY	198	GCCCCAAAACCTCTTCCTGGTGTCTCTGGCCCTGGCGCCAGATCCTGTTGGCCACGCTGCT	257
Db	564	CGTCACCAACTATTTCATCGTGAACCTGGCCGTGGCCGACCTGCTGCTGAGCGCCACCGT	623
QY	258	CATCCCTTCTCGCTGGCCCAAGGTCATGGGCTACTGCTACTGCTGCGCAAGGCTTGCTG	317
Db	624	ACTGCCCTTCTCGGCCACCAAGAGGTTCTGGGCTTCTGGGCTTGGCGGCTTCTG	683
QY	318	CGAGATCTACCTGGCGCTGCGCTGCTCTTCTGACAGTCTGTCATCGTGCACCTGTGCGC	377
Db	684	CGACGTATGGCGCGCGCTGACGTGCTGTGTCACGCGCTTCATCCTCAGCCTTGAC	743
QY	378	CATCAGCCTGGACCGCTACTGCTTCATCACAAGGCCATCGAGTACAACCTGAAGCGCAC	437
Db	744	CATCTCCGTGAGCCGCTACGTGGCGCTGCGCCACTCACTCAAGTACCAAGCCATCATGAC	803
QY	438	GCCGCGCCGATCAAGGCCATCATCATCACCCTGTGGGTACTCTCGGCGTCATCTCTT	497
Db	804	CGAGCGCAAGGGCGCGCCCATCTGCCCCCTGCTGTGGGTGTAAGCCCTGGTGTCTCGT	863
QY	498	CCGCGCGCTCATCTCCATGAGAGAAGAGGGCGCGCGCGCGCGCCGACCGGGCGAGCC	557
Db	864	AGGGCCCT-----GCTGGCTGAAGAGCCCGTGCCTGACGAGCG	908
QY	558	GCGCTGCGAGATCAACGACGAAGTGTGCTACGTCACTGCTGCTGTCATCGGCTCTCTT	617
Db	909	CTTCTGCGTATCACCGAGAGGCGGGCTACGCTGCTCTCTCTCCTCGTGTGCTCTCTA	968
QY	618	CGCTCCCTGCTCATCATGATCTCTGTCTACGTGCGCATCTACAGATGCG-----CAA	671
Db	969	CCTGCCCATGCGCGTCACTGTGTCATGTACTGCCGCGTACGTGTGCGCGCAGAC	1028
QY	672	GCGTGCACCCGCGTGCACCCAGCCGCGGGGTCCGAGACCCGCTGCCGCGCGCGCGG	731
Db	1029	CACGCGCAGCCTCGAGCGAGCGCTCAAGCGCGCAGCGCAAGGCCCTCCGAGGTGTGCT	1088
QY	732	GGGCACCGAGCGCAGGCCCAAGGGTCTGGGCCCCCGAGCGCAGCGCGGGCGGGGGCGC	791
Db	1089	GCGCATCCACTGTGCGCGCGCGCGCCACAGGGCGCCGACGGGGCGCACGGCATGCGCAGCGC	1148
QY	792	AGAGGCCGAACCGCTGCCCCAACCAAGTCAACGCGCGCCCCCTGGCGAGCCGCGC	844
Db	1149	CAAGGGCCACACCTTCCGACGCTGCTCTCCGTGCGGCTGCTCAAGTCTCTCC	1201

RESULT 15
 US-08-468-939-1
 ; Sequence 1, Application US/08468939
 ; Patent No. 5714381
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Jonathan A. Bard et al.
 ; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
 ; TITLE OF INVENTION: Receptors and Uses Thereof
 ; NUMBER OF SEQUENCES: 6
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: COOPER & DUNHAM LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ;

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: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/468,939
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 41337-1B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0526
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2140 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: N
: ANTI-SENSE: N
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 178..1893
: OTHER INFORMATION:
:
US-08-468-939-1

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Query Match	11.4%;	Score 153.4;	DB 1;	Length 2140;
Best Local Similarity	52.0%;	Pred. No. 9.8e-20;		
Matches 433; Conservative	0;	Mismatches 376;	Indels 24;	Gaps 3;

QY	18	GGACGCGGGCAACGCCGAAGCTGGAAACGGGACCCGAAGGCGCGGGGGGGGGGGCCCCGGGCCAC	77
Db	387	GGAGCCGGGGAGCGCGGGGGCGGGGGCGGCAGACTGAATGGCACGCGCGCGCTCGGGGGACT	446
QY	78	CCCTTACTCCTTCGAGGTGACGCTGACCGTGTTGCTTGCGCGCGCTGCTCATGTGCT	137
Db	447	GGTGTGAGCGCGCGAAGGCGCGTGGGCGTGGCGCTTCTCTGCAGCC--TTCATCCTTA	503
QY	138	CACC GTGTTGCGCAACGTGCTCGTCATCATGCGCGTGTTCACGAGCGCGCGCTCAAGGC	197
Db	504	GGCGGTGCGAGTAACCTGCTGTGATCCTCTCAAGTGGCGCTGCACACCGCCACCTGCAGAC	563
QY	198	GCCCCAAAACCTCTTCCTGTGTCTCTGCGCTCGGCCGACATCCTGTTGGCCACGCTCGT	257
Db	564	CGTCACCAACTATTTCATCGTGAACCTGGCGCGTGCCGACCTGCTGTAGCGCCACCGT	623
QY	258	CATCCCCTTCTTCGCTGGCCCAACGAGGTATGGGCTACTGTTACTTTCGGCAAAGCTTGTG	317
Db	624	ACTGCCCTTCTTCGGCCACCACATGAGAGTTCTGGGCTTCTGGGCTTTTGGCCGCGCTTCTG	683
QY	318	CGAGATCTACCTGGCGGCTCGACGTGCTCTTCTGACAGTGTCTCATGTCGACCTGTGCGC	377
Db	684	CGACGTATGGCGCCCGCTGACGTGCTGTGCTGACAGCGCTTCATCTCAGCCTGTGCAC	743
QY	378	CATCAGCTTGGACCGCTACTGTCTCATCACACAGGCCATGAGTACAACCTGAAGCGCAC	437
Db	744	CATCTCCGTGACCGGTACGTGGGCGTGGCCACTCACTCAAGTACCAGCCATCATGAC	803
QY	438	GCCGCGCCGCATCAAGGCCATCATCACCGTGTGGGTCACTCGGCGCTCATCTCTT	497
Db	804	CGAGCGCAAGCGCGCGCCATCTCTGGCCCTGCTCTGGGTCTGTAAGCCCTGTTGTGTCCGT	863
QY	498	CCGCGCGCTCATCTCCATCGAGAAGAGGCGCGCGCGCGCGCGCCGACCGCGCGCGAGCC	557
Db	864	AGGCGCCCT-----CGTGGCGCTGGAAGAGCGCCGTGCCCCCTGACGAGCG	908
QY	558	GGCGTGGAGATCAACGACGAGAAGTGTACGTCACTCTGTTGTCATCGGCTCCTTCTT	617

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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/334,698
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/952,798
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 376901
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 977-9550
: TELEFAX: (212) 664-0525
: TELEX: (212) 422523 COOP UI
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2140 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: N
: ANTI-SENSE: N
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 178..1893
: OTHER INFORMATION:
:
: US-08-334-698-1

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Query Match      11.4%; Score 153.4; DB 1; Length 2140;
Best Local Similarity 52.0%; Pred. No. 9.8e-20;
Matches 433; Conservative 0; Mismatches 376; Indels 24; Gaps 3;

OY 18 GGACGCGGGCAACGCGAGCTGGAACGGGACCGAGCGCGGGGGGGCGCGCGCGGCCAC 77
Db 387 GGAGCGGGGAGCGCGGGCGCGCGCGCGAGCTGAATGGAACGCGCGCGCGTGGGACT 446
OY 78 CCTTACTCCCTGAGGTGACGTGACGCTGTGTGCTGCGCGCGCGCTGCTATGCTGCT 137
Db 447 GGTGTGAGCGCGCAGGGCGGTGGCGCTGCTCTCTGCGCAGCC--TTTATCTTAT 503
OY 138 CACGCTTTCGGCAACGCTGCTCATCATCGCGCTGTTCACGAGCGCGCGCTCAAGC 197
Db 504 GCGCGTGGCAGGTAACCTGCTTCATCTCTCAGTGGCTGCAACCGCCACCTGACAG 563
OY 198 GCGCCAAACCTCTTCTGCTGCTGCTGCGCTGCGCGCGCATCTGCTGCGCAGCTCT 257
Db 564 CGTACCACTATTTCATCTGAACCTGCGCGTGGCGCGCATCTGCTGAGCGCCACCT 623
OY 258 CATCCCTTCTCGCTGCGCAACGAGTATGCGCTACTGCTACTTGGCAAGGCTTGGTG 317
Db 624 ACTGCCCTTCTCGCGCACCATGAGGTTCTGGGCTTCTGCGCTTGGCGCGCTTCTG 683
OY 318 CGAGATCTACCTGCGCTGACGTGCTCTTCTGACAGTGTCCATCGTGACCTGACCTG 377
Db 684 CGAGGTATGGGCGCGCTGACGTGTGTGTGACAGCGCTCCATCTCAGCGCTGAC 743
OY 744 CATCTCGTGGACCGGTACGTGGCGCTGCGCCACTCACTCAAGTACCCAGCCATCATG 803
OY 438 GCGCGCGCATCAAGGCTATCATCAACGCTGTGGTCACTCTGCGCGTCACTCTCT 497
Db 804 CGAGCGCAAGGCGCGCGCATCTGCGCTGCTGTGGTGTAGCCCTGTGTGTCTCT 863
OY 498 CCGCGCGCTCATCTCATCGAGAAGAGGCGCGCGCGCGCGCGCGCGCGCGAGCC 557
Db 864 AGGCGCGCT-----GCTGGGCTGGAAGGAGCCCGTGGCGCGCGCGCGAGCG 908
OY 558 GCGCTGCGAGATCAACGACAGAGAGTGTACGTCACTCTGCTGTCATCGGCTCTCT 617

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Db 909 CTCTGCGGTATCACCGAGAGCGCGGCTACGCTGTCTTCTCTCCGTGTGCTCTTCA 968
OY 618 CGTCCCTGCTCATCATGATCTCTGTCTACGTGCGCATCTACAGATCGC-----CAA 671
Db 969 CCTGCCATGGCGGTATCGTGTCACTACTGCGCGGTGTACGTGTGCGCGCAGCAC 1028
OY 672 GCGTGCACCGCGGTGCCACCGAGCGCGCGGGTCCGAGCGCGCTGCGCGCGCGGG 731
Db 1029 CACGCGCAGCGCTGAGGACGCGCTCAAGCGCGAGCGAGCGCGCTCCGAGGTGCT 1088
OY 732 GCGCACCAGCGCGAGCGCCCAAGGCTGTGGGCGCGCGAGCGCGCGCGCGGGGGCG 791
Db 1089 GCGCATCCACTGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCATGCGCAGCGC 1148
OY 792 AGAGCGCGAAGCGCTGCCACCGCATCAACGCGCGCGCGCTGCGCGAGCGCGCGC 844
Db 1149 CAAGGCGCACACTTCCGACAGCTCGCTCTCGGTGCGCGCTGCTCAAGTCTCTCC 1201

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RESULT 14
US-08-228-932-1
: Sequence 1, Application US/08228932
: Patent No. 557861
:
: GENERAL INFORMATION:
: APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
: APPLICANT: Theresa A. Branche, John M. Wetzel and Paul R. Hartig
: TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
: TITLE OF INVENTION: PROSTATIC HYPERPLASIA
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: COOPER & DUNHAM
: STREET: 30 Rockefeller Plaza
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10112
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/228,932
: FILING DATE: 13-APR-1994
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 977-9550
: TELEFAX: (212) 664-0525
: TELEX: (212) 422523 COOP UI
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2140 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: N
: ANTI-SENSE: N
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 178..1893
: OTHER INFORMATION:
:
: US-08-228-932-1

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Query Match      11.4%; Score 153.4; DB 1; Length 2140;
Best Local Similarity 52.0%; Pred. No. 9.8e-20;
Matches 433; Conservative 0; Mismatches 376; Indels 24; Gaps 3;

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Db 1144 AGGCGCTGAGCGCGG 1159

RESULT 12

US-08-475-742-15
; Sequence 15, Application US/08475742
; Patent No. 6121015

GENERAL INFORMATION:

; APPLICANT: O'Malley, Karen L
; APPLICANT: Todd, Richard D
; TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor
; FILE REFERENCE: WU 102 CON DIV
; CURRENT APPLICATION NUMBER: US/08/475,742
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: US 08/261,293
; EARLIER FILING DATE: 1994-06-16
; EARLIER APPLICATION NUMBER: US 08/014,013
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 15
; LENGTH: 2428
; TYPE: DNA
; ORGANISM: CDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2428)
; OTHER INFORMATION: Rat d2 receptor sequence
; PUBLICATION INFORMATION:
; TITLE: Cloning and expression of a rat D2 dopamine receptor
; TITLE: cDNA.
; JOURNAL: Nature
; VOLUME: 336
; PAGES: 783-787
; DATE: 1988
US-08-475-742-15

Query Match 11.5%; Score 154.6; DB 3; Length 2428;
Best Local Similarity 48.98; Pred. No. 6e-20;
Matches 595; Conservative 0; Mismatches 604; Indels 18; Gaps 6;

QY 115 CTGGCCGGCCTGCTCATGCTGCTCACCSTGTTCGGCAACGTGCTCGTCATCGCCGTG 174
Db 142 CTGCTCACCTCTCATCTTTATCATCGTCTTTGGCAATGTGCTGGTGCATGGCTGTA 201
QY 175 TTCACGAGCGCGCGCTCAAGCGCGCCCAAAACCTCTTCTGCTGCTGCTGCGCTGGCC 234
Db 202 TCCCGAGAGAGGCTTTCAGACACCACCACCACTACTTGATAGTCAGCCTTGCTGGCT 261
QY 235 GACATCTGCTGGCCACGCTGCTCATCCCTTTCGCTGCGCAACGAGTCATGGGCTAC 294
Db 262 GATCTCTGCTGGCCACTGCTAATGCCGTGGTGTCTACCTGAGGTGGTGGTGAG 321
QY 295 TGGTACTTCGGCAAGGCTTGGTCGAGATCTACCTGGCGCTCGACGTGCTTCTGCACG 354
Db 322 TGGAAATTCAAGCATTCACGTGACATCTTGTCACTCTGATGTCAATGATGTGCACA 381
QY 355 TCGTCCATCGTGACCTGTGGCCCATCAGCCCTGGACCGCTACTGTGCATCACACAGGCC 414
Db 382 GCAAGCATCTGACCTGTGTGGCCATCAGCATGACAGGTACACAGCTGGCAATGCCC 441
QY 415 ATCGAGTACAAC--CTGAAGCGCAGCGCGCGCGCATCAAGGCCATCATCACCGTG 471
Db 442 ATGCTGTATAACACACGCTACAGCTCCAAGCGCGGAGTTACTGTCAATGATGCCATTGTC 501
QY 472 TGGGTCACTCGGGCGCTCATCTCTTCCGCGCGCTCATCTCCATCGAGAGAAGGCGGCG 531
Db 502 TGGGTCTGTCTTCACCATCTCTCTGCCACACTGCTCTTGGACTCAACAATACAGACCAG 561
QY 532 GCGCGGCGCGCAGCGCGCGAGCGCGCTGCGAGATCAACGACGAGAGTGTACGTC 591
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Db 619 TACGTGCCCCCTTCATCGTCACTCTGCTGTATATCAAAATCTACATCGTCTCCGGAAG 678
QY 652 CGCATCTACAGATCGCCAAAGCTGCGACCCCGCGTGCACCCAGCCCGGGGTCCGGAC 711
Db 679 CGCCGGAAGCGGGTCAACACCAAGCGCAGCAGTGCAGCTTTCAG-AGCCAACCTGAAGAC 737
QY 712 GCCGTGCG 771
Db 738 ACCACTCAAGGCAAC----TGTACCCACCCTGAGGACATGAAACTGTGCACCGTTATC 792
QY 772 AGCG 831
Db 793 ATGAAGTCTAATGGAGTTTCCAGTGAACAGCGGAGAAATGATGCTGCCCGCGAGCT 852
QY 832 GCGGAGCG 888
Db 853 CAGGAGCTGGAATGGAGATGCTGTCAAGCACAGCAGCCCGCCAGAGAGACCGCGTATAGC 912
QY 889 TCGTCTTCGGAACCAAGCG 948
Db 913 CCCATCCCTCCAGTCAACCAAGCTCACTCTCCCTGATTCATCCACCAAGCGCGCTACAT 972
QY 949 GGCAAGCGCAAGCG 1008
Db 973 AGCAACCTGACAGTCTCTGCCAAACAGAGAAGAAATGGGCAAGATTGTCAATCCC 1032
QY 1009 CCGGGCGGAGCGGGGATCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1068
Db 1033 AGGATTTGCCAAGTTCTTTGAGATCCAGACCATGCCCCAATGGCAAAACCGGACCTCCCTT 1092
QY 1069 GCCAAGCGCTCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1128
Db 1093 AAGACGATGAGCCCGCAGAAAGCTCTCCCAAGCAGAGAAGAGAGAAAGCCACTCAGATGCTT 1152
QY 1129 GCCGTGCTCATCGGAGTGTTCGTGTGCTGCTGCTCCCTTCTTCTTACCTACAGCTC 1188
Db 1153 GCCATTTCTCTCGGTGTGTTCATCATCTGCTGCTGCCCTTCTTCTCATCAGCAGATCTG 1212
QY 1189 ACGGCGGTGCG--GTGCTCGGTGCGCAGCAGCGCTCTTCAAAATCTTCTTCTGCTGGCG 1245
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QY 1246 TACTGCAACAGCTGTTGAACCGCGGTCACTTACACCATCTTCAACACAGATTCGCGCG 1305
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Db 1333 GCCTTCAAGAAGATCTT 1349

RESULT 13

US-08-334-698-1
; Sequence 1, Application US/08334698
; Patent No. 5556753

GENERAL INFORMATION:

; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible


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Db 304 GCGCGCGCGCGCGCGCGCGCGCTGAACGCTTCGGGGGGCGCTGGCGCGGATGCGCGGC 363
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Db 364 GCGCGCGCGCGCGCGCGCTTCTGCGACGCTGACCGCGGTGCTGCGCGCGCTCATGGC 423
QY 123 CCTGCTCATGCTGCTCAACCGCTGTTGCGCAAGCTGCTGCTCATCATCGCGCTGTTACAG 182
Db 424 GCTGCTCATGCTGCGCACGCTGCTGCGCAACGCGCTGCTCATGCTGCGCTTCTGCGCG 483
QY 183 CCGCGCGCTCAAGCGCGCGCGCGCGCGCGCTTCTGCTGCTGCTGCTGCTGCGCGCGCG 242
Db 484 CTCGAGCCTCCGACCGCACCAACAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
QY 243 GGTGGCCACGCTGCTCATCCCTTCTGCTGCGCGCGCGCGCGCGCGCTGCTGCTGCTG 302
Db 544 GCTGCGCGCGCTTCTGCTCATCCCACTGATGTAACCTTACGCTGCTGCTGCTGCTGCT 603
QY 303 CCGCAAGGCTTGTGCGAGATCTACCTGCGCGCTGACGCTGCTTCTGCTGCTGCTGCT 362
Db 604 CCGCGCGCGCGCTTCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
QY 363 CGTGACCTGTGCGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
Db 664 CTTCAACATGCTGCTCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 723
QY 423 C---AACCTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 479
Db 724 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 783
QY 480 CTCGCGCGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 539
Db 784 GCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
QY 540 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 599
Db 844 CATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 903
QY 600 GTGCATGCGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 659
Db 904 TTCCACCTGAGTCTTCTTACGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
QY 660 CCAGATGCGCAAGCGCTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719
Db 964 CTTGAACATCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1023
QY 720 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 776
Db 1024 CGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1083
QY 777 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 836
Db 1084 GCAGAAGGGGCGAGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1143
QY 837 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 852
Db 1144 AGCGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1159
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RESULT 11

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US-09-642-514-5
: Sequence 5, Application US/09642514
: Patent No. 6437100
: GENERAL INFORMATION:
: APPLICANT: Lovenberg, Timothy
: APPLICANT: Erlander, Mark
: APPLICANT: Pyatt, Jayashree
: APPLICANT: Huvar, Arne
: TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
: FILE REFERENCE: SUBTYPE
: FILE REFERENCE: ORT1290
: CURRENT APPLICATION NUMBER: US/09/642,514
: CURRENT FILING DATE: 2000-08-21
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: PRIOR APPLICATION NUMBER: US 09/167,354
: PRIOR FILING DATE: 1998-10-06
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 2699
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-514-5
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Query Match 12.2%; Score 164.8; DB 4; Length 2699;
Best Local Similarity 51.2%; Pred. No. 8.8e-22;
Matches 438; Conservative 0; Mismatches 412; Indels 6; Gaps 2;
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QY 3 GGGCTCCCTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 62
Db 304 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 363
QY 63 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 122
Db 364 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 423
QY 123 CTTGCTCATGCTGCTCAACCGCTGTTGCGCAAGCTGCTGCTCATCATCGCGCTGTTACAG 182
Db 424 GCTGCTCATGCTGCGCACGCTGCTGCGCAACGCGCGCTGCTCATGCTGCGCTTCTGCGCG 483
QY 183 CCGCGCGCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 242
Db 484 CTCGAGCCTCCGACCGCACCAACAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
QY 243 GGTGGCCACGCTGCTCATCCCTTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 302
Db 544 GCTGCTCATGCTGCGCACGCTGCTGCGCAACGCGCGCTGCTCATGCTGCTGCGCGCG 603
QY 303 CCGCAAGGCTTGTGCGAGATCTACCTGCGCGCTGACGCTGCTTCTGCGACGCTGCTCAT 362
Db 604 CCGCGCGCGCGCTTGTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
QY 660 CCAGATGCGCAAGCGCTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719
Db 904 TTCCACCTGAGTCTTCTTACGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
QY 660 CCAGATGCGCAAGCGCTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719
Db 964 CTTGAACATCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1023
QY 720 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 776
Db 1024 CGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1083
QY 777 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 836
Db 1084 GCAGAAGGGGCGAGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1143
QY 837 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 852
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QY 540 CCGCGAGCCGCGCGAGCCGCGCTGCGAGATCAACGACCAGAAAGTGTACGTATCTGTC 599
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Db 546 CATCCCCGAGGGCCACTGCTATAGCCAGTTCCTTACAACTGGTACTTCCTCATCACGGC 605
QY 600 GTGCATCGGCTCTCTCTGCTCCCTGCTCATCATGATCCTGGTCTACGTGCGCATCTA 659
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 606 TTCCACCCCTGAGTCTTTTACGCCCTTCCTCAGCGTCAACCTTCTTTAACTCAGCATCTA 665
QY 660 CCAGATCGCCAAAGCTGCGACCCCGCTGCGACCCAGCCCGGGTCCGGACGCCGCTGCG 719
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 666 CCGAACAATCCAGAGCGCACCCCGCTCGCGCTGGATGGGGCTCGAGAGGCGAGCCGGCCC 725
QY 720 CGCGCCGCGGGGGGCGACCGAGCGC--AGGCCCAAGGGTCTGGGCCCCGAGCGCAGCGC 776
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 726 CGAGCCCCCTCCCGAGGCCACGCCCTCACCACCCCCACCGCTGGCTGGGGCTGCTG 785
QY 777 GGGCCCGGGGGGCGAGAGCCGCAACCGCTGCCACCACCGCTCAACGCGGCCCTGGCGA 836
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 786 GCAGAGGGGCGACGGGGAGGCCATGCGCGCTGCACAGGTATGGGGTGGAGCGCGCGGT 845
QY 837 GCCCGCGCGCGCGG 852
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Db 846 AGCGCGTGAGCGCGG 861
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RESULT 9

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US-09-167-354-5
; Sequence 5, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-167-354-5
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Query Match 12.2%; Score 164.8; DB 3; Length 2699;
Best Local Similarity 51.2%; Pred. No. 8.8e-22;
Matches 438; Conservative 0; Mismatches 412; Indels 6; Gaps 2;

QY 3 GGGCTCCCTGACGCGGAGCGGGGCAACGCGAGCTGGAACGGGACCGAGCGCGGGGG 62
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 GCGGGGCGCGCGCGGAGCGGCGCTGAAACGCTTGGGGGCGCTGGCGGCGATGCGGGC 363
QY 63 CGGGCGCGGGGCGCAACCCCTTACTCCCTGACGCTGACGCTGCTGCTGCTGGCCG 122
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 GCGGGGCGGGGCGCGGCTTCTCGGACGCTGACCGCGGCTGCTGCGCGCTCATGGC 423
QY 123 CCTGCTCATGCTGCTACCGTGTTCGGCAACGCTGCTCATCATCGCGGTGTTCACGAG 182
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 424 GCTGCTCATGCTGCGCACGCTGCGCAACGCGCTGCTCATGCTGCGCTTCTGCGCGA 483
QY 183 CCGCGGCTCAAGGCGCGCCCAAAACCTTCTCTGCTGCTGCTGCGCTGCGCGCATCT 242
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 484 CTGAGCCTTCGACACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGACTTCT 543
QY 243 GGTGGCACGCTGCTCATCCCTTCTGCTGCGCAACGAGGTCAATGGCTACTGTACTT 302
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 544 CGTGGGCGCTTCTGCTCATCCCACTGTATGTATCCCTPACGTGCTGACAGGCGCGTGA 603
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QY 303 CGGCAAGGCTTGTGCGAGATCTACTGGCGCTCGACGTGCTCTTTCGACGTCGTCAT 362
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 604 CGGCGGGGGCCTTGCAAGCTGTGGCTGTAGTGACTACTGCTGTGCACTCTCTGTC 663
QY 363 CTTGCACTGTGCGCATCAGCCTTGACCGGCTACTGTCCATCACACAGCCATCGAGTA 422
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 664 CTTCACATCGTGTCTATCAGCTACGACCGCTTCTGTGCTCACCCGAGCGTCTCATA 723
QY 423 C---AACCAGAAGCGCACGCGCGCGCATCAAGGCCATCATCATCACCGTGTGGTCA 479
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 724 CCGGGCCCAAGAGGTGACACGCGCGCGCGGCGAGTGGGGAAGATGCTGCTGGTGTG 783
QY 480 CTGGGCGCTCATCTCTTCCCGCGCTCATCTCCATCGAGAAGAAGGGCGGGCGCGG 539
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 784 GGCCTTCTGCTGTACGAGACCAACCATCTGAGCTGGGAGTACCTGTCCGGGGCAGCTC 843
QY 540 CCGCGAGCCGCGCGAGCGCGCTGCGAGATCAACGACCAAGAAGTGTACGTATCTGTC 599
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 844 CATCCCGGAGGGCCACTGCTATGCGGAGTCTTCTTACAACTGGTACTTCCATCACGGC 903
QY 600 GTGATCGGCTCTCTTCTGCTCCCTGCTCATATGATCTGTCTACGTGCGCATCTA 659
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 904 TTCCACCTTGAGTCTTTTACGCCCTTCTCCTCAGCGTCACTTCTTTAACCTCAGCATCTA 963
QY 660 CCAGATCGCCAAAGCTGCGACCCCGCTGCCACCCAGCGCGCGGGTCCGAGCGCTGCG 719
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 964 CCGAACAATCCAGAGCGCGCACCCGCTCCGCGTGGATGGGGCTCGAGAGGCGAGCGGCC 1023
QY 720 CGCGCGCGCGGGGCGACCGAGCGC--AGGCCCAAGGCTTGGGCCCCGAGCGCAGCGC 776
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1024 CGAGCCCCCTCCCGAGGCCCGCCCTCACCACCCCGCTGGCTGGGGCTGCTG 1083
QY 777 GGGCCCGGGGGGCGCAGAGGCGCAACCGCTGCCACCCAGCTCAACGCGCGCGCTGGCGA 836
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1084 GCAGAGGGGCGACGGGAGGCCATGCCGCTGCACAGGTATGGGGTGGGTGAGCGGCGGT 1143
QY 837 GCCCGCGCGCGCGG 852
      ||| ||| ||| ||| |||
Db 1144 AGCGCGTGAGCGCGG 1159
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RESULT 10

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US-09-642-855-5
; Sequence 5, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-5
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Query Match 12.2%; Score 164.8; DB 4; Length 2699;
Best Local Similarity 51.2%; Pred. No. 8.8e-22;
Matches 438; Conservative 0; Mismatches 412; Indels 6; Gaps 2;

QY 3 GGGCTCCCTGACGCGGAGCGGGGCAACGCGAGCTGGAACGGGAGCGCGCGGGGG 62
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-855-6
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Query Match          12.2%; Score 164.8; DB 4; Length 1335;
Best Local Similarity 51.2%; Pred. No. 8.1e-22;
Matches 438; Conservative 0; Mismatches 412; Indels 6; Gaps 2;
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QY 3 GGGCTCCCTGCAGCGCGGCAACGCGGAGCTGGACGGGACCGGCGCGGGGG 62
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 6 GCGCGCGCGCGCGCGCGCGCTGAACGCTTCGGGGCGCGCTGGCGGCGATGCGCGC 65

QY 63 GCGCGCGCGCGCGCGCGCTTACTCCCTGCAGGTGACGCTGACGCTGTGCTGCGCCGG 122
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 66 GCGCGCGCGCGCGCGCGCTTCTCGGACGCTTGACCGCGGCTGCGCGGCTCATGGC 125

QY 123 CTTGCTCATGCTGCTCACCCTGTTCGGCAACGCTGCTCATCATCGCCGTTCACGAG 182
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 126 GCTGCTCATGCTGCGCACGCTGCTGGCAACGCGCTGCTCATGCTGCGCTTCGTGGCGA 185

QY 183 CCGCGCGCTCAAGCGCGCGCAAAACCTCTTCTGCTGCTCTGCGCTCGCGCCGACATCCT 242
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Db 186 CTGCAAGCTTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGACTTCTCT 245

QY 243 GGTGGCCACGCTGCTCATCCCTTCTGCTGCGCAACGAGGTATGGCTACTGTTACTT 302
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 246 GCTGCGCGCGCTTCTGCTCATCCACTGTATGTATACCTTACCTGCTGACAGGCGCGTGAACCTT 305

QY 303 CGGCAAGGCTTGTGCGAGATCTACCTGGCGCTCGACGCTCTTCTGACAGCTGCTCAT 362
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 306 CGGCGCGCGCGCTTGCACAGCTGTGGCTGTGAGTGAATACCTGCTGTGACCTCTCTCTGC 365

QY 363 CGTGACCTGTGCGCATACCTTGACCGCTACTGCTCATCACACAGGCGCATCGAGTA 422
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 366 CTTCACATCGTGTCTATCACTACGACCGCTTCTGCTGCTGACCGCGGCTCTCATATA 425

QY 423 C---AACCTGAAGCGCAGCGCGCGCGCATCAAGGCCATCATCACCGTGTGGTCAAT 479
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 426 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGTGGGAAAGATGCTGTGCTGTGGTGTCT 485

QY 480 CTGCGCGCTCATCTCTTCCCGCGCTCATCTCCATCGAAGAAGGCGCGCGCGCGCG 539
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 486 GGCCTTCTGCTGTACGAGACCAACCATCTGAGCTGGGAGTACCTGTCCGGGGGCAAGCTC 545

QY 540 CCGCGCAGCGCGCGCGCGCGCTGCGAGATCAACGACCAAGAGTGTACTCATCTCTGTC 599
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 546 CATCCCGCGAGGCGCATGCTATGCGAGTCTCTTCTTACAACCTGTACTTCTCATCACGGC 605

QY 600 GTGCATCGGCTCTTCTTCCGCTCCCTGCTCATCATGATCTGCTTACGTGCGCATCTTA 659
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 606 TTCCACCGCTGAGTCTTTACGCGCTTCTTCAAGCTTCAACCTTCAACCTCAAGCATCTTA 665

QY 660 CCAGATCGCAAGCGTTCGCAACCGCGGTGCCAGCCGCGGGGTCCGAGCGCGCTGCG 719
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 666 CCTGAACATCCAGAGCGGCAACCGCGCTCCGCTGGATGGGCTCGAGAGCGACCGCGGCC 725

QY 720 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 776
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 726 CGAGCGCGCTTCCGAGGCGCGCGCGCTTACCAACCGCGCGCTGCTGTGGGCTGCTG 785

QY 777 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 836
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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Db 786 GCAGAGGGGCAAGGGGAGGCGCATGCCGCTGCACAGGTATGGGTGGGTGAGGCGCGCT 845
QY 837 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 852
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 846 AGCGCGTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 861
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RESULT 8
US-09-642-514-6
; Sequence 6, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
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; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-514-6
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Query Match          12.2%; Score 164.8; DB 4; Length 1335;
Best Local Similarity 51.2%; Pred. No. 8.1e-22;
Matches 438; Conservative 0; Mismatches 412; Indels 6; Gaps 2;
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QY 3 GGGCTCCCTGCAGCGCGGCAACGCGGAGCTGGACGGGACCGGCGCGGGGG 62
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 6 GCGCGCGCGCGCGCGCGCGCTGAACGCTTCGGGGCGCGCTGGCGGCGATGCGCGC 65

QY 63 GCGCGCGCGCGCGCGCGCTTACTCCCTGCAGGTGACGCTGACGCTGTGCTGCGCCGG 122
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 66 GCGCGCGCGCGCGCGCGCTTCTCGGACGCTTGACCGCGGCTGCGCGGCTCATGGC 125

QY 123 CTTGCTCATGCTGCTCACCCTGTTCGGCAACGCTGCTCATCATCGCCGTTCACGAG 182
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 126 GCTGCTCATGCTGCGCACGCTGCTGGCAACGCGCTGCTCATGCTGCGCTTCGTGGCGA 185

QY 183 CCGCGCGCTCAAGCGCGCGCGCAAAACCTCTTCTGCTGCTCTGCGCTCGCGCCGACATCCT 242
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 186 CTGAGGCTTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGACTTCTCT 245

QY 243 GGTGGCCACGCTGCTCATCCCTTCTGCTGCGCAACGAGGTATGGCTACTGTTACTT 302
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 246 GCTGCGCGCGCTTCTGCTCATCCACTGTATGTATACCTTACCTGCTGACAGGCGCGTGAACCTT 305

QY 303 CGGCAAGGCTTGTGCGAGATCTACCTGGCGCTGACGCTCTTCTGACAGCTGCTCAT 362
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 306 CGGCGCGCGCGCTTGCACAGCTGTGGCTGTAGTGAATACCTGCTGTGACACCTCTCTGC 365

QY 363 CGTGACCTGTGCGCATACCTTGACCGGCTACTGCTCATCACACAGGCGCATCGAGTA 422
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 366 CTTCACATCGTGTCTCATCAGCTACGACCGCTTCTGCTGCTCATCACCGCGGCTCTCATATA 425

QY 423 C---AACCTGAAGCGCAGCGCGCGCGCATCAAGGCCATCATCACCGTGTGGTCAAT 479
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 426 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 485

QY 480 CTGCGCGCTCATCTCTTCCCGCGCTCATCTCCATCGAAGAAGGCGCGCGCGCGCG 539
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 486 GGCCTTCTGCTGTACGAGACCAACCATCTTGAAGCTGGGAGTACCTGTCCGGGGGCAAGCTC 545
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QY      243 GGTGGCCACGCTCGTCATCCCTTTCTGCCTGGCCCAACGAGGCTCATGGGCTACTGGTACTT 302
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Db      536 CGTCGGCGCCTTCTGCATCCCACTGTATGTACCCCTACGTTGTAACAAGGCCGCTGACCCTT 595
QY      303 CGGCAAGGCTTGTTGCGAGAATCTACCTGGCGCTCGACGTCGCTCTTCTGCAAGTGTCCAT 362
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      596 CGGCCGGGGCCTCTGCAGAGCTGTGGCTGGTAGTGGACTACCTGCTGTGCACCTCCTCTGC 655
QY      363 CGTGCACTGTGCGCCATCAAGCTTGGACCGCTACTGCTGCATCACACAGGCCATCGAGTA 422
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Db      656 CTTCACATCGTGCCTCATCACTACGACCGCTTCCCTGTCCGCTCACCCGAGCGGTCTCATATA 715
QY      423 C---AACC TGAAGCGCACCGCGCGCCGCATCAAGGCCATCATCAACCGTGTGGTCAAT 479
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      716 CCGGGCCCAAGCAGGGGTGACACGCGGGCGGCGAGTGGCGGAAGATGCTGCTGGTGTGGTGTCT 775
QY      480 CTCGGCCGTCATCTCTCTCCCGCGCGCTCATCTCCATCGAAGAAGGGCGGGCGGGCGGG 539
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      776 GGCTTCTCTGTGTACGGAACAGCCATCTCGAGCTGGAGTAAGTCTCCGGGGCAGCTC 835
QY      540 CCCGACGCGCGCGAGCCGCGCTGCGAGATCAACGACCAAGTGTAGCTCATCTCTGTC 599
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Db      836 CATCCCCGAGGCGCACGTCATGCGAGTCTTCTTACAACGTGTACTTCTCATCACGCG 895
QY      600 GTGCATCGGCTCTTCTTCCCTCCCTGCTCATCATGATCTGTGTACTGCGCATCTA 659
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Db      896 TTCCACCTTGAGTTCTTTAACGCCCTTCTCTCAGCGTCACCTCTTTAACTCAGCATCTA 955
QY      660 CCAGATCGCCAAGCGTCCGACCCCGCGTGCACACCCAGCCGCGGGGTCCGGACGCCGTGCG 719
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      956 CCTGAACATCCAGAGGCGCAACCCGCCCTCCGGCTGATGGGGCTCGAGAGGACGCCGGCCC 1015
QY      720 CCGCGCCCGCGGGGGGCGACCGAGCGC--AGGCCCAAGGGTCTGGGGCCCCGAGCGACGCG 776
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1016 CGAGCCCCCTCCCGAGGCGCCACCCCTCACACACCCCCACCCCGCTGCTGCGGCTGCTG 1075
QY      777 GGGCCCCGGGGGGCGCAGAGGCCGAACCGCTGCCCCACCCAGCTTCAACGGCGCCCTGGCGCA 836
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Db      1076 GCAGAAAGGGGCGACGGGGAGGCCATTGCCGCTGCACAGGTATGGGGTGGGTGAGGGCGCCGT 1135
QY      837 GCCCGCGCGCGCGCGG 852
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Db      1136 AGCGCGCTGAGCGCGG 1151

RESULT 6
US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvart, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-167-354-6
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QY	3	GGGCTCCCTGCAGCGCCGGACGCGGGGCAACGCGAGCTGGAAACGGACCCGAGCGCCGGGGGG	62
Db	6	GCGCGCGCCGCCGACGGGGCCGCTGAACGCTTCGGGGGCGCTGGCGGGCGATGCGGGC	65
QY	63	CGCGCCCCGGGCCACCCCTTACTCCCTCGAGGTGACGCTGACGCTGCTGTGCTGCGCGG	122
Db	66	GGCGGGCGGGGGCGGGCTTCTCGGACGCTTGACCGCGGTCTGGCCGCGCTCATGCG	125
QY	123	CCTGCTCATGCTGCTCAACCGTGTTCGGCAAGTGTCTGTCATCATCGCCGTGTTACAGAG	182
Db	126	GCTGCTCATGCTGCGCCACGCGTGTGGGCAACGCGCTGGTCATGCTCGCCTTCGTGGCCGA	185
QY	183	CCGCGCGCTCAAGGCGCCCCCAAAACCTCTTCCTGTTGTCTCTGCGCTCGGGCAGATCCT	242
Db	186	CTCGAGCCTCCGCACCCAGAACAACTTCTTCCTGCTCAACCTCGCCATCTCCGACTTCCT	245
QY	243	GGTGGCCACGCTGCTCATCCCTTCTCGCTGGCCCAACGAGTCAATGGGCTACTGCTACTT	302
Db	246	CGTCGGCGCTTCGATCCACTGTATGTATACCCTACGTGTGACAGGCGCGCTGGACTT	305
QY	303	CGGCAAGGCTTGGTGCAGAGATCTACCTGGCGCTCGACGTGCTCTCTGCACGTGCTCAT	362
Db	306	CGGCGGGGCTCTGCACAAGCTGTGGCTGTAGTGAGTACTCTGCTGTGCACCTCCTGCG	365
QY	363	CGTGCACTGTGGCGCATCAGCCCTGGACCGCTACTGTCTCATCACACAGGCCATCGAGTA	422
Db	366	CTTCAACATCGTCTCATCAGCTACGCTACGCGCTTCTGTCGTGCACCCGAGCGGTCTATA	425
QY	423	C---AACCTGAAGCGCACGCGCGCGCATCAAGGCCATCATCACCGTGTGGGTAT	479
Db	426	CCGGGCCACAGAGGTGACACGCGCGGGCAGTGGGAAGATCTGTGTGGGTCT	485
QY	480	CTCGGCGTATCTCTCCCGCGCTCATCTCCATCGAGAAAGAGGGCGCGCGCGG	539
Db	486	GGCCTTCTGCTGTACGGACCAAGCCATCCTGAGCTGGAGTACTGTCCGGGGCAGCTC	545
QY	540	CCCCGACCGCGCCGACCGCGCTGCGAGATCAACGACCAAGAGTGGTACGTCACTCTGTC	599
Db	546	CATCCCCGAGGGCCACTGCTATGCCAGTTCTTACAACTGTGTACTTCTCATCACGGC	605
QY	600	GTGCATCGGCTCTCTTCTGCTCCCTGCTCATCATGATCTGTGCTTACGTGGCATCTA	659
Db	606	TTCACCCCTGGAGTCTTTPACGCGCTTCTCTCAGCGTCACCTTCTTAACTCAGCATCTA	665
QY	660	CCAGATCGCCAAAGCTGACACCCGCGTGCACCCAGCCGCGGGGTCCGAGCGCCGTGCG	719
Db	666	CCTGAACATCCAGAGGCGCACCCGCGCTCGGCTGATGGGCTCGAAGGACGCGCGCC	725
QY	720	CGCGCGCGCGGGGACCCGAGCGC--AGGCCCAAGGTGTGGGCCCCCGAGCGCAGCGC	776
Db	726	CGAGCCCCCTCCCGAGGGCCAGCCCTCAACACCCACCGCCCTGGCTGTGGGCTGTG	785
QY	777	GGGCGCGGGGGCGCAGAGGCGCGAACCCTGCCCCACCCAGTCAACGGCGCCCTGTGCGA	836
Db	786	GCAGAAGGGGCGACGGGGAGGCCATGCCCTGCACAGGTATGGGGTGGGTGAGGCGGGCT	845
QY	837	GCCCCGCGCGCGCGG 852	
Db	846	AGCGGCTGAGGCGGG 861	

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RESULT 7
US-09-642-855-6
; Sequence 6, Application US/09642855
; Patent No. 6413743
;
; GENERAL INFORMATION:
;
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE

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: REFERENCE/DOCKET NUMBER: MNI-032
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)742-4214
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2689 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 291..1625
: US-08-985-090-1

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Query Match      12.3%; Score 166.4; DB 2; Length 2689;
Best Local Similarity 51.3%; Pred. No. 4.5e-22;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;

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QY 3 GGGCTCCCTGCAGCCGGACGGGCAACGGAGCTGGAAAGGGAACCGGCGGGGGG 62
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QY 63 CGCGCGCGGGGCAACCCCTTACTCCCTGCAGGTGACGCTGACGCTGTGCTGGCGGG 122
Db 356 GCGCGCGGGGGCGCGCGCTTCGCGCAAGCTGACCGCGCGTGTGGCGCGCTCATGCGC 415
QY 123 CTTGCTCATGCTGCTCACCCTGTTGCGCAACGCTGCTCATCATCGCGCTGTTGCGAG 182
Db 416 GCTGCTCATGCTGCGCACGCTGCTGCGCAACGCGCTGCTCATGCTGCGCTTGTGGCGGA 475
QY 183 CCGCGGCTCAAGGCGCGCCCAAAACCTTCTGCTGCTGCTGCGCTGCGCGCAATCCT 242
Db 476 CTCGAGCCTCCGACACCGAACAACCTTCTGCTGCTCAACCTCGCATCTCCGACTTCCT 535
QY 243 GGTGGCAAGCTGCTCATCCCTTCTCGCTGGCCAAAGAGTATGGGCTACTGCTACTT 302
Db 536 CGTGGCGGCTTCTGCATCCCACTGATATGTAACCTACGCTGACAGAGCGCGTGAACCTT 595
QY 303 CGGCAAGGCTTGTGCGAGATCTACCTGCGGCTGACGCTGCTTCTGCAAGCTGCTCAT 362
Db 596 CGGCGGGGCGCTTGCAGAGCTGTGCTGAGTAGTGAATGCTGCTGCAACCTTCTGCTGC 655
QY 363 CGTGCACTGTGCGCATCAGCTGAGACCGCTACTGCTCATGCTCATCACAGGCGCATGATA 422
Db 656 CTTCAACATGCTGCTCATGCTAGACACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 715
QY 423 C--AACCTGAAGCGCACGCGCGCGCATCAAGGCGCATCATCATCACCGTGTGGGTCAT 479
Db 716 CCGGGCCAGCAGGCTGACAGCGCGGGGAGTAGTGCAGAAATGCTGCTGTGGGTGCT 775
QY 480 CTCGGCGCTCATCTCTTCCCGCGCTCATCTCATGAGAAGAAGGGCGGGCGGGGG 539
Db 776 GGGCTTCTGCTGTACGAGCACGACCATCTGAGCTGGAGTAGTCTCGGGGGCGAGCTC 835
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Db 836 CATCCCCAGAGGGCGACTGCTATGCGGAGTCTTCTTACACTGTGTAATCTCTCATACGGC 895
QY 600 GTGCATGCGCTCTTCTGCTGCTGCTGCTCATCATGATGCTGCTTACGTGCGCATCTA 659
Db 896 TTCCACCTGGAGTCTTCTTACGCGCTTCTCTAGCGCTACCTTCTTAACTCAGCATCTA 955
QY 660 CCAGATCGCAAGCGTGCACCGCGGTGCCACCGAGCGCGGGGTCCGGAGCGCGTGC 719
Db 956 CCTGAACATCCAGAGCGCACCGCTTCGGCTGATGGGCTCGAGAGGCAAGCGCGGCC 1015
QY 720 CGCGCGCGGGGGGCGACCGAGCGC--AGGCCCAAGGTTCTGGGCGCGGAGCGAGCGC 776
Db 1016 CGAGCCCTCTCCGAGGCGCACCGCTCACACCGCCACCGCGCTGGCTGTGGGGTCTG 1075
QY 777 GGGCGGGGGGGCGAGAGGCGGAACGCTGCCACCCAGCTCAACGGCGCGCCCTGGGGA 836

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Db 1076 GCAGAAGGGGCGAGGGAGGCGCATGCCGCTGCACACAGTATGGGTGGGTGAGGGCGCGCT 1135
QY 837 GCGCGCGCGCGCGGG 852
Db 1136 AGCGGCTGAGGCGCGG 1151

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RESULT 5

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US-09-165-543-1
; Sequence 1, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

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COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:

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ATTORNEY/AGENT INFORMATION:

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; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214

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INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-09-165-543-1

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Query Match      12.3%; Score 166.4; DB 3; Length 2689;
Best Local Similarity 51.3%; Pred. No. 4.5e-22;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;

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QY 3 GGGCTCCCTGCAGCGGACGGGCGCAACGGAGCTGGAACGGGAGCGGCGGGGGG 62
Db 296 GCGCGCGCGCGCGGAGCGGGCGCTGAACGCTTCGGGGGGCGCTGGCGGCGAGCGCGGGC 355
QY 63 CGCGCGCGGGGCAACCCCTTACTCCCTGCAAGGTGACGCTGACGCTGTGCTGGCGGG 122
Db 356 GCGCGGGGCGCGCGCGCTTCTGCGCAAGCTGACCGCGGTGTGCGCGCTCATGCGC 415
QY 123 CTTGCTCATGCTGCTCACCCTGTTGCGCAACGCTGCTCATCATCGCGCTGTTCAAGAG 182
Db 416 GCTGCTCATGCTGCGCACGCTGCTGCGCAACGCGCTGCTCATGCTGCTGCTGCGCGGA 475
QY 183 CCGCGGCTCAAGGCGCGCCCAAAACCTTCTGCTGCTGCTGCTGCTGCTGCGCTGCGGACATCT 242
Db 476 CTCGAGCCTCCGACACCGAACAACCTTCTGCTGCTCAACCTCGCATCTCCGACTTCCT 535

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QY 837 GCCCGCGCGCGCGG 852
Db 846 AGCGCTGAGCGCGG 861

RESULT 3

US-09-165-543-3
; Sequence 3, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-09-165-543-3

Query Match 12.3%; Score 166.4; DB 3; Length 1335;
Best Local Similarity 51.3%; Pred. No. 4.1e-22;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;

QY 3 GGGCTCCCTGCAGCGCGGAGCGGGCAACGCGAGCTGGAACGGGACCGAGCGCGGGGG 62
Db 6 GCGGCGCGCGCGCGAGCGCGCTGAACGCTTCGGGGCGCGCTGGCGCGAGCGCGCGG 65
QY 63 CGGCGCGCGCGCGCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGTGCTGCGCGG 122
Db 66 GCGGCGCGCGCGCGCGCGCTTCGCGCAGCCTGGACCGCGGCTGCTGCGCGCTCATGGC 125
QY 123 CTTGCTCATGCTGCTACCGGTGTTCGGCAACGCTGCTCATCATCGCGGTTCACGAG 182
Db 126 GCTGCTCATGCTGCGCACGGTGTGGCAACCGCGCTGCTCATGCTCGCTGTGCGCGA 185
QY 183 CCGCGCGCTCAAGCGCGCGCAAAACCTCTTCCTGTGTCTCTGGCCTCGCGCGACATCCT 242
Db 186 CTGAGAGCTTCGACACCGCAACAACCTTCTTCCTGCTCAACCTCGCCATCTCCGACTTCT 245
QY 243 GGTGGCCACGCTGTCATCCCTTCTCTGCTGGCCACGAGGTGATGGGCTACTGTGTA 302

Db 246 CGTCGGCGCCTTCTGCATCCCACTGTATGTAACCTACGCTGCTGACAGCGCGCTGACCTT 305
QY 303 CGGCAAGGCTTGGTGCAGATCTACCTGCGCGCTCGACGTGCTTCTTGACAGTCTGTCAT 362
Db 306 CGGCGGGGCGCTTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGCACCTCCTCTGC 365
QY 363 CGTGACCTGTGCGCCATCAGCCTTGACCGCTACTGTGTCATCAGACAGGCCATCGAGTA 422
Db 366 CTTCACATCTGCTCATCAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 425
QY 423 C---AACCTGAAGCGCACGCGCGCGCGCATCAAGCCATCATCATCACCGTGTGCTCAT 479
Db 426 CCGGCGCGCAGAGGCTGACACGCGCGCGCGCAGTGGGAAGATGCTGTGCTGTGCTGCT 485
QY 480 CTCGCGCTCATCTCCTTCCCGCGCTCATCTCCATCGAGAGAAGGGCGGGCGGGG 539
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QY 540 CCGCAGCGCGCGCGAGCGCGCGCTGCGAGATCAACGACCAAGAGTGTACGTATCTCTC 599
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QY 600 GTGATCGGCTCTCTCTGCTCCCTGCTCATCATGATCTGCTTACGTGCGCATCTA 659
Db 606 TTCCACCCCTGAGTCTTTTACGCGCTTCTCAGCGTACACCTTTTAACTCAGCATCTA 665
QY 660 CCAGATCGCGCAAGCGTGCACCCCGCTGCCACCCAGCGCGCGCGGCTCCGAGCGCTGCG 719
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QY 777 GGGCGCGGGGCGCAGAGCGCGCAACCGCTGCCACCCAGCTCAAGCGCGCGCTGCGCA 836
Db 786 GCAGAGAAGGGGACGGGAGGCCATGCCCTGCACAGAGTATGGGTGAGGCGGCGCT 845
QY 837 GCCCGCGCGCGCGG 852
Db 846 AGCGCTGAGCGCGG 861

RESULT 4

US-08-985-090-1
; Sequence 1, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030

QY 188 CGCTCAAGGCGCCCAAAACCTCTTCTGCTGTCTGTGCGCTCGGCCGACATCCTGTGG 247
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QY 248 CCACGCTCGTCATCCCTTCTCGCTGGCCAAAGAGTCATGGGCTACTGTACTTCCGCA 307
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Db 794 CCCTTCTGTGCTGCCCTCAACGTGGCTTACTGATCCCTGGGCGCTGGGAGTTCCGCA 853
QY 308 AGGCTTGGTGCAGATCTACCTTGGCGCTCGACGTGCTCTTCTGCACGTCGTCATCGTGC 367
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Db 854 TCCACCTGTGCAAGCTGTGGCTTACCTGCGACGTGCTGTGCTGACACTAGCTTCATCCTGA 913
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QY 428 TGAAGCGCACGCGCGCCGATCAAGGCCATCATCACCCTGTGGGTCTCTCGGCCG 487
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QY 488 TCATCTCTTCCCGCCCTCATCTCCATCGAAGAAGAGGCGCGCGCGCGCGCGCAGC 547
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QY 548 CGGCGGAGCGCGCTGCGAGATCAACGACGAGAGTGTACGTCTCATCTCGTGTGATCG 607
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Db 1085 CAAGCGCCACGCGCTGAGAGTGAACCTCGACGAGAGGCTACGTGATCTACTCTCGCTGG 1144
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QY 668 CCAAGCGTCGACCGCGTGCACCCAGCGCGCGGGGTCCGAGCGCGCGCGCGCGCGC 727
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Db 1265 CCACTGAGCTCGAGCCGATGGCAA 1289

RESULT 2
US-08-985-090-3
; Sequence 3, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silverl
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-08-985-090-3
Query Match 12.3%; Score 166.4; DB 2; Length 1335;
Best Local Similarity 51.3%; Pred. No. 4.1e-22;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;
QY 3 GGGCTCCCTGCAGCCGAGCGCGGCCAACGCGAGCTGGAACGGGACCGAGCGCGCGGGG 62
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QY 63 CGGCGCGCGCGCGCGCGCGCTTCTGCGCAAGCTTGGGGCGCTGCGCGCGCGCGCGCGC 122
111111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 66 GCGCGCGCGCGCGCGCGCGCTTCTGCGCAAGCTTGGGGCGCTGCGCGCGCGCGCGCGC 125
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QY 600 GTGCATCGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
11
Db 606 TTCCACCTTGAGTCTTTCAGCGCTTCTCTGAGCTGACCTTCTTAACTTCAGCATCTA 665
QY 660 CCAGATCGCAAGCGTGCACCGCGCTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCG 719
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Db 666 CTGAACATCCAGAGCGCACCGCGCTGCGAGTGGGCTGAGAGCGACCGCGCGC 725
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QY 777 GGGCG 836
11
Db 786 GCAGAAGGGGCGAGGCG 845

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 06:16:02 ; Search time 72.1176 Seconds
(without alignments)
5740.812 Million cell updates/sec

Title: US-09-636-259B-2

Perfect score: 1350

Sequence: 1 atgggtccctgcagccgga.....gggacaggaagcgatcgtg 1350

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	173	12.8	3335	1	US-07-676-174A-1
2	166.4	12.3	1335	2	US-08-985-090-3
3	166.4	12.3	1335	3	US-09-165-543-3
4	166.4	12.3	2689	2	US-08-985-090-1
5	166.4	12.3	2689	3	US-09-165-543-1
6	164.8	12.2	1335	3	US-09-167-354-6
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16	153.4	11.4	2140	2	US-08-406-855A-1
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19	153.4	11.4	2140	3	US-09-206-899-1
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23	152.2	11.3	1621	1	US-08-722-001-13
24	151.8	11.2	1776	1	US-08-722-001-29
25	150.4	11.1	1956	1	US-08-313-553-6
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28	147.2	10.9	1645	2	US-08-461-812-1	Sequence 1, Appli
29	142	10.5	1134	1	US-08-087-772A-14	Sequence 14, Appl
30	142	10.5	1227	1	US-07-916-901-1	Sequence 1, Appli
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33	140.8	10.4	1581	3	US-08-767-993-8	Sequence 8, Appli
34	140.4	10.4	1227	1	US-08-351-473B-7	Sequence 7, Appli
35	139.8	10.4	1338	3	US-09-165-543-6	Sequence 6, Appli
36	139.8	10.4	1690	2	US-08-461-812-3	Sequence 3, Appli
37	139.8	10.4	3244	3	US-09-165-543-4	Sequence 4, Appli
38	139.4	10.3	1610	1	US-08-056-051-5	Sequence 5, Appli
39	139.4	10.3	1610	1	US-07-928-611-21	Sequence 21, Appl
40	139.4	10.3	1610	2	US-08-487-811A-21	Sequence 21, Appl
41	139.4	10.3	1610	4	US-09-060-694-21	Sequence 21, Appl
42	139.4	10.3	1610	4	US-09-378-074-21	Sequence 21, Appl
43	139.4	10.3	1610	5	PCT-US93-07370-21	Sequence 21, Appl
44	138.2	10.2	1601	1	US-08-722-001-7	Sequence 7, Appli
45	138.2	10.2	1997	1	US-08-722-001-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-07-676-174A-1
: Sequence 1, Application US/07676174A
: Patent No. 5344776
: GENERAL INFORMATION:
: APPLICANT: Ventor, J. Craig
: TITLE OF INVENTION: Octopamine receptor
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
: STREET: Eleventh Floor, 1615 L. Street, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20036-5601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/676,174A
: FILING DATE: 19910328
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Scott, Watson T.
: REGISTRATION NUMBER: 26,581
: REFERENCE/DOCKET NUMBER: WTS/5683/79117/KIK
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)861-3000
: TELEFAX: (202)822-8944
: TELEX: 6714627 CUSH
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3335 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 319..2121
: US-07-676-174A-1

Query Match 12.8%; Score 173; DB 1; Length 3335;
Best Local Similarity 56.2%; Pred. No. 3e-23;
Matches 351; Conservative 0; Mismatches 265; Indels 9; Gaps 1;

QY 128 TCATGCTGCTCACCCTGTTCCGCAACGTCGTCATCATCGCCGTTTCACGACCGCG 187
Db 674 TTAATGCTGCTGACCATCATCGGGAACATCTCTGATCTGAGTGTGTTCACTAACAAC 733

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Perfect score: 1350
Sequence: 1 atgggctccctgcagccgga.....gggacaggaagcgatcgtg 1350

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

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Maximum Match 100%
Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	446	33.0	1344	9	US-10-077-870-1	Sequence 1, Appli
2	446	33.0	1344	10	US-09-825-923-1	Sequence 1, Appli
3	444.6	32.9	1353	9	US-10-077-870-3	Sequence 3, Appli
4	444.6	32.9	1353	10	US-09-825-923-3	Sequence 3, Appli
5	171.8	12.7	2625	9	US-09-954-531-995	Sequence 995, App
6	166.4	12.3	1335	9	US-09-349-755-3	Sequence 3, Appli
7	166.4	12.3	1335	9	US-09-166-334-3	Sequence 3, Appli
8	166.4	12.3	1335	10	US-09-350-206-3	Sequence 3, Appli
9	166.4	12.3	2689	9	US-09-349-755-1	Sequence 1, Appli
10	166.4	12.3	2689	9	US-09-166-334-1	Sequence 1, Appli
11	166.4	12.3	2689	10	US-09-350-206-1	Sequence 1, Appli
12	153.4	11.4	2140	9	US-10-005-010-1	Sequence 1, Appli
13	147.2	10.9	1645	12	US-10-005-010-1	Sequence 1, Appli
14	147.2	10.9	1973	10	US-09-864-761-3769	Sequence 3769, Ap
15	142	10.5	1185	10	US-09-993-844-13	Sequence 13, Appli
16	142	10.5	3683	10	US-09-895-211-1	Sequence 1, Appli
17	139.8	10.4	694	10	US-09-864-761-17258	Sequence 17258, A
18	139.8	10.4	1338	9	US-09-349-755-6	Sequence 6, Appli
19	139.8	10.4	1338	9	US-09-166-334-6	Sequence 6, Appli

20	139.8	10.4	1338	10	US-09-350-206-6	Sequence 6, Appli
21	139.8	10.4	1690	12	US-10-005-010-3	Sequence 3, Appli
22	139.8	10.4	1749	10	US-09-855-991A-1	Sequence 1, Appli
23	139.8	10.4	3244	9	US-09-349-755-4	Sequence 4, Appli
24	139.8	10.4	3244	9	US-09-166-334-4	Sequence 4, Appli
25	139.8	10.4	3244	10	US-09-350-206-4	Sequence 5, Appli
26	135	10.0	1639	9	US-10-185-991-5	Sequence 12, Appli
27	134.8	10.0	1356	10	US-09-993-844-12	Sequence 12, Appli
28	130.8	9.7	1738	9	US-10-185-991-3	Sequence 178, App
29	128.8	9.5	2173	10	US-09-822-830A-178	Sequence 12, Appli
30	127.2	9.4	1647	10	US-09-829-631A-12	Sequence 9, Appli
31	126	9.3	1113	10	US-09-993-844-9	Sequence 1, Appli
32	126	9.3	3451	10	US-09-811-286-1	Sequence 214, App
33	126	9.3	3451	10	US-09-954-456-214	Sequence 1598, Ap
34	126	9.3	3451	10	US-09-954-456-1598	Sequence 2, Appli
35	126	9.3	3659	12	US-10-044-090-27	Sequence 27, Appli
36	126	9.3	3659	10	US-09-897-006-34	Sequence 34, Appli
37	124.4	9.2	9511	10	US-09-829-631A-7	Sequence 7, Appli
38	123	9.1	1914	10	US-09-829-631A-9	Sequence 9, Appli
39	123	9.1	2108	10	US-09-829-631A-9	Sequence 3, Appli
40	117.6	8.7	3437	10	US-09-895-211-3	Sequence 1620, Ap
41	114.8	8.5	2048	12	US-10-052-589-1	Sequence 20536, A
42	113.2	8.4	2108	10	US-09-917-800A-1620	Sequence 5, Appli
43	106.2	7.9	803	10	US-09-864-761-20536	Sequence 249, App
44	101	7.5	1119	9	US-10-083-168-5	
45	100.2	7.4	2595	10	US-09-964-824A-249	

ALIGNMENTS

RESULT 1
US-10-077-870-1
; Sequence 1, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077, 870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1341)
; OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protei
US-10-077-870-1

Query Match	33.0%;	Score 446;	DB 9;	Length 1344;
Best local Similarity	62.9%;	Pred. No. 2.4e-78;		
Matches 827;	Conservative 0;	Mismatches 415;	Indels 72;	Gaps 6;
QY 78	CCCTTACTCCCTGAGGTGACGCTGACGCTGCTGCTGCGCGGCTGCTCATGCTGCT	137		
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QY 138	CACCGTGTTCGGCAAGTGTCTGTCATCATGCCGCTGTTACAGCAGCGCGGCTCAAGGC	197		
DB 75	TACCATCTTCGGCAAGCTCTGTGTCATCTGCTGTGTGACCAAGCGCTCGTGGCGC	134		
QY 198	GCCCCAAACCTTCTCTGCTGTCTCTGCTGCGCGACATCCTGTGGCCACGCTCGT	257		
DB 135	CCCTCAGAACCTGTCTCTGCTGCTGCTGCGCGCGCCGACATCCTGTGGCCACGCTCAT	194		
QY 258	CATCCCTTCTCTGCTGCGCAAGAGGTGATGGCTACTGTGTAATTCGCGCAAGGCTTGGTG	317		

Db	195	CATCCCTTTCTTCGCTGGCCCAACGAGCTGCTGGGCTACTGTGACTTCCGGCCACGTGTG	254
QY	318	CGAGATCTACCTGGCGCTGACGTGCTTCTGTGCACGTCGTCCAATCGTGCACCTGTGCGC	377
Db	255	CGAGGTGTACTCTGGCGCTGACGTGCTTCTGTGCACCTCGTCCATCGTGCACCTGTGCGC	314
QY	378	CATGAGCTTGAGCCGCTACTGTGTCATTCACACAGGCCATCGAGTACAACTGAGCGCAC	437
Db	315	CATGAGCTTGAGCCGCTACTGGCGCTGAGCCGCGCGCTGGAGTACAACTCCAAGCGCAC	374
QY	438	GCCGCGCCGCATCAAGGCCATCATCAACCGTGTGGTCAATCTGGCCGCTATCTCCTT	497
Db	375	CCCCGCGCCGATCAAGTGCATCATCTCTCACTGTGTGGCTCATCGCCGCGCTCATCTCGCT	434
QY	498	CCCCGCGCTCATCTCCATCGAGAGAGAGGGCGGGCGGGCGGGCGGCGGCGGAGCC	557
Db	435	GCCGCGCCGCTCATCT-----ACAAGGGCGAGCAGGGCGCCGAGCGCGCGCGGCC	485
QY	558	GCGCTGCGAGATCAACGACAGAGAGTGTACGTCATCTCGTGTGATCGGCTCCTTCTT	617
Db	486	CCAGTGCAGAGCTCAACCAAGAGGCGCTGTACATCCTGGCCCTCCAGCATCGGATCTTCTT	545
QY	618	CGCTCCCTTGCCCTCATCATGATCCTGTGTCTACGTGGCGATCTACAGATCGCCCAAGCCTCG	677
Db	546	TGCTCTCTTGCCCTCATCATGATCTCTGTCTACCTGGCGCATCTGATCGCCCAACGCGAG	605
QY	678	CACCCGCGTGCCACCCA-----GCGCGCGGGTCCGGACGCGCTCG	718
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QY	719	CCGCGCGCGCGGGGG-----CACCGAGCGCAGGCCCAAGGGTCTGG	760
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Db	726	TGCCAGAGAGTCAACGCGACACTCGAAGTCCACTGGGAGAGAGAGAGGGAGAGCCCC	785
QY	813	CCAGCTCAACGGCGCCCTGCGGAGCCCCGCGCGCGCGCGCGCGCGCGAGACCGCGCT	872
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QY	873	GGACCTGGAGGAGAGCTGTCTTCCGACACGCGCCGAGCGGCCCTCCAGGGCCCCGACAGC	932
Db	846	GGGCCAGAGAGGAGGTGTGTGAGGACATCTCCAGAGGATGAAGCTGAAGAGAGGAAGA	905
QY	933	CGAGCGCGGTCCCCCGGGGCAAGGCCAAGGCCGAGCGGCAAGTGAAGCCGGCGGACAG	992
Db	906	GGAGGAGGAGGAGTGTGAACCCCAAGGAGTGCAGTGTCTCCGGCCTCAGCTTGACGCC	965
QY	993	CCTGCCCGCGCGGGCGGGGGCGAGCGGGATCGGGACGCCCGGCTGCAGGGCGGGGGA	1052
Db	966	CCCCGTGCAGCAGCCACAGGGGCTCCCGGGTCTGGCCACCTACGTGGCCAGGTGCTCT	1025
QY	1053	GGAGCGCGTCGGGGCTGCCA-----AGGCGTCGCGCTGGCGCGGGCGGCGAGAACG	1103
Db	1026	GGGCGAGGGGCGTGGGTGTATAGGTGGGCGAGTGGGCGTGCAGCGGGCGCAGCTGACCG	1085
QY	1104	CGAGAGCGCTTCAACGTTGCTGTGCTGGCGGTGTGTCATCGAGTGTTCGTGTGTGCTGTT	1163
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QY	1164	CCCCCTTCTTCTTCACTTACCTACACGCTCAGCGCGCTGGG-----TGCTCGGTCACG	1214
Db	1146	CCCCCTTCTTCTTCACTTACAGCCTGGGCGCATCTGCCGGAAGCACTGCAAGGTGCCCA	1205
QY	1215	CACGCTCTTCAAAATCTTCTTCTGTGTGCGGCTACTTGAACAAGCTCGTTGAACCCGCTCAT	1274
Db	1206	TGGCTCTTCTTCAAGTCTTCTTCTGTGATCGGCTACTTGAACAAGCTCACTGAACCTGTAT	1265
QY	1275	CTACACCATCTTCAACCAAGATTTCCGCGCGCGCTTCAAGAAGATCCTCTGTG	1328
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RESULT 2
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; Sequence 1, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snaplr, Amtr
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulou, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Nyyss"nen, Kristina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kaunonen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT APPLICATION NUMBER: US/09/825,923
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422,985
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1341)
; OTHER INFORMATION: Coding sequence for variant human
; OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1

Query Match          33.0%; Score 446; DB 10; Length 1344;
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Matches 827; Conservative 0; Mismatches 415; Indels 72; Gaps 6,

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DB 15 CCCCTACTCCGTCGAGGCCACAGCGCCCATAGCGCGGCATCACCCTTCTCTCTT 74

QY 138 CACCGTGTTCGGCAACGTCGCTGTCATCATCGCCGCTTTCACGAGCGCGCTCAAGC 197
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DB 75 TACCATCTTCGGCAACGCTGTCATCTGCTGCTGTGTGACCAAGCGCTCGCTGCGGC 134

QY 198 GCCCCAAAACCTTCTCTGCTGTCGTCCTGCGCTCGGCGACATCCTGTGGCCACGCTCGT 257
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QY 258 CATCCCTTTCCTGCTGCGCAAGAGGTGATGGGCTACTGTGACTTCGGCAAGGCTTGCTG 317
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QY 318 CGAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGTCGTCATCGTGACCTGTGCGC 377
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QY 438 GCCGGCGCGCATCAAGGCCATCATCATCACCCTGTGGGTGATCTGCGCGCTCATCTCCCT 497
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DB 375 CCCGGCGCGCATCAAGTGCATCATCTCTCAGCTGTGTGGCTCAATCGCGCGCTCATCTCCCT 434

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OY      498 CCCGCCGCTCATCTCCATCGAGAGAAGGGCGGCGGCGGCCCCCGCAGCCGCCGAGCC 557
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OY      558 GCGCTGCAGATCAACGACGACGAAGTGTACTGTCATCTGCTGTCATCGGCTCTTCTT 617
          | ||| | |||| | || ||||| | | ||||| | | ||||| | |||||
Db      486 CCAGTGCAAGCTCAACCAGAGGCCCTGTATCATCTGTGACCTCCAGCATCGAATCTTTCTT 545

OY      618 CGCTCCCTGCTCATCATGATCCTGTGTACTGTCGCATCTACAGATCGCCAAGCGTGC 677
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Db      546 TGCTCCCTGCTCATCATGATCCTGTGTACTACCTGCGCATCTACCTGATCGCAAAACGAG 605

OY      678 CACCCGCGTGCACCCA-----GCGCGCGGGGTCCGAGCGCCGTGC 718
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Db      606 CAACCGCAGAGGTCCAGGGCCCAAGGGGGGGGCGCTGGGCGAGGTGAGTCCAGACGACCCC 665

OY      719 CCGCGCGCGCGGGGG-------CACCGAGCGCAGGCGCCCAAGGCTTGG 760
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Db      666 ACCCGACCATGGTGGGGCTTGGCCCTCAGCCAACTGCCAGCCCTGGGCTGTGTGGCTTC 725

OY      761 GCCCCGACGCGCAGCGCGGGCGCGGG-------GCGCGCAGAGGCGCAACGCTGCCAC 812
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Db      726 TGCAGAGAGGTCAACGGACTCGAAGTCCACTGGGGAAGAAGAGAGGGGAGAACCC 785

OY      813 CCAGCTCAACGCGCCCCCTGCGGAGCCCCGCGCGCGCGCGCGCGCAGACCGCGCT 872
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Db      786 TGAAGATACTGGGACCCGCGGCTTGCCACCAGTTGGGCTGCCCCCTCCAACTCAGGCCA 845

OY      873 GGACCTGAGAGAGAGCTCGTCTTCCGACCAACGCGCAGCGGCGCTCCAGGGCGCCGACACC 932
          || ||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db      846 GGGCCAGAGAGAGGAGGTGTTGTGGGGCATCTCCAGAGGATGAAGCTGAAGAGAGGAAGA 905

OY      933 CGAGCGCGGTCCCCGGGGCAAGGCCAGCGCCGAGCGCAGGTGAAGCCGGCGACAG 992
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OY      993 CTGCGCGCGCGCGCGGGCGCGGGCGAGCGGGGATCGGAGCGCCGCGCTGCAGGGCGCGGGA 1052
          || ||| |||| | |||| | |||| | |||| | |||| | |||| |
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OY      1053 GGAGCGCGCTCGGGGCTGCCA-----AGGCGTCGCGCTGGCGCGGGCGGCGAGAACCG 1103
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Db      1026 GGGCAGGGGCGTGGGTGCTAATAGGTGGGCGAGTGTGGCGTCGACGGGCGCAGCTGACCCG 1085

OY      1104 CGAGAACGCTTCACGTTCTGCTGCGCGCTGCTGTCATCGAGTGTCTGCTGCTGCT 1163
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1086 GGAGAACGCTTCACCTTCGCTGCGCTGTGTGTAATTGGCGTTTTTGTGCTCTGCTGTT 1145

OY      1164 CCCCTCTTCTTACCTACGCTACAGGCTCAGGCGCTGGG-----TGTCTCGTGGCCAGC 1214
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1146 CCCCTCTTCTTACGCTACAGGCTGGGGCGCCATCTGCCCGAAGCAGCTGCAGAGTGGCCCA 1205

OY      1215 CACGCTCTTCAATCTTCTCTGTGTTGCGCTACTGCAACAGCTCGTTGAACCCGGTCA 1274
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1206 TGGCTCTTCCAGTCTTCTTCTGTGATCGGCTACTGCAACAGCTCAGTGAACCTGTTAT 1265

OY      1275 CTACACATCTTCAACACACGATTTCCGCGCGCGCTTCAAGAAGATCCTGTGCG 1328
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1266 CTACACATCTTCAACACAGAGACTTCCGCGCTTCCGAGGATCCTGTGCGCG 1319

RESULT 3
US-10-077-870-3
; Sequence 3, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20

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; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
US-10-077-870-3

Query Match      32.9%; Score 444.6; DB 9; Length 1353;
Best Local Similarity 63.3%; Pred. No. 4.5e-78;
Matches 838; Conservative 0; Mismatches 404; Indels 81; Gaps 7;

QY 78 CCCTTACTCCCTGCAGTGTGACGCTGCTGTGTGCTGCGCCGCTGCTCATGCTGCT 137
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15 CCCCTACTCCGTCAGCGCACAGCGGCATAGCGCGGCATCACCTTCTCATTTCTTT 74

QY 138 CACCGTGTTCGGCAACGTCCTCGTCATCATCGCCGTTTCACGAGCGCGGCTCAAGCC 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75 TACCATCTTCGGCAACGCTGTGTCATCCTGCTGTGTGACCAAGCGCTCGCTGCGCC 134

QY 198 GCCCCAAACCTCTTCTGCTGTCTCTGCGCTGCGCCGACATCCTGTGGCCACGCTCT 257
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 135 CCCTCAGAACCTGTTCCTGTGTCTGCTGCGCCGCGCCGACATCCTGTGGCCACGCTCAT 194

QY 258 CATCCCTTTCCTGCTGCGCCCAACGAGTCTATGGGCTACTGTACTTCCGCAAGGCTTGGTG 317
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 195 CATCCCTTTCCTGCTGCGCCCAACGAGTCTGTGGGCTACTGTACTTCCGCGCCACGTGGTG 254

QY 318 CGAGATCTACCTGGCGGCTGCAGCTGCTCTTCTGCACGTCGTCATCGTGACCTGTGCGCC 377
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Db 255 CGAGGTGTACCTGGCGGCTGCAGCTGCTCTTCTGCACCTGTCATCGTGACCTGTGCGCC 314

QY 378 CATCAGCCTGGACCGGCTACTGTTCCATCACACAGGCCATCGAGTACAACTGAAAGCGCAC 437
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 315 CATCAGCCTGGACCGGCTACTGCGCCGTGAGCGCGCGCTGAGTACAACTGAAAGCGCAC 374

QY 438 GCCGCGCCGATCAAGGCCATCATCAACCCTGTGGTCACTCTCGGCCGTACTCTCTT 497
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 375 CCCGCGCCGATCAAGTGTATCATCTCACTGTGTGCTCATCGCCGCGTCACTCTCGCT 434

QY 498 CCCGCGGCTCATCTCCATCGAAGAAGGGCGGCGGCGGCGCCGACGCCGCGGACGCC 557
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 435 GCCGCGCCGCTCATCT-----ACAAGGGCGACCAAGGGCCCCCAGCCGCGGCGGCC 485

QY 558 GCGCTGCGAGATCAACGACGACGAAGTGGTACGTCATCTGCTGTCATCGGCTCTTCTT 617
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 486 CCAAGTCAAGCTCAACGACGAGGCGCTGTATCATCTGCGCTCCAGCATCGGATCTTCTT 545

QY 618 CGCTCCCTGCTCATCATGATCTCTGTCTACGTGCGCATCTTACAGATCGCCAAAGCTCG 677
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 546 TGCTCTTGTGCTCATCATGATCTCTGTCTACCTGCGCATCTTACCTGATCGCCAAAGCAG 605

QY 678 CACCCGCGTGCCACCAC-----GCCGCGGCGGTCCGGACGCGGTCG 718
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 606 CAACCGCAGAGTCCCAAGGGCCAAAGGGGCGCTGCGGCAAGGTGATCCAAAGCAGCCCCG 665

QY 719 CCGCGCGCGCGGGGG-----CACCGAGCGCAGGCCCAAGGCTCTGG 760
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 666 ACCCGACCATGTTGGGGCTTTGGCCCTCAGCCAAACTGCCAGCCCTGGCCTCTGTGTGCTTC 725

QY 761 GCCCGGAGCGCAGCGCGCGCGCG-----GGCGCAGAGGGCGAACCCTGTCCCAACC 813
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 726 TGCCAGAGAGGTCAACGACACTCGAAGTCCACTGGGGAGAAAGAGAGAGGGGAGAACCCC 785

QY 814 CAGCTCAACGGCGCCCTGCGGAGACCGCGCGCGCGCGCGCGCGGACACCGACCGCGCTG 873
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 786 TGAAGATACTGGGACCGCGGCGCTTGCCACCCAGTTGGGCTGCGCTTCCCAACTCAGGCCA 845
874 GACCTGGAGAGAGTCTGTTCCGACCACGCGCGGCGGCTTCCAGGGCGCGCAGACCG 933

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Db 846 GGGCCAGAAAGAGGGTGTGTGTGGGCGATCTCCAGAGGATGAAGCTGAAGAGAGAGA 905
QY 934 GAGCGCGGTCCCCGGGCAAAAGGCAAGGCCCGAGCGCAGGTGAAGCCGGCGACAGC 993
Db 906 GGAGGAGGAGGAGGAGGAAGAGTGTGAACCCAGGCGAGTGCCAGTGTCTCCGGCTCAGC 965
QY 994 CTGCGCGGGCGGGCGGGGGCGGCGACGGGATCGGG-----ACGCGGCT 1038
Db 966 TTGCAGCCCCCGCTGCAGCAGCCACAGGGCTCCGGGTGCTGGCCACCCTACGTGGCCA 1025
QY 1039 GCAGGGCGGGGAGAGCGCGTCCG---GGCTGCCAAGGCGTCCGCTGGCGCGGGCG 1094
Db 1026 GGTGCTCCTGGGAGGGGCGTGGGTGCTAATAGGTGGGAGTGTGGCTGCAGCGGGCA 1085
QY 1095 GCAGAACCGCGAGAGCGCTTCAAGTTCGTGCTGGCCGTGTCATCGAGTGTCTGTGT 1154
Db 1086 GCTGACCCGGGAGAGCGCTTCACTTCGTGCTGGCTGTGTCATGGCGTTTGTGCT 1145
QY 1155 GTGCTGTTCCCTCTCTTCTTCACTTACAGCTCACGGCGTCCGG-----TGCTC 1205
Db 1146 CTGCTGGTCCCTCTCTTCTTCACTTACAGCTGAGCGCGCCATCTGCCGAAGCACTGCAA 1205
QY 1206 CGTGCCACGACGCTCTTCAATTTCTTCTGTGGTTCGGCTACTGCAACAGCTCGTTGAA 1265
Db 1206 GGTGCCCATGGCTCTTCCAGTTCCTTCTGTGATCGGCTACTGCAACAGCTCACTGAA 1265
QY 1266 CCGGTCATCTACCATCTTCAACCAAGATTTCCGGCGGCTTCAAGAGATCTCTGTG 1325
Db 1266 CCCTGTATCTACCATCTTCAACCAAGACTTCCGGCGTCCGCTTCCGAGGATCTCTGTG 1325
QY 1326 TCG 1328
Db 1326 CCG 1328
RESULT 4
US-09-825-923-3
; Sequence 3, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Nyyss"nen, Kristiina
; APPLICANT: Salonen, Riiita
; APPLICANT: Kauhanen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT APPLICATION NUMBER: US/09/825,923
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422,985
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
; OTHER INFORMATION: protein

US-09-825-923-3
Query Match 32.9%; Score 444.6; DB 10; Length 1353;
Best Local Similarity 63.38; Pred. No. 4.5e-78;
Matches 838; Conservative 0; Mismatches 404; Indels 81; Gaps 7;
QY 78 CCTTACTCCCTGCAGGTGACGCTGACGCTGTGTGCTTGGCGGCTTCATGCTGCT 137
Db 15 CCTTACTCCGTGCAGGCGACAGCGCCATAGCGCGGCCATCACCTTCTCATTTCTT 74
QY 138 CACGCTGTTCCGCAACGTGCTGTCATCATCGCGTGTTCACGAGCGCGGCTCAAGGC 197
Db 75 TACCATCTTCGGCAACGCTCTGTGTCATCCTGGCTGTGTGACCAAGCGCTCGCGGC 134
QY 198 GCCCAAAACCTCTTCTGTGTCTCTGCGCTCGGCGACATCCTGTGTGCCACGCTCGT 257
Db 135 CCTCAGAACCTGTTCCTGTGTGCTGCGCGCGCGGACATCCTGTGTGCCACGCTCAT 194
QY 258 CATCCCTTCTCGCTGGCCCAAGGTCATGGGCTACTGTGTACTTCGGCAAGCTTGTG 317
Db 195 CATCCCTTCTCGCTGGCCCAAGGTCATGGGCTACTGTGTACTTCCGGCGACGTTGTG 254
QY 318 CGAGTCTACCTGGCGCTGCAGCTGCTCTTGTGACGTCGTCATCGTGTGACCTGTGCGC 377
Db 255 CGAGTGTACCTGGCGCTGCAGCTGCTCTTGTGACCTGTCATCGTGTGACCTGTGCGC 314
QY 378 CATCAGCTTGACCGCTACTGTGTCATCACACAGGCCATGAGTACAACTGAAGCGCAC 437
Db 315 CATCAGCTTGACCGCTACTGTGGCGCTGAGCGCGCGCTGAGTACAACTGAAGCGCAC 374
QY 438 GCCGCGCGCATCAAGGCCATCATCATCACCGTGTGGTCACTCGCGCTCATCTCCTT 497
Db 375 CCGCGCGCATCAAGTGCATCATCTCATCTGTGTGCTCATCGCGCGCTCATCTCCTT 434
QY 498 CCGCGCGTCATCTCATGAGAAGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 557
Db 435 GCGCGCGCTCATCT-----ACAAGGCGACAGGGCGCGCGCGCGCGCGCGCGCGC 485
QY 558 GCGCTCGAGATCAACGACGAGAAGTGTAGTCACTCTGCTGTCATCGGCTCTTCTT 617
Db 486 CCAGTGCAAGCTCAACGACGAGCGCTGTACATCTCGGCGCTCCAGCATCGATCTTCTT 545
QY 618 CGCTCCCTGCTCATGATCTCTGTGTACGTGCGCATCTACAGATCGCCAGCGTGC 677
Db 546 TGTCTCTTGCCTCATGATGATCTTGTCTACCTGCGCATCTACCTGATCGCCAAACGAG 605
QY 678 CACCGCGTGCCACCCA-----GCCGCGGGGTCCGAGCGCGTGC 718
Db 606 CAACCGCAGAGGTCCAGGGCCAGGGGGCGCTGGGCGAGGTGAGTCCAGCAGCGCCCG 665
QY 719 CCGCGCGCGCGGGG-----CAGCGAGCGGAGCGCGCAAGGGTCTGG 760
Db 666 ACCCGACCATGGTGGGCTTTGGCCTCAGCCAACTGCGACCGCTCTGTGTGCTTC 725
QY 761 GCCCGAGCGCAGCGCGCGCGG-----GGCGCAGAGCGCGCAAGCGCTGCCACC 813
Db 726 TGCCAGAGAGTCAACGAGACTCGAAGTCCACTGGGAGAGAGAGAGGGGAGACCC 785
QY 814 CAGTCAACGGCGCGCGCTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 873
Db 786 TGAAGTACTGGGACCGCGGCTTGCCACCCAGTTGGGCTGCGCTTCCAACTCAGGCCA 845
QY 874 GACCTGAGAGAGAGCTCGTCTCCGACCAAGCGCGCGCGCTCCAGGGCGCGCAGACCC 933
Db 846 GGGCCAGAAAGAGGTGTGTGGGCGATCTCCAGAGATGAAGCTGAAGAGAGGAAGA 905
QY 934 GAGCGCGTCCCCGGGCAAAAGGCAAGGCCCGAGCGCAGGTCGAAGCGCGCGCAGACAGC 993
Db 906 GGAGGAGGAGGAGGAGGAAGTGTGAACCCAGGCGAGTCCAGTGTCTCGGCGCTCAGC 965
QY 994 CTGCT 1038
Db 966 TTGCAGCCCCCGCTGCAGAGCCACAGGCGCTCCGCGGTGCTGCGCACCCCTACGTGGCCA 1025


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; Sequence 3, Application US/09349755
; Patent No. US20020166131A1
;
; GENERAL INFORMATION:
;   APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
;   TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
;   NUMBER OF SEQUENCES: 39
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: LAHIVE & COCKFIELD, LLP
;     STREET: 28 State Street
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: USA
;     ZIP: 02109
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/349,755
;   FILING DATE: 08-Jul-1999
;   CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/042,780
;   FILING DATE: <Unknown>
;   APPLICATION NUMBER: US 08/985,090
;   FILING DATE: 04-DEC-1997
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Elizabeth A. Hanley
;   REGISTRATION NUMBER: 33,505
;   REFERENCE/DOCKET NUMBER: MNI-032CP
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617)227-7400
;     TELEFAX: (617)742-4214
;
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1335 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1..1335
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-349-755-3

Query Match      12.3%; Score 166.4; DB 9; Length 1335;
Best Local Similarity 51.3%; Pred. No. 4.4e-24;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;

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Db 306 CGGCGGGGGCCTCTGCAAGCTGTGGCTGTAGTAGACTACCTGTGTGCACTCTCTGTC 365
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Db 366 CTTCACATCGTGTCTATCAGCTACGACCGCTTCTGTGCTACCCGCGGTCTCATATA 425
QY 423 C--AACCTGAAGCGCAGCGCGCGCATCAAGCCATCATCATCACCGTGTGGTCAAT 479
Db 426 CGGGGCCAGCAGGCTGACACAGCGCGCGGACAGTGGGAAGATGCTGTGTGGTGTCT 485
QY 480 CTGCGCCGTATCTCTCTCCCGCGCTCATCTCCATCGAAGAAGAGGGCGCGCGCGG 539
Db 486 GGCTTCTCTGTGTACGAGACCGCATCTGAGCTGGAGATACCTGTCCGGGGGACGCTC 545
QY 540 CCGGACGCGCGCGCGCGCGCTGCGAGATCAAGACAGAGAGTGGTACGTATCTGTC 599
Db 546 CATCCCCGAGGGCCACTGCTATGCCGAGTCTCTACAACTGTACTTCTCATCACGCG 605
QY 600 GTGCATCGGCTCTCTCTCCCTCCCTGCTCATATGATCTGTGTACGTGCGCATCTA 659
Db 606 TTTCACCCCTGAGTCTTTTACGCCCTTCTCTCAGCGTCAACCTTCTTACCTCAAGCATCTA 665
QY 660 CCAGATGCGCAAGCGTGCACACCGCGGTGCCACCCAGCCGCGGGGTCCGAGCGCGTCCG 719
Db 666 CTTGAACATCCAGAGGCGCACCCGCGCTCCGCTGGATGGGGCTCGAGAGGCGACGCGGCC 725
QY 720 CGCGCGCGCGGGGCGCACCGAGCGC--AGGCCAAGGGTCTGGGCGCGCGAGCGCGC 776
Db 726 CGAGCCCCCTCCGAGGCGCCAGCCCTCACACACCCCAACGCGCTGCTGTGGGCTGCTG 785
QY 777 GGGCGCGGGGCGCAGAGCGCCGAGCCGCTGCCACCCAGCTCAACGCGCGCCCTGGCGA 836
Db 786 GCAGAAGGGGCACGGGAGGCCATGCGCGCTGCACAGGTATGGGTGGGTGAGCGCGCGCT 845
QY 837 GCGCGCGCGCGCGCGG 852
Db 846 AGCGGCTGAGGCGCGG 861

RESULT 7
US-09-166-334-3
; Sequence 3, Application US/09166334
; Patent No. US20020168708A1
;
; GENERAL INFORMATION:
;   APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
;   TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
;   NUMBER OF SEQUENCES: 39
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: LAHIVE & COCKFIELD, LLP
;     STREET: 28 State Street
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: USA
;     ZIP: 02109
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/166,334
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/042,780
;     FILING DATE:
;     APPLICATION NUMBER: US 08/985,090
;     FILING DATE: 04-DEC-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Elizabeth A. Hanley
;     REGISTRATION NUMBER: 33,505
;     REFERENCE/DOCKET NUMBER: MNI-032CP
;   TELECOMMUNICATION INFORMATION:

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Db	246	CGTCGGCGCCTTCTG	CATCCACATGTATGT	ACCCTACGTTGCTG	ACAGCGCGCTG	CACTT	305		
QY	303	CGGCAAGGCTTGGT	CGAGATCTACCTGG	CGCTCGACGTGCT	TTCTGCAGCTG	CTCAT	362		
Db	306	CGGCGGGGCTCTG	CAAGCTGTGGTGGT	AGTGGACTACCTG	CTGTGCACCTCC	CTTGC	365		
QY	363	CGTGACCTGTGGCC	ATCAGCCTGGA	CCGCTACTGTG	TCATCACAGG	CCATCAGTA	422		
Db	366	CTTCAACATCTGCT	CTCATCAGCTAC	GAACCGCTTCT	GTGGTCA	CCCCGAGCGGTCT	CATA 425		
QY	423	C---AACCTGAAG	CGGCACGCGCGCG	CGCATCAAGGCC	ATCATCACCG	GTGGTCA	479		
Db	426	CCGGGCCACG	AGGGGTGACACG	CGCGGGGACGTG	CGGAAGATGCT	GCTGTGTGGT	GCT 485		
QY	480	CTCGGCGCTCAT	CTCTCTCCCGCG	CTCATCTCCAT	CGAGAAGGGCG	CGCGCGG	539		
Db	486	GGCTTCTCTGT	GTACGAGCACCAT	CTCTGAGCTGG	AGTAACCTGT	CCGGGGGCA	CTC 545		
QY	540	CCCGACGCCG	CGGACGCGGCTG	CGAGATCAACG	ACAGAAAGTGT	AGTCATCTG	CTC 599		
Db	546	CATCCCCGAG	GGCCACTGCTAT	GCCGAGTTCTT	CTACAAC	TGTA	CTTCC	CATCACGGC 605	
QY	600	GTGCATCGGCT	CTCTCTTCGCT	CTCCCTGCTCAT	CTATGATCTG	GTCTACG	TGCGCATCTA 659		
Db	606	TTCCACCC	TGGAGTTCTTT	ACGCCCTTCT	CTCAGCGTCA	CACTTCTT	TAACTCAGCA	CTTA 665	
QY	660	CCAGATCGCC	AAGCGTGCAC	CCCGCTGCCAC	CCAGCGCGGGG	TCCGGAGCG	CCCTCGC 719		
Db	666	CCTGAACAT	CAAGAGGCG	CACCGCTCCG	GCTGATGGG	CTCGAGAGG	CAGCGGCC 725		
QY	720	CGGCGCGCGG	GGGCGCACCG	AGCGC---AGG	CCCAAGGTTGG	CGCCCGAGCG	CAAGCC 776		
Db	726	CGAGCCCC	CTCCCCGAG	CGCCACCA	CCACCCACCG	CTGTGCTG	GGGCTGCTG 785		
QY	777	GGGCGCGGGG	CGACAGAGCG	CAACCGCTG	CCCAACCA	CAAGCTCA	AGGCGC	CCCTGCGCA 836	
Db	786	GCAGAA	GGGGGCA	CGGGGAGG	CCATGCGC	CTGCACAG	GTATGGG	TGGTGAGAGGCGGCC	CT 845
QY	837	GCCCCGCG	CGCGCGG	852					
Db	846	AGCGGCT	GAGCGCGG	861					

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RESULT 9
US-09-349-755-1
; Sequence 1, Application US/09349755
; Patent No. US20020166131A1
;
GENERAL INFORMATION:
;
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
;
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
;
NUMBER OF SEQUENCES: 39
;
CORRESPONDENCE ADDRESS:
;
ADDRESSEE: LAHIVE & COCKFIELD, LLP
;
STREET: 28 State Street
;
CITY: Boston
;
STATE: Massachusetts
;
COUNTRY: USA
;
ZIP: 02109
;
COMPUTER READABLE FORM:
;
MEDIUM TYPE: Floppy disk
;
COMPUTER: IBM PC compatible
;
OPERATING SYSTEM: PC-DOS/MS-DOS
;
SOFTWARE: PatentIn Release #1.0, Version #1.25
;
CURRENT APPLICATION DATA:
;
APPLICATION NUMBER: US/09/349,755
;
FILING DATE: 08-Jul-1999
;
CLASSIFICATION: <Unknown>
;
PRIOR APPLICATION DATA:
;
APPLICATION NUMBER: US/09/042,780
;
FILING DATE: <Unknown>
;
APPLICATION NUMBER: US 08/985,090
;
FILING DATE: 04-DEC-1997
;

```

```

: ATTORNEY/AGENT INFORMATION:
: NAME: Elizabeth A. Hanley
: REGISTRATION NUMBER: 33,505
: REFERENCE/DOCKET NUMBER: MNI-032CP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)742-4214
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2689 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 291..1625
: SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-349-755-1

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Query Match	12.3%;	Score 166.4;	DB 9;	Length 2689;
Best Local Similarity	51.3%;	Pred. No. 4.8e-24;		
Matches 439;	Conservative	0;	Mismatches 411;	Indels 6;
				Gaps
QY 3	GGGCTCCCTGCAGCCGGACGCGGGCAACGGCAGCTGGAAACGGGACCGAGCGCGGGGG	62		
Db 296	GGCGGCGCGCCCGACGGGGCCGTGACGGCTTCGGGGGCGCTGGGGGGCGAGCGCGCGG	355		
QY 63	CGCGCGCGGGGCCACCCCTTACTCCCTGACGGTGACGCTGACGCTGGTGTGCTGGCCGG	122		
Db 356	GGCGGGGGGGGGCGCGCGCGCTTCTCGGCAGCCCTGGACCGCGGGTGTGCGCCGCTCATGGC	415		
QY 123	CCTGCTCATGCTGCTCAACCGTGTTCGGCAACGTGCTCGTCATCATCGCCGTGTTCACGAG	182		
Db 416	GCTGCTCATGCTGGCCACCGTGTGCGGCAACGCGCTGGTCATGCTTCGCTTGTGGCCGA	475		
QY 183	CGCGCGCTCAAGCGCGCCCCAAAACCTTCCTGCTGTGTCTGTGCGCTGGCCGACATCCT	242		
Db 476	CTCGAGCCTCCGACCCAGAACAACTTCCTGCTCAACCTCGGCATCTCCGACTTCCT	535		
QY 243	GGTGGCCACGCTGTCATCCCTTCTCGCTGGCCAAACGAGGTCAATGGCTACTGTACTT	302		
Db 536	CGTCGGCGCCTTCGTCATCCCACTGTATGTAACTTACGTGCTGACAGGCCGCTGACCTT	595		
QY 303	CGGCAAGCCTTGGTTCGAGATCTACCTGGCGCTCGACGTGCTTCTTCGACGTGCTCCAT	362		
Db 596	CGGCGGGGCGCTTCGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGACACCTCCTTGC	655		
QY 363	CGTGACCTGTGGCCCATCAGCCTGGACCGCTACTGTCATCACAGGCCATCGAGTA	422		
Db 656	CTTCAACATCGTGTCTATCAGCTACGACCGCCTTCCTGTGCTACCCGAGCGGTCATATA	715		
QY 423	C---AACCTGAAGCGCACGCGCGCGGCATCAAGGCCATCATCATCACCCTGTGGTCA	479		
Db 716	CCGGGCCACGAGGGTGACACGCGGGGCGAGTGGGAAGATGCTGTGTGGTGT	775		
QY 480	CTCGGCGCTCATCTCTTCCCGCGCTCATCTCCATCGAGAAGAGGGCGGGCGGGCGG	539		
Db 776	GGCCTTCCTGCTGTACGGAACCAAGCCATCTCTGAGCTGGAGTACCTGTCCGGGGGACGCTC	835		
QY 540	CCCGCAGCGGGCGGAGCGCGCTGGCGAGATCAACGACGAGAAGTGTATCGTATCTGTC	599		
Db 836	CATCCCGAGGGCCACTGCTATGCCGAGTCTTCTACAACGTGTACTTCTCATCACGGC	895		
QY 600	GTGCATGCGCTCTTCTTCTGCTCCTTCGCTCATCATGATCTGTGCTACGTCGCACTTA	659		
Db 896	TTCCACCCCTGAGTCTTTTACGCCCTTCTCAAGCTCACCTTCTTAACTCAGCATCTA	955		
QY 660	CCAGATCGCCAAAGCTCGCACCCCGCGTGCACCCAGCCGCGGGGTCCGGACGCGCTGCG	719		
Db 956	CCTGAACATCCAGAGGGCCACCCGCGCTCCGGCTGGATGGGGCTCGAGAGGACGCGCGGCC	1015		
QY 720	CGCGCGCGGGGGGACCCGAGCGC--AGGCCCAAGGGTCTGGGCCCCCGAGCGCAGCGC	776		


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Db 1016 CGAGCCCCCTCCCGAGGCGCCCTCACACACCCCGCCCTGGCTGCTGGGCGTGTG 1075
QY 777 GGGCGGGGGGGGGCGCAGAGCGCGAAGCGCTGCCACCCAGCTCAACGGCGCCCTGGCGA 836
Db 1076 GCAGAGGGGGCGACGGGGAGCGCATGCCGCTGCACAGGTATGGGTGGGTGAGGGCGCGCT 1135
QY 837 GCGCGCGCGCGCGGG 852
Db 1136 AGCGCGCTGAGCGCGGG 1151

RESULT 10
US-09-166-334-1
; Sequence 1, Application US/09166334
; Patent No. US20020168708A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,334
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE:
; APPLICATION NUMBER: US 08/985,090
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-09-166-334-1

Query Match 12.3%; Score 166.4; DB 9; Length 2689;
Best Local Similarity 51.3%; Pred. No. 4.8e-24;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;
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Db 416 GCTGCTCATGTGGCCACGCGTGTGGGCAACGCGCTGTGTCATGCTCGCTTGTGGCGA 475
QY 183 CCGCGCGCTCAAGGCGCCCGCAAAACCTCTTCTGTGTGTCTGTGGCCCTGGCGACATCT 242
Db 476 CTCGAGCCTCCGACACCCAGAACAACTTCTTCTGCTCAACCTGCGCATCTCCGACTTCT 535
QY 243 GGTGGCCACGCTCGTCATCCCTTCTTCTGCTGGCCAAAGAGTCAATGGGCTACTGTACTT 302
Db 536 CGTCGGCGGCTTCTGATCCACATGATGTACCTACGTGCTGACAGGCGCGCTGACCTT 595
QY 303 CGCAAGGCTTGGTGGAGATCTACCTGGCGCTGCAGCTGCTTCTGACGTCGTCAT 362
Db 596 CGGCGGGGCGCTTGCAGAGCTGTGGCTGGTAGTGACTACTGCTGTGCACCTCTCTGC 655
QY 363 CGTGCACTGTGCGCCATCAGCCCTGGACCGCTACTGTGCTCATCACAGGCCATCGAGTA 422
Db 656 CTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGCTGCTGACCCGAGCGGTCTCATTA 715
QY 423 C---AACCAGAGCGCACGCGCGCGGCATCAAGGCCATCATCACCGGTGGTGCAT 479
Db 716 CCGGGCCAGCAGGGGTGACACGCGGCGGGCAGTGGCGGAAGATGCTGCTGTGTGGTCT 775
QY 480 CTGCGCGCTCATCTCTTCCCGCGCTCATCTCATCGAAGAAAGGCGGCGCGCGG 539
Db 776 GGCTTCTGCTGTACGAGCACCATCTGTAGCTGGAGTACCTGTCCGGGGCGAGCTC 835
QY 540 CCGCGAGCGCGCGAGCGCGCTGGAGATCAACGACAGAGAGTGTAGCTCATCTCTC 599
Db 836 CATCCCGAGGGGCGCACTGTATGCGGAGTCTTCTTACAACTGTACTTCTCATACAGGC 895
QY 600 GTGATCGGCTCTCTTCTGCTGCTGCTCATCATGATGCTGTAGCTGCGCATTA 659
Db 896 TTCACCTTGAGATTCTTTACGCGCTTCTTCTTACAGCTTCTTTAACCTCAGCATCTA 955
QY 660 CCAGATCGCAAGCGTGCACACCGCGGTGCCACCCAGCGCGCGGGGTCCGAGCGCCGTCG 719
Db 956 CCGTACATCCAGAGGCGCACCGCGCTCCGGCTGGATGGGGCTCGAAGGACGCGCGCC 1015
QY 720 CGCGCGCGCGGGGGCGACCGAGCGC---AGGCCAAGGCTGTGGCCCCGAGCGCAAGCG 776
Db 1016 CGAGCCCCCTCCCGAGGCGCCAGCCCTCACACCCCGCCCTGTGGGTGGGTGCTG 1075
QY 777 GGGCGGGGGGGCGCAGAGGCGCGAACCCTGCCCCACCCAGCTCAACGGCGCCCTGGCGA 836
Db 1076 GCAGAGGGGGCAGCGGGAGCGCATGCGCTGCACAGGTATGGGTGGGTGAGGCGCGCT 1135
QY 837 GCGCGCGCGCGCGGG 852
Db 1136 AGCGCTGAGGCGCGG 1151

RESULT 11
US-09-350-206-1
; Sequence 1, Application US/09350206
; Patent No. US20020099199A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/350,206
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-09-350-206-1

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Query Match 12.3%; Score 166.4; DB 10; Length 2689;
Best Local Similarity 51.3%; Pred. No. 4.8e-24;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;

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QY 3 GGGCTCCCTGAGCGCGGAGCGGGAACGCGAGCTGGAACGCGGAGCGCGCGGGGG 62
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 296 GCGCGCGCGCGCGCGAGCGGCGCGTGAACGCTTCGGGGCGCGTGGCGGCGGCGG 355

QY 63 GCGCGCGCGCGCGCGCGCGCTTACTTCCCTGAGGTGACGCTGACGCTGCTGCTGCGCGG 122
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 356 GCGCGCGCGCGCGCGCGCGCTTCTCGGAGCGCTGACCGCGGCTGCGCGCGCTCATGGC 415

QY 123 CCTGCTCATGCTGCTTACACCGTGTTCGGCAACGTGCTCATCATCGCCGTTTCAGAG 182
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 416 GCTGCTCATGCTGCGCACGCGTGTGGCAACGCGCTGCTCATGCTCGCCTTCGTGCGCGA 475

QY 183 CCGCGCGCTCAAGCGCGCGCGCAAAACCTTCTGCTGTGTCTGTGCGCGCTCGCGCACATCT 242
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 476 CTCGAGCCTCCGACCGACAGAACACTTCTTCTGCTCAACCTCGCCATCTCCGACTTCCT 535

QY 243 GGTGGCCACGCTCGTCATCCCTTTCGCGTGGCCACGAGGTCATGGGCTACTGTACTT 302
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 536 CGTCGGCGCGCTTGCATCCCACTGTATGTACCTACGTGCTGACAGGCGCGCTGACCTT 595

QY 303 CGGCAAGGCTTGGTCGAGATCTACCTGGCGCTCGACGTGCTTCTTCACGTCGTCAT 362
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 596 CGGCGGGGCGCTTGCAGAGCTGTGGCTGTAGTGAGTACCTGCTGTGCACCTCCTCTGC 655

QY 363 CGTGACCTGTGGCGCATCAGCCTGAGCGGCTACTGTCATCATCACAGGCCATCGAGTA 422
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 656 CTTCAACATCTGTCTCATCAGCTACGACCGGCTTCTGTGCGGTACCGGAGGCTCTCATTA 715

QY 423 C--AACCTGAAGCGCACGCGCGCGCGCATCAAGGCCATCATCACCGTGTGGGTCT 479
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 716 CCGGCGCCAGAGGGGTGACACGCGCGGCGAGTGCGGAAGATGCTGTGTGGGTGCT 775

QY 480 CTCGGCGCTCATCTCTTCCCGCGCTCATCTTCATCGAGAAAGAGGGCGGCGGCGG 539
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 776 GGCTTCTCTGTCTACGAGCAGCCATCTGAGCTGGAGTACCTGTCCGGGCGAGCTC 835

QY 540 CCGCGAGCGCGCGAGCGCGCGCTGCGAGATCAACGACGAGAGTGTACGTCATCTGTC 599
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 836 CATCCCGAGGGCGCACTGCTATGCGGAGTTCTTCTACAACTGTGTACTTCTCATCACGGC 895

QY 600 GTGCATGGGCTCTTCTTCCCTGCTCCCTCATCATGATCCTGTGTTACGTCGCGCATCTA 659
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 896 TTCACCCCTGAGTTCTTTACGCGCCTTCTCTACGCGTACACCTTCTTTAACCTCAGCATCTA 955

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QY 660 CCAGATCGCCAGCGCTCGCACCCGCGGTGCCACCCAGCCGCGGGGTCCGAGCGCGTCCG 719
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 956 CCGAATCCAGAGGCGCGACCGCGCTCCGGCTGATGGGGCTCGAGAGGACCGCGGCC 1015

QY 720 CGCGCGCGCGCGCGCACCGAGCGC--AGGCCCAAGGCTCTGGGCGCGCGAGCGCAGCGC 776
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1016 CGAGCCCCCTCCCGAGGCGCCAGCCCTCACACACCCCGCGCTGCTGGGGCTGCTG 1075

QY 777 GGGCGCGGGGGCGAGAGCGCGAACCCTGCCCCACCCAGCTCAACGCGCGCGCTGGCGGA 836
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1076 GCAGAGGGGCGACGGGAGGCGCATGCGCTGCACAGGATGGGGTGTGAGGCGGCCGT 1135

QY 837 GCCCGCGCGCGCGG 852
   | | | | | | | | | |
Db 1136 AGCGCTGAGCGCGG 1151

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RESULT 12
US-10-185-991-1

; Sequence 1, Application US/10185991
; Publication No. US20030022900A1

; GENERAL INFORMATION:

; APPLICANT: Charles Gluchowski, et al.
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN PROSTATIC HYPERPLASIA

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/185,991
; FILING DATE: 28-Jun-2002

; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/444,783
; FILING DATE: <unknown>

; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 2140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N

; FEATURE:
; NAME/KEY: CDS
; LOCATION: 178..1893
; OTHER INFORMATION:

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-10-185-991-1

Query Match 11.4%; Score 153.4; DB 9; Length 2140;
Best Local Similarity 52.0%; Pred. No. 1.5e-21;
Matches 433; Conservative 0; Mismatches 376; Indels 24; Gaps 3;

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QY 18 GGACCGGGCAACGGAGCTGGAAACGGAGCGCGCGGGGGCGCGCGCGCGCCAC 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 387 GGAGCGGGGAGCGCGCGCGCGCGCGCGAGCTGAATGGACAGCGCGCGCGGGGACT 446
QY 78 CCTTACTCCCTGCAGGTGACGCTGACGCTGGTGGCCCTGGCCGCTGCATGCTGCT 137
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 447 GGTGGTAGCGCGCAGGGCGGTGGCGCTGGCGCTCTCCCTGGCAGCC--TTATCCTTAT 503
QY 138 CACCGTGTTCGCAACGTGCTCGTCATCATCGCCCTGTTCACGAGCGCGCGCTCAAGGC 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 504 GGGCGTGGCAGGTAACTGCTGTGTCATCCTCTCAAGTGGCCCTGCACACCGCCACTGCAGAC 563
QY 198 GCGCCAAACCTCTTCTGCTGCTCTGCGCTCGCCCGACATCCTGCTGGCCACGCTCGT 257
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 564 CGTCACCAACTATTTCATGTAACCTGGCGCGGTGGCCGACCTGCTGCTGAGCGCCACCGT 623
QY 258 CATCCCTTCTCGCTGGCCAAACGAGTATGGGCTACTGCTACTTCGGCAAGGCTTGTG 317
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 624 ACTGCGCTTCTCGCGCCACCATGGAAGTTCTGGGCTTCTGGGCTTGGCGCGCTTCTG 683
QY 318 CGAGATCTACCTGGCGCTGACGCTGCTCTTCTGACGCTGTCATGTCGACCTGTGCGC 377
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 684 CGACGTATGGCGCGCGCGCTGACGCTGCTGCTGACGCGCTCCATCCTCAAGCTTGTGAC 743
QY 378 CATCAGCCTGGACCGCTACTGCTCATCACAGGCCATCGATACCAACTGAAGCGCAC 437
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 744 CATCTCGTGGACCGGTACGTGGCGCTGCGCCACTCACTCAAGTACCCAGCCATCATGAC 803
QY 438 GCGCGCGCATCAAGCCATCATCATCACGCTGTGGTCACTCGCGCTCATCTCCTT 497
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 804 CGAGCGCAAGCGCGCGCATCTGCGCTGTCTGGTCTGAGCCCTGGTGGTCCGT 863
QY 498 CCGCGCGCTCATCTCATTCAGAGAAGAGGGCGCGCGCGCGCGCGCGCGCGAGCC 557
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 864 AGGGCCCT-----GCTGGGCTGGAAGAGGCCGCTGCCCTGACGAGCG 908
QY 558 GCGCTGCGAGATCAACGACAGAGTGTAGTCACTCTGCTGCTGCTGCTGCTCTT 617
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 909 CTCTGCGTATACCGAGAGAGGGCGGCTACGCTGCTCTCTCTCTCTCTCTCTCTA 968
QY 618 CGCTCCCTGCTCATCATGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 969 CCTGCGCATGGCGGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1028
QY 672 GCGTCGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1029 CACGCGCAGCTGAGGAGCGGCTCAAGCGCGAGCGAGGCAAGGCTTCGAGGTGCT 1088
QY 732 GGGCACCAGAGCGAGGCCCAAGGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 791
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1089 GCGCATCTACTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1148
QY 792 AGAGCGCAACCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 844
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1149 CAAGGCGCACACTTCCGCAAGCTCGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCT 1201
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RESULT 13
US-10-005-010-1

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; Sequence 1, Application US/10005010
; Patent No. US2002015149A1
; GENERAL INFORMATION:
; APPLICANT: Weinsbank et al, Richard L.
; TITLE OF INVENTION: Method of obtaining A Composition Comprising A 5-HT1D
; FILE REFERENCE: 36536-BA
; CURRENT APPLICATION NUMBER: US/10/005,010
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/371,705
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
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; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (284)..(1414)
US-10-005-010-1
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Query Match 10.9%; Score 147.2; DB 12; length 1645;
Best Local Similarity 52.9%; Pred. No. 2.4e-20;
Matches 348; Conservative 0; Mismatches 298; Indels 12; Gaps 1;

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QY 67 GCGCGCGCACCCCTTACTCCCTGACGTGACGCTGACGCTGCTGCTGCTGCTGCTGCTG 126
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Db 365 GCTTGGATCCCAAGAGACCCCTCAGCGCGCTCAAGATCTCCCTGGCGTGTCTTCCGTG 424
QY 127 CTCATGCTGCTCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 186
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 425 ATCACACTGGCCACAGTCTCTCCAAATGCCCTTGTACTCAACCATCTTACTACACAGG 484
QY 187 GCGCTCAAGCGCGCGCCCAAAACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 485 AAGCTCCACACCCCTGCAACTACCTGATTGGCTCCCTGGCCACACCGACCTTGTGTT 544
QY 247 GCCACGCTCGTCACTCCCTTCTGCTGCGCAACGAGTATGGGCTACTGCTGCTGCTGCTG 306
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 545 TCCATCTTGTGTAATGCCCATCAGCATCGCCCTATACCATCACCCACACCTGGAATTTGGC 604
QY 307 AAGGCTGTGCGAGATCTACTGCGCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 366
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 605 CAATCTTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 664
QY 367 CACCTGTGCGCATCAGCCTGAGCGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 665 CATCTGTGTCTATGCTGCTGAGAGTACTGGGCAATCAAGATGCCCTGGAATACAGT 724
QY 427 CTGAAGCGACCGCGCGCGCGCATCAAGCCATCATCATCAACCGTGTGCTGCTGCTGCTG 486
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 725 AAACGAGAGCGGCTGCGCACGCGCGCACCATGATGCGCATGTCTGGGCACTCCATC 784
QY 487 GTCATCTCTTCCCGCGCTCATCTCCATCGAAGAAGGGCGCGCGCGCGCGCGCGCGAG 546
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 785 TGCACTCTCATCCCGCGCTCTCTGCGCGGAGCGCAAGCC-----CCAGGAG 832
QY 547 CCGCGCGAGCGCGCTGCGAGATCAACGACAGAGAGTACGTATCTGCTGCTGCTGCTG 606
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 833 GAGATGTGGAATGTCTGTGTAACACCTCTCAGATCTCTACACCATCTTACTCACTGT 892
QY 607 GGTCTCTTCTGCTCCCTGCTCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 893 GGGGCTTCTACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 952
QY 667 GCCAAGCTGCGACCGCGCTGCGACCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 724
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 953 GCGCGGAACCGCATCTGAAATCCACCCTCACTCTTAATGGGAAGCGCTTACACGAGGCC 1010
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RESULT 14

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US-09-864-761-3769/c
; Sequence 3769, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
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; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3769
; LENGTH: 1973
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL049576.15
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
; US-09-864-761-3769
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Query Match 10.9%; Score 147.2; DB 10; Length 1973;
Best Local Similarity 52.9%; Pred. No. 2.5e-20;
Matches 348; Conservative 0; Mismatches 298; Indels 12; Gaps 1;
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QY 67 GCCCGGCCACCCCTTACTCCCTGAGGTGACGCTGACGCTGCTGCTGCGCGCGCTG 126
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Db 1234 GCTTGGATGCCAGACCTCCAGCGGCTCAAGATCTCCCTTGCGGTGCTTTCGTC 1175

QY 127 CTCATGCTGCTCACCGTGTTCGCAACGTGCTGTCATCATGCGCGCTTTCACGAGCGC 186
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1174 ATCACACTGGCCACAGTCTCTCAATGCCCTTTGACTCACCAACCATCTTACTCACCAGG 1115

QY 187 GCGCTCAAGGGCCCCAAACCTCTTCTGCTGTCTCTGCGCTCGGCCGACATCCTGGTG 246
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY 247 GCCACGCTGCTCATCCCTTCTCGCTGGCCCAACGAGTGCATGGGCTACTGTACTTCGGC 306
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   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY 367 CACCTGTGCGGCATCAGCCTGACCGCTACTGTTCATCACAGGCGCATCGAGTACAAC 426
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Db 934 CATCTCTGTGTCATTTGCTCTGACAGGTACTGGCAATCAGATGCCCTGAATACAGT 875
QY 427 CTGAGCGCAGCGCGCGCGCATCAAGCCATCATCATCACCGTGTGGTCACTCGGCC 486
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Db 874 AAACGACGACGGCTGGCCACGGCCACCATGATCGCATTTGCTGGCCATCTCCATC 815
QY 487 GTCATCTCTTCCCGCGCTCATCTCCATCGAGAAGAGGGCGCGCGCGCCGACAG 546
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QY 547 CCGGCGGAGCGCGCTGCGAGATCAACGACCAAGAGTGTACGTATCTCGTGTGATC 606
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QY 607 GGTCTCTTCTTCCCTCCCTGCTCATCATGATCTCTGTCTACGTTGCGCATCTACCAATC 666
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QY 667 GCCAAGCTGCGCACCCGCGTGCACACCAACCGCGCGGTCCGAGCCGTCGCGCGC 724
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RESULT 15
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; Sequence 13, Application US/09993844
; Patent No. US20020106739A1
; GENERAL INFORMATION:
; APPLICANT: Oakley, Robert H.
; APPLICANT: Barak, Lawrence S.
; APPLICANT: Laporte, Stephane A.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Modified G-Protein Coupled Receptors
; FILE REFERENCE: 033072-026
; CURRENT APPLICATION NUMBER: US/09/993,844
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,772
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/260,363
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1185
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence of beta3-AR-V2R chimera
; US-09-993-844-13
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Best Local Similarity 52.6%; Pred. No. 2.4e-19;
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Db 121 GGGGCCCTGCTGGCGCTGGCGTGTGCTGGCCACCGTGGAGGCAACCTGTGTCATCGTG 180

QY 169 GCGGTGTACAGAGCGCGCGCTCAAGGCGGCCCAAAACCTCTTCTGCTGTCTGTGCC 228
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Db 181 GCCATGCGCTGACTCCGAGACTCCAGACCAATGACCAACAGTGTTCGTGACTTCGCTGCC 240

QY 229 TCGGCGGACATCTGTGTGGCCACGCTGTCATCCCTTCTCGCTGGCCAAAGAGTCAAG 288
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 GCAAGCCGACCTGTGTATGGGACTCTCTGTGTGCGCGCGGCCACCTTGGCGTGAAT 300

QY 289 GGCTACTGTGACTTCGGCAAGGCTTGTGCGAGATCTACCTGGCGCTGCACGTGCTCTTC 348
   ||| ||||| | | | | | | | | | | | | | | | | | | | | | |
Db 301 GGCCACTGGCGGTGGCGCCACTGCGTGGAGCTGTGACCTCGGTGGAACGTGCTGTGT 360

QY 349 TGCACGTGCTCATGCTGACCTGTGCGGCATCAGCCTGACCGCTACTGTGCATCACA 408
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Db 361 GTGACCGCGCAGCATGCAAAACCTGTGCGCCCTGGCCGTGACCGCTACTGTGTGACC 420
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 11:01:28 ; Search time 11.7706 Seconds
(Without alignments)
7844.310 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	41	100.0	1350	23	AAI99918	Human alpha-2AAR v
2	39.4	96.1	1350	23	AAI99917	Human alpha-2AAR e
3	25	61.0	14855	22	ABA15164	Human nervous syst
4	25	61.0	22028	24	ABA93286	Human acetyl-Coenz
5	25	61.0	22028	24	ABA93288	Human acetyl-Coenz
6	24.2	59.0	978	23	ABLI0491	Drosophila melanog
7	23.6	57.6	3036	22	AAF44733	Novel protein kina
8	23.4	57.1	1733	24	ABQ47498	Oligonucleotide fo
9	23.4	57.1	1733	24	ABQ47499	Oligonucleotide fo

10	23.4	57.1	7353	24	ABL32072	Human immune syste
11	23.4	57.1	7353	24	AAD28362	Human chemically t
12	22.4	54.6	36	21	AAZ94312	Rat cholecystokint
13	22.4	54.6	37	21	AAZ94369	Human alpha 2A adr
14	22.4	54.6	2286	23	AAZ94369	DNA encoding novel
15	22.4	54.6	2286	23	AAZ94369	DNA encoding novel
16	22.4	54.6	2286	23	AAZ94369	DNA encoding novel
17	22.4	54.6	2286	23	AAZ94369	DNA encoding novel
18	22.4	54.6	2286	23	AAZ94369	DNA encoding novel
19	22.4	54.6	2286	23	AAZ94369	DNA encoding novel
20	22.4	54.6	2286	23	AAZ94369	DNA encoding novel
21	22.2	54.1	1396	22	AAK65897	Human LKBI gene fr
22	22.2	54.1	1396	22	AAK65897	Human LKBI gene fr
23	22.2	54.1	1396	22	AAK65897	Human LKBI gene fr
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25	22.2	54.1	1396	22	AAK65897	Human LKBI gene fr
26	22.2	54.1	1396	22	AAK65897	Human LKBI gene fr
27	22.2	54.1	1396	22	AAK65897	Human LKBI gene fr
28	21.8	53.2	967	22	AAI35843	Human immune/haema
29	21.8	53.2	967	22	AAI35843	Human immune/haema
30	21.8	53.2	967	22	AAI35843	Human immune/haema
31	21.6	52.7	1733	24	ABQ47500	Human genomic regl
32	21.6	52.7	1733	24	ABQ47501	Pseudomonas aerugi
33	21.6	52.7	1733	24	ABQ47501	Porcine BAC-PIGF2-
34	21.6	52.7	1733	24	ABQ47501	Human musculoskele
35	21.6	52.7	1733	24	ABQ47501	Human CDNA sequenc
36	21.6	52.7	1733	24	ABQ47501	Human CDNA clone (
37	21.4	52.2	10672	23	AAZ94369	Oligonucleotide fo
38	21.2	51.7	1008	18	AAT85901	Human immune syste
39	21.2	51.7	1008	18	AAT85901	Human immune syste
40	21.2	51.7	1008	18	AAT85901	Human immune syste
41	21.2	51.7	1008	18	AAT85901	Human immune syste
42	21.2	51.7	1008	18	AAT85901	Human immune syste
43	21.2	51.7	1008	18	AAT85901	Human immune syste
44	21.2	51.7	1008	18	AAT85901	Human immune syste
45	21.2	51.7	1008	18	AAT85901	Human immune syste

ALIGNMENTS

RESULT 1	
AAI99918	
ID	AAI99918 standard; DNA; 1350 BP.
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AC	AAI99918;
XX	
DT	18-FEB-2002 (first entry)
XX	
DE	Human alpha-2AAR variant encoding DNA.
XX	
KW	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW	polymorphic site; allelic variant; cardiovascular disease;
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW	phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..1353
FT	/*tag= a
FT	/product= "alpha-2AAR"
FT	replace(753,C)
FT	/*tag= b
FT	
XX	
PN	WO200179561-A2.
XX	
PD	25-OCT-2001.
XX	
PF	17-APR-2001; 2001WO-US12575.
XX	
PR	17-APR-2000; 2000US-0551744.
PR	10-AUG-2000; 2000US-0636259.

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PR 19-OCT-2000; 2000US-0692077.
XX
XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;
PI
XX
DR WPI: 2001-611728/70.
DR P-PSDB; AAM52123.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
PS Disclosure; Page 152; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (ggggcgggcgcg) or (B) (ggggcggtcgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR variant
CC gene.
XX
SQ Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;

Query Match 100.0%; Score 41; DB 23; Length 1350;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGCACCGAGCGCGAGGCCCAAGGGTCTGGGCCCCGAGCG 41
Db 730 GGGGGCACCGAGCGCGAGGCCCAAGGGTCTGGGCCCCGAGCG 770

RESULT 2
AAI99917
ID AAI99917 standard; DNA; 1350 BP.
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XX AAI99917;
AC
XX 18-FEB-2002 (first entry)
DT
XX Human alpha-2AAR encoding DNA.
DE
XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2AAR;
KW GenBank Accession AF281308; chromosome 10; ds.
XX
OS Homo sapiens.
XX
XX
FH Key 1.1353
FT CDS Location/Qualifiers
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FT /product= "alpha-2AAR"
XX
XX PN WO200179561-A2.
XX
XX PD 25-OCT-2001.
XX
XX PF 17-APR-2001; 2001WO-US12575.
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XX PR 17-APR-2000; 2000US-0551744.
XX PR 10-AUG-2000; 2000US-0636259.
XX PR 19-OCT-2000; 2000US-0692077.
XX
XX PA (LIGG/) LIGGETT S B.
XX PA (SMAL/) SMALL K M.
XX
XX PI Liggett SB, Small KM;
XX
XX DR WPI: 2001-611728/70.
XX DR P-PSDB; AAM52122.
XX
XX PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX PT determining whether an individual is at increased risk of developing a
XX PT disease associated with the corresponding receptor comprises detecting
XX PT a polymorphic site -
XX
XX PS Example 7; Page 151; 163pp; English.
XX
XX CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
XX CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
XX CC alpha2A or alpha2C or fragment or complement of; and
XX CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
XX CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
XX CC or a site comprising (A) (ggggcgggcgcg) or (B) (ggggcggtcgag) at
XX CC positions 961-972 of (III). The method may be used for genotyping an
XX CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
XX CC whether an individual is at increased risk of developing a disease
XX CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
XX CC polymorphic site which correlate to disease selected from cardiovascular
XX CC disease, central nervous system disease and combinations of these. In
XX CC addition, the technique may be used to predict an individual's response
XX CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
XX CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
XX CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
XX CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
XX CC these) by detecting the polymorphic site and correlating the site to a
XX CC predetermined response (where the response is correlated to adenylyl
XX CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
XX CC levels). The present sequence is that of the human alpha-2AAR gene
XX CC (GenBank Accession AF281308).
XX
SQ Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;

Query Match 96.1%; Score 39.4; DB 23; Length 1350;
Best Local Similarity 97.6%; Pred. No. 0.00026;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGGCACCGAGCGCGAGGCCCAAGGGTCTGGGCCCCGAGCG 41
Db 730 GGGGGCACCGAGCGCGAGGCCCAACGCTCTGGGCCCCGAGCG 770

RESULT 3
ABA15164
ID ABA15164 standard; DNA; 14855 BP.
XX
XX ABA15164;
AC
XX 23-JAN-2002 (first entry)
DT
XX Human nervous system related polynucleotide SEQ ID NO 7495.
DE Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
XX
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KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antislaking; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX Homo sapiens.
XX WO200159063-A2.
XX PD 16-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01334.
XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 11-JUL-2000; 2000US-0217487.
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PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.

PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	08-DEC-2000;	2000US-0251989.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
XX	(HUMA-)	HUMAN GENOME SCI INC.
PA	Rosen CA,	Barash SC, Ruben SM;
XX	WPI;	2001-541565/60.
DR	Nucleic acids encoding	3224 human nervous system antigen polypeptides,
PT	useful for preventing,	diagnosing and/or treating nervous system
PT	cancers and metastases -	
XX	Disclosure;	SEQ ID NO 7495; 1701pp + Sequence Listing; English.
PS	The invention relates to novel genes	(ABA11004-ABA21534) and proteins
CC	(ABBI4678-ABBI8001) useful for preventing,	treating or ameliorating
CC	medical conditions e.g. by protein or gene therapy.	The genes are
CC	isolated from a range of human tissues disclosed	in the specification.
CC	The nucleic acids, proteins, antibodies and	(ant)agonists are useful
CC	in the diagnosis, treatment and prevention of:	(a) cancer, e.g. breast
CC	and ovarian cancer and other cancers of the	adrenal gland, bone, bone
CC	marrow, breast, gastrointestinal tract,	liver, lung, or urogenital;
CC	(b) immune disorders e.g. Addison's disease,	allergies, autoimmune
CC	haemolytic anaemia, autoimmune thyroiditis,	diabetes mellitus, Crohn's
CC	disease, multiple sclerosis, rheumatoid	arthritis and ulcerative
CC	colitis; (c) cardiovascular disorders such	as myocardial ischaemias;
CC	(d) wound healing; (e) neurological diseases	e.g. cerebral anoxia and
CC	epilepsy; and (f) infectious diseases such	as viral, bacterial, fungal
CC	and parasitic infections.	
CC	Note: The sequence data for this patent did	not form part of the
CC	printed specification, but was obtained	in electronic format directly
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences.	
XX	Sequence	14855 BP; 3335 A; 3554 C; 4013 G; 3953 T; 0 other;
SQ	Query Match	61.0%; Score 25; DB 22; Length 14855;
	Best Local Similarity	75.6%; Pred. No. 16;
	Matches	31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY	1	GGGGGCACCGAGCGGCCCCAAGGTCTGGGCCCGAGCG 41
Db	265	GCGCGCTTCAAGGTGAGGCCCGAGGCTCTGGCGCGAGTG 305
RESULT 4		
ABA93286		
ID	ABA93286 standard; DNA; 22028 BP.	
XX	ABA93286;	
AC	22-APR-2002 (first entry)	
DT		
XX	Human acetyl-Coenzyme A acyltransferase 1	gene SEQ ID NO:1.
DE		
KX	Human; acetyl-Coenzyme A acyltransferase;	ACAAL; chromosome 3p23-p22;
KW	peroxisomal 3-oxoacyl-Coenzyme A thiolase;	SNP; genotype; haplotype;
KW	single nucleotide polymorphism; polymorphic	variant; enzyme; gene; ds.
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	variation	replace(3546,A)
FT		/tag= a
FT	variation	/standard_name= "single nucleotide polymorphism (SNP)"
FT		replace(3637,A)
FT		/tag= b
FT	variation	/standard_name= "single nucleotide polymorphism (SNP)"
FT		replace(4033,T)
FT		/tag= c

FT	variation	/standard_name= "single nucleotide polymorphism (SNP)" replace(4157,T) /tag= d /standard_name= "single nucleotide polymorphism (SNP)" replace(4176,A) /tag= e /standard_name= "single nucleotide polymorphism (SNP)" replace(4276,C) /tag= f /standard_name= "single nucleotide polymorphism (SNP)" replace(9110,G) /tag= g /standard_name= "single nucleotide polymorphism (SNP)" replace(9182,A) /tag= h /standard_name= "single nucleotide polymorphism (SNP)" replace(9600,G) /tag= i /standard_name= "single nucleotide polymorphism (SNP)" replace(11702,T) /tag= j /standard_name= "single nucleotide polymorphism (SNP)" replace(11756,C) /tag= k /standard_name= "single nucleotide polymorphism (SNP)" replace(13390,T) /tag= l /standard_name= "single nucleotide polymorphism (SNP)" replace(14441,G) /tag= m /standard_name= "single nucleotide polymorphism (SNP)" replace(14872,C) /tag= n /standard_name= "single nucleotide polymorphism (SNP)" replace(14931,C) /tag= o /standard_name= "single nucleotide polymorphism (SNP)" replace(15471,C) /tag= p /standard_name= "single nucleotide polymorphism (SNP)" replace(15486,G) /tag= q /standard_name= "single nucleotide polymorphism (SNP)" replace(18004,T) /tag= r /standard_name= "single nucleotide polymorphism (SNP)" replace(18192,T) /tag= s /standard_name= "single nucleotide polymorphism (SNP)"
XX		WO200187903-A2.
XX		22-NOV-2001.
XX		03-MAY-2001; 2001WO-US14330.
XX		18-MAY-2000; 2000US-205022P.
PA		(GENA-) GENAISSANCE PHARM INC.
PA		(DUDA/) DUDA A E.
XX		
PI		Chew A, Koshy B;
XX		
DR		WPI; 2002-164134/21.
XX		
PT		Isolated polynucleotide, comprising a polymorphic variant of the
PT		acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A
PT		thiolase) gene useful for providing haplotype information and in
PT		therapy for treating related disorders -
XX		
PS		Claim 19; Fig 1A-I; 93pp; English.
XX		
CC		The present invention describes a polypeptide (I) which is a polymorphic

CC variant (PV) of the acetyl-Coenzyme A acyltransferase (peroxisomal
CC 3-oxoacyl-Coenzyme A thiolase) ACAAI protein (AB05516). ACAAI is located
CC on chromosome 3p23-p22. (I) can be encoded by ABA93286 (or ABA93288)
CC where the sequence comprises one of the haplotypes shown in Table 4 or
CC one of the haplotype pairs shown in Table 3, where Tables 3 and 4 are
CC given in the specification. The polynucleotide encoding ACAAI can be used
CC for providing haplotype and genotype information of an individual.
CC Furthermore, the polynucleotide is useful for the treatment of disorders
CC related to its abnormal expression or function. The present sequence
CC represents the human ACAAI gene, featuring all the single nucleotide
CC polymorphisms (SNP) possible, from the present invention.
XX

5Q Sequence 22028 BP; 4811 A; 5599 C; 6137 G; 5481 T; 0 other;

Query Match 61.0%; Score 25; DB 24; Length 22028;
Best Local Similarity 75.6%; Pred. NO. 16;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGGGGCACCGACGCGCCCAAGGCTGTGGCCCCGAGCG 41
|| ||| | || ||||| ||||| ||||| ||||| |
Db 4199 GCGGCTTCAAGTGAGGCCCGAGGCTGTGGCGCCGAGTG 4239

RESULT 5
ABA93288
ID ABA93288 standard; DNA; 22028 BP.
XX
AC ABA93288;
XX
DT 22-APR-2002 (first entry)
XX
DE Human acetyl-Coenzyme A acyltransferase 1 gene SEQ ID NO:99.
XX
KW Human; acetyl-Coenzyme A acyltransferase; ACAAI; chromosome 3p23-p22;
KW peroxisomal 3-oxoacyl-Coenzyme A thiolase; SNP; genotype; haplotype;
KW single nucleotide polymorphism; polymorphic variant; enzyme; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200187903-A2.
XX
PD 22-NOV-2001.
XX
PF 03-MAY-2001; 2001WO-US14330.
XX
PR 18-MAY-2000; 2000US-205022P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
PA (DUDA/) DUDA A E.
XX
PI Chew A, Koshiy B;
XX
DR WPI; 2002-164134/21.
XX
PT Isolated polynucleotide, comprising a polymorphic variant of the
PT acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A
PT thiolase) gene useful for providing haplotype information and in
PT therapy for treating related disorders -
XX
PS Disclosure; Page 85-93; 93pp; English.
XX
CC The present invention describes a polypeptide (I) which is a polymorphic
CC variant (PV) of the acetyl-Coenzyme A acyltransferase (peroxisomal
CC 3-oxoacyl-Coenzyme A thiolase) ACAAI protein (AB05516). ACAAI is located
CC on chromosome 3p23-p22. (I) can be encoded by ABA93286 (or ABA93288)
CC where the sequence comprises one of the haplotypes shown in Table 4 or
CC one of the haplotype pairs shown in Table 3, where Tables 3 and 4 are
CC given in the specification. The polynucleotide encoding ACAAI can be used
CC for providing haplotype and genotype information of an individual.
CC Furthermore, the polynucleotide is useful for the treatment of disorders
CC related to its abnormal expression or function. The present sequence
CC represents the human ACAAI gene, where all the single nucleotide
CC polymorphisms (SNP) possible have been given in the sequence using the

CC standard ambiguity codes.
XX
SQ Sequence 22028 BP; 4808 A; 5592 C; 6133 G; 5476 T; 19 other;

Query Match 61.0%; Score 25; DB 24; Length 22028;
Best Local Similarity 75.6%; Pred. NO. 16;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGGGGCACCGACGCGCCCAAGGCTGTGGCCCCGAGCG 41
|| ||| | || ||||| ||||| ||||| ||||| |
Db 4199 GCGGCTTCAAGTGAGGCCCGAGGCTGTGGCGCCGAGTG 4239

RESULT 6
ABL10491
ID ABL10491 standard; cDNA; 978 BP.
XX
AC ABL10491;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25955.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB66388.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 25955; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 978 BP; 277 A; 241 C; 242 G; 218 T; 0 other;

Query Match 59.0%; Score 24.2; DB 23; Length 978;
Best Local Similarity 78.4%; Pred. NO. 29;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGCACCGACGCGCCCAAGGCTGTGGCCCCGAG 39
|| ||| | ||||| ||||| ||||| ||||| |
Db 126 GGAACCTGGGGCAGCCCAAGGCTCAGGTACCCGAG 162

```
RESULT 7
AAF44733/c
ID AAF44733 standard; cDNA; 3036 BP.
XX
XX AAF44733;
AC
XX 27-MAR-2001 (first entry)
DT
XX Novel protein kinase cDNA, SEQ ID NO: 114.
DE
XX
XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
XX
XX Homo sapiens.
OS
XX WO200073469-A2.
PN
XX 07-DEC-2000.
PD
XX 26-MAY-2000; 2000WO-US14842.
PF
XX 28-MAY-1999; 99US-0136503.
PR
XX (SUGEN-) SUGEN INC.
PA
XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
PI
XX WPI; 2001-032161/04.
DR P-PSDB; AAB65704.
DR
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers .
PT
XX Example 4; Fig 2; 310pp; English.
PS
XX The present sequence encodes a novel protein kinase. The nucleic acids
CC and the protein kinases they encode may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure,
CC oxidative-stress related disorders, chronic inflammatory bowel disease,
CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
CC reproductive disorders.
CC
SQ Sequence 3036 BP; 595 A; 964 C; 918 G; 559 T; 0 other;
Query Match 57.6%; Score 23.6; DB 22; Length 3036;
Best Local Similarity 86.7%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 11 AGCGCAGGCCCAAGGCTCTGGCCCCGAGC 40
      |||||
DB 2393 AGCGCAGGCCCAAGGCTCTGGCCCCCTCAGC 2364
```

```
RESULT 8
ABQ47498
ID ABQ47498 standard; DNA; 1733 BP.
XX
```

```
AC ABQ47498;
XX
XX 12-JUL-2002 (first entry)
DT
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 34089.
DE
XX Human; cytosine methylation; 5'-Cpg-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
XX Homo sapiens.
OS
XX WO200218632-A2.
PN
XX 07-MAR-2002.
PD
XX 01-SEP-2001; 2001WO-EP10074.
PF
XX 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
PR
XX (EPIC-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI
XX WPI; 2002-371829/40.
DR
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA .
PT
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
PS
XX
```

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-Cpg-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (11) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.

```
SQ Sequence 1733 BP; 252 A; 211 C; 585 G; 685 T; 0 other;
Query Match 57.1%; Score 23.4; DB 24; Length 1733;
Best Local Similarity 73.2%; Pred. No. 54;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 1 GGGGCCACCGAGCGCCCAAGGCTCTGGCCCCGAGCG 41
      |||||
DB 990 GGGGGTATCGAGCGTAGGTTTAACGGTTTGGGTTTCGAGCG 1030
```

```
RESULT 9
ABQ47499/c
ID ABQ47499 standard; DNA; 1733 BP.
XX
AC ABQ47499;
XX 12-JUL-2002 (first entry)
DT
```


XX 02-JUL-2001; 2001WO-EP07540.
PF
XX 30-JUN-2000; 2000DE-1032529.
PR
PR 01-SEP-2000; 2000DE-1043826.
XX
XX (EPIC-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2002-154759/20.
DR
XX
PT Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT gene -
PS
XX Claim 1; Page 32-36; 190pp; English.
XX
CC The invention relates to nucleic acids comprising a segment of chemically
CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC useful for detecting cytosine methylations. The pretreated DNA is useful
CC for the diagnosis or therapy of behavioural disorders, neurological
CC disorders and cancer, in particular major depressive disorder, Tourette's
CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC drug abuse, alcoholism, personality traits, compulsive gambling, human
CC immunodeficiency virus dementia, migraine, behaviours in schizophrenic
CC and schizoaffective patients, and suicidal behaviour in patients with
CC schizophrenia. The nucleic acid is useful for detecting the methylation
CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC (SNPs). The present sequence is human chemically treated genomic DNA.
XX
SQ Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;
QY
Query Match 57.1%; Score 23.4; DB 24; Length 7353;
Best Local Similarity 73.2%; Pred. No. 54;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Db 5730 GGGGGTATCGAGCGTAGGTTTAACGGTTTGGGTTTCGACG 5770
RESULT 12
AAZ94312/C
ID AAZ94312 standard; DNA; 36 BP.
XX
AC AAZ94312;
XX
DT 03-JUL-2000 (first entry)
XX
DE Rat cholecystokinin CCKB receptor PCR primer.
XX
KW G protein coupled receptor; cholecystokinin CCKB receptor;
KW rat; alpha-2A adrenergic receptor; human; screening; PCR primer;
KW ss.
XX
OS Rattus sp.
XX
PN WO200012704-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US20011.
XX
PR 01-SEP-1998; 98US-0098704.
XX
PA (PAUS/) PAUSCH M H.
PA (LAIM/) LAI M.
PA (SILV/) SILVERMAN S.
PA (BIRS/) BIRSAN C.
PA (BAUM/) BAUMBAUCH W.

PA (TSEN/) TSENG E.
PA (KAJK/) KAJKOWSKI E M.
PA (OZEN/) OZENBERGER B A.
XX
XX Pausch MH, Lai M, Silverman S, Birsan C, Baumbauch W, Tseng E;
PI Kajkowski EM, Ozenberger BA;
XX
DR WPI; 2000-246753/21.
XX
XX
PT Novel host cells comprising heterologous G protein-coupled receptor
PT modified to be constitutively active, useful for high throughput
PT screening assays for e.g. drugs, insecticides or nematocides -
XX
PS Example 3; Page 25; 75pp; English.
XX
CC This is the DNA sequence of a primer that was used in the PCR
CC amplification of DNA encoding the N-terminal portion (including 22
CC amino acids proximal to the 5th transmembrane domain) of rat
CC cholecystokinin CCKB receptor, a G protein coupled receptor (GPCR).
CC The PCR product was used in the construction of an intracellular
CC loop 3 (IC3) deleted CCKB receptor mutant. Deletion of a portion
CC of IC3 of mammalian GPCRs is correlated with improved functional
CC expression in yeast cells with retention of full ability to couple
CC to the heterotrimeric G protein. The invention relates to mutant
CC GPCRs with constitutively activating mutations that permit the
CC detection of the receptors' functional activity in the absence of
CC activation ligands, host cells that contain mutations that promote
CC the functional activity of the GPCRs, host cells expressing such
CC receptors, and vectors useful for making such cells. The host cells
CC are useful in high throughput screening assays for therapeutic drugs,
CC insecticides, nematocides etc., and are especially useful for assays
CC using orphan receptors.
XX
SQ Sequence 36 BP; 2 A; 15 C; 16 G; 3 T; 0 other;
QY
Query Match 54.6%; Score 22.4; DB 21; Length 36;
Best Local Similarity 95.8%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 36 GCCCAACGGTCTGGGCCCGGAGCG 13
RESULT 13
AAZ94369/C
ID AAZ94369 standard; DNA; 37 BP.
XX
AC AAZ94369;
XX
DT 03-JUL-2000 (first entry)
XX
DE Human alpha 2A adrenergic receptor PCR primer.
XX
KW G protein coupled receptor; GPCR; human;
KW alpha 2A adrenergic receptor; drug screening; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200012705-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US20013.
XX
PR 01-SEP-1998; 98US-0098704.
XX
PA (PAUS/) PAUSCH M H.
PA (WESS/) WESS J.
PI Pausch MH, Wess J;
XX WPI; 2000-246754/21.
DR

XX New G protein-coupled receptors with a mutation in an intracellular
PT domain, useful for high throughput screening assays for e.g. drugs,
PT insecticides or nematocides -
XX
PS Example 5; Page 16; 37pp; English.

This is the DNA sequence of a primer that was used in the PCR amplification of DNA encoding the N-terminal portion (including 39 amino acids proximal to the 5th transmembrane domain) of human alpha 2A adrenergic receptor, a G protein coupled receptor (GPCR). The PCR product was used in the construction of an intracellular loop 3 (IC3) deleted receptor mutant. Deletion of a portion of IC3 of mammalian GPCRs is correlated with improved functional expression in yeast cells with retention of full ability to couple to the heterotrimeric G protein. The invention provides modified GPCRs having a mutation in IC3 that results in an improved functional response in cell-based assays. The modification promotes growth stimulation by a GPCR agonist, especially by improving coupling between the receptor and a heterotrimeric G protein. Polynucleotides encoding the mutated GPCR, chimeric GPCR, vectors and host cells are also claimed. The modified GPCRs can be used in improved high throughput screening assays (especially in yeast cells) for therapeutic drugs, insecticides, nematocides etc.

SQ Sequence 37 BP; 2 A; 15 C; 17 G; 3 T; 0 other;

Query Match	54.6%;	Score 22.4;	DB 21;	Length 37;
Best Local Similarity	95.8%;	Pred. NO. 1.2e+02;		
Matches 23; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 18 GCCCAAGGCTCTGGGCCCCGAGCG 41
||||| |||||||||||||||
Db 37 GCCCAACGGTCTGGGCCCCGAGCG 14

RESULT 14

AAS67824
ID AAS67824 standard; cDNA; 2286 BP.

AC AAS67824;

DT 13-FEB-2002 (first entry)

DNA encoding novel human diagnostic protein #3628.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN W0200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Llu C, Tang YT;

WPI; 2001-639362/73.

P-PSDB; ABG03637.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -

PPS Claim 1; SEQ ID No 3628; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

50 Sequence 2286 BP; 604 A; 575 C; 617 G; 490 T; 0 other;

Query Match	54.68;	Score 22.4;	DB 23;	Length 2286;
Best Local Similarity	72.58;	Pred. No. 1.2e+02;		
Matches 29;	Conservative	0;	Mismatches 11;	Indels 0;
				Gaps 0;

QY 2 GGGGCACCGAGCGGACAGGCCCAAGGGTCTGGGCCCGAGCG 41
 ||||| ||||| | | ||||| ||||| |||
 Db 2055 GGGGCACCGAGCGGCGCTGAACCTAGGGCGCCCGGGCCGCGG 2094

RESULT 15

AAS71762
ID AAS71762 standard; cDNA; 2286 BP.

AC AAS71762;

DT 13-FEB-2002 (first entry)

DNA encoding novel human diagnostic protein #7566.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN W0200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR P-PSDB; ABG07575.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 1; SEQ ID No 7566; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 2286 BP; 604 A; 575 C; 617 G; 490 T; 0 other;

Query Match 54.6%; Score 22.4; DB 23; Length 2286;
Best Local Similarity 72.5%; Pred. No. 1.2e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 GGGGCACCGAGCGCAGGCCCAAGGCTCTGGCCCCGAGCG 41
||||| ||||| | | | ||||| ||||| |||||
Db 2055 GGGGCACCGAGGGCCTGAACCTAGGGCCCCGGCCGCGCG 2094

Search completed: February 15, 2003, 14:30:43
Job time : 25.0206 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 12:34:42 ; Search time 81.5273 Seconds
(without alignments)
8144.696 Million cell updates/sec

Title: US-09-636-259B-2_COPY_730_770

Perfect score: 41
Sequence: 1 gggggcaccgcagcgagcc.....aagggtctgggccccgagcg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	39.4	96.1	453	14	BQ129312
C 2	39.4	96.1	492	14	BM967243
C 3	39.4	96.1	561	14	BM967248
4	25.2	61.5	606	9	AI935256
5	25	61.0	235	9	AV250353
C 6	25	61.0	463	14	BM800068

C 7	25	61.0	529	14	BM704323	BM704323	UI-E-CK1-
8	25	61.0	606	14	BM671529	BM671529	UI-E-CK1-
C 9	25	61.0	793	13	BI952735	BI952735	HVSMem000
10	25	61.0	3689	11	AK014589	AK014589	Mus muscu
11	24.2	59.0	259	13	BI243119	BI243119	RE40676.5
12	24.2	59.0	297	13	BI482295	BI482295	RE64967.5
13	24.2	59.0	393	13	BI589545	BI589545	RH02982.5
14	24.2	59.0	438	13	BI353926	BI353926	GM25615.5
15	24.2	59.0	448	13	BI241551	BI241551	RE38647.5
16	24.2	59.0	457	13	BI578058	BI578058	RE71856.5
17	24.2	59.0	467	13	BI584252	BI584252	RH23291.5
18	24.2	59.0	468	13	BI239413	BI239413	RE35892.5
19	24.2	59.0	470	9	AA567681	AA567681	HL01628.5
20	24.2	59.0	503	13	BI634092	BI634092	RH37305.5
21	24.2	59.0	525	13	BI585510	BI585510	RH25106.5
22	24.2	59.0	526	13	BI576424	BI576424	RH32981.5
23	24.2	59.0	526	13	BI615125	BI615125	RH44663.5
24	24.2	59.0	533	13	BI361680	BI361680	RE46007.5
25	24.2	59.0	537	9	AI402612	AI402612	GH21861.5
26	24.2	59.0	537	13	BI613704	BI613704	RH42922.5
27	24.2	59.0	546	9	AI403493	AI403493	GH22945.5
28	24.2	59.0	552	9	AI259030	AI259030	LP02351.5
29	24.2	59.0	554	9	AI404885	AI404885	GH24737.5
30	24.2	59.0	572	13	BI590050	BI590050	RH03608.5
31	24.2	59.0	573	13	BI237477	BI237477	RE33712.5
32	24.2	59.0	576	13	BI606741	BI606741	RH73530.5
33	24.2	59.0	586	13	BI357417	BI357417	RE43901.5
34	24.2	59.0	589	13	BI589749	BI589749	RH03232.5
35	24.2	59.0	591	13	BI165996	BI165996	RE06013.5
36	24.2	59.0	607	13	BI568381	BI568381	RH39817.5
37	24.2	59.0	613	13	BI357318	BI357318	RE43752.5
38	24.2	59.0	614	13	BI172535	BI172535	RE15053.5
39	24.2	59.0	614	13	BI590298	BI590298	RH03895.5
40	24.2	59.0	626	13	BI615346	BI615346	RH44953.5
41	24.2	59.0	639	9	AI114144	AI114144	GH10841.5
42	24.2	59.0	640	9	AI135240	AI135240	GH12908.5
43	24.2	59.0	644	12	BE974991	BE974991	bs37d09.Y
44	24.2	59.0	663	13	BI369569	BI369569	RE55787.5
45	24.2	59.0	665	13	BI629282	BI629282	RH58125.5

ALIGNMENTS

RESULT 1
BQ129312/c 453 bp mRNA linear EST 29-APR-2002
LOCUS i334d05.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
DEFINITION CDNA clone IMAGE:6136736 5' similar to SW:A2AA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.

ACCESSION BQ129312
VERSION BQ129312.1 GI:20203223
SOURCE EST.

ORGANISM human.

REFERENCE
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Rittler,E., Ronko,I., Bennett,J., Cardenas ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)

TITLE
JOURNAL COMMENT
Other_ESTs: i334d05.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812

Fax: 617-495-8557
Email: dmeltone@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center This clone is
available royalty-free through LBNL; please contact the IMAGE
consortium (info@image.lbnl.gov) for further information
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco.

FEATURES
source

1..453
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6136736"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 41 a 189 c 164 g 59 t
ORIGIN

Query Match 96.1%; Score 39.4; DB 14; Length 453;
Best Local Similarity 97.6%; Pred. No. 0.0035;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGAGCCCAAGGCTGTGGCCCCGAGCG 41
|||||
Db 441 GGGGGCACCAGCGAGCCCAAGGCTGTGGCCCCGAGCG 401

RESULT 2
BM967243/c

LOCUS 492 bp mRNA linear EST 29-APR-2002
DEFINITION i132c09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
CDNA clone IMAGE:6136336 5' similar to SW:A2AA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ; mRNA sequence.
BM967243

ACCESSION BM967243.1 GI:19561038
VERSION
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

1 (bases 1 to 492)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Seearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
, M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T.,
, Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: i132c09.x1

TITLE
JOURNAL
COMMENT

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812

Fax: 617-495-8557
Email: dmeltone@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 455.

FEATURES
source

1..492
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6136336"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 44 a 202 c 182 g 64 t
ORIGIN

Query Match 96.1%; Score 39.4; DB 14; Length 492;
Best Local Similarity 97.6%; Pred. No. 0.0036;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGAGCCCAAGGCTGTGGCCCCGAGCG 41
|||||
Db 441 GGGGGCACCAGCGAGCCCAAGGCTGTGGCCCCGAGCG 401

RESULT 3

BM967248/c 561 bp mRNA linear EST 29-APR-2002
LOCUS
DEFINITION i132d04.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
CDNA clone IMAGE:6136374 5' similar to SW:A2AA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ; mRNA sequence.
BM967248

ACCESSION BM967248.1 GI:19561047
VERSION
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

1 (bases 1 to 561)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Seearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
, M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T.,
, Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: i132d04.x1

TITLE
JOURNAL
COMMENT

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Glibco
High quality sequence stop: 445.
Location/Qualifiers
1. 561

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6136374"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
Superscript Plasmid library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 63 a 215 c 210 g 73 t
ORIGIN

Query Match 96.1%; Score 39.4; DB 14; Length 561;
Best Local Similarity 97.6%; Pred. No. 0.0037;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGGGCAGCGAGCGAGCGCCCAAGGGTCTGGGCCCCGAGCG 41
|||||
Db 441 GGGGGCAGCGAGCGAGCGCCCAAGCGTCTGGGCCCCGAGCG 401

RESULT 4
AI935256 606 bp mRNA linear EST 08-MAR-2000
LOCUS wp16a07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464980 3',
DEFINITION mRNA sequence.
ACCESSION AI935256
VERSION AI935256.1 GI:5674126
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 606)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 652 Std Error: 0.00
Seq primer: -40UP from Glibco
High quality sequence stop: 390.
Location/Qualifiers
1. 606

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2464980"
/clone_lib="NCI_CGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
metastatic)"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Lung; Vector: pRT3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
pooled lung tumor tissue, and was then primed with a Not I
- oligo(dT) primer. Double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pRT3 vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT 113 a 219 c 197 g 77 t
ORIGIN

Query Match 61.5%; Score 25.2; DB 9; Length 606;
Best Local Similarity 78.9%; Pred. No. 1.6e+02;
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 3 GGGCAGCGAGCGCAGGCCCAAGGCTCTGGGCCCCGAGC 40
| | | | |
Db 146 GAGCGCGCGCCCGCAGGGCCAGCGCTCTGGCCCCGAGC 183

RESULT 5
AV250353 235 bp mRNA linear EST 04-NOV-1999
LOCUS AV250353 RIKEN full-length enriched, 0 day neonate head Mus
DEFINITION musculus cDNA clone 4833422109 3', mRNA sequence.
ACCESSION AV250353
VERSION AV250353.1 GI:6237812
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 235)
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Horii,F.,
Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai
C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata
Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,
Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y.,
Wataniki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T.,
Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al. 1999)
Unpublished (1999)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Wataniki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
Y.
Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES

source

Location/Qualifiers
1. .235
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4833422109"
/clone_lib="RIKEN full-length enriched, 0 day neonate
head"
/sex="mixed"
/tissue_type="head"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATCTCGATTATTAAATTATCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified Bluescript KS(+) after bulk excision
from Lambda FLC I."

BASE COUNT

52 a 58 c 66 g 59 t

ORIGIN

Query Match 61.0%; Score 25; DB 9; Length 235;
Best Local Similarity 75.6%; Pred. No. 1.6e+02;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 GGGGGCACCGACGCGAGCCCAAGGCTCTGGCCCCGAGCG 41
|||||
Db 94 GGGGGCACCAAGGCGCAGACCAATGCTGTGGCTGAGCG 134

RESULT 6
BM800068/c

LOCUS

DEFINITION

BM800068 463 bp mRNA linear EST 05-MAR-2002
AGENCOURT_6415956 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531068
5', mRNA sequence.

ACCESSION

BM800068
BM800068.1 GI:19116891

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 463)
NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

JOURNAL

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LLM12212 row: c column: 05
High quality sequence stop: 462.

FEATURES

source

Location/Qualifiers
1. .463
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5531068"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
Average insert size 2.1 kb.

BASE COUNT 90 a 160 c 130 g 83 t

ORIGIN

Query Match 61.0%; Score 25; DB 14; Length 463;
Best Local Similarity 75.6%; Pred. No. 1.8e+02;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 GGGGGCACCGACGCGAGCCCAAGGCTCTGGCCCCGAGCG 41
|||||
Db 358 GGGGGCACCGACGCGAGCGCGGCTGTGGCGCAGAGGG 318

RESULT 7
BM704323/c

LOCUS

BM704323 529 bp mRNA linear EST 28-FEB-2002
UI-E-CK1-afj-j-22-0-UI.r1 UI-E-CK1 Homo sapiens cDNA clone
UI-E-CK1-afj-j-22-0-UI 5', mRNA sequence.

ACCESSION

BM704323
BM704323.1 GI:19017581

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers
1. .529
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-CK1-afj-j-22-0-UI"
/clone_lib="UI-E-CK1"
/tissue_type="Retina Foveal and Macular"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: PT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CK1 is a normalized cDNA library containing the

following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 83 a 173 c 161 g 111 t 1 others
ORIGIN

Query Match 61.0%; Score 25; DB 14; Length 529;
Best Local Similarity 75.6%; Pred. No. 1.8e+02;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 GGGGGCACCAGCGCAGCCCAAGGCTGTGGCCCCGAGCG 41
|||||
Db 288 GGGGGCACCAGCGCAGCGCAGCCCGCTGGCGCAGAGGG 248

RESULT 8

LOCUS BM671529 606 bp mRNA linear EST 27-FEB-2002
DEFINITION UI-E-CK1-afj-j-22-0-UI.s2 UI-E-CK1 Homo sapiens cDNA clone
ACCESSION UI-E-CK1-afj-j-22-0-UI 3', mRNA sequence.
VERSION BM671529
KEYWORDS BM671529.1 GI:18981427
SOURCE EST.
ORGANISM human.
HOMO sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 606)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477

COMMENT

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.iowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
POLYA=Yes.

FEATURES

Source

Location/Qualifiers
1..606
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-CK1-afj-j-22-0-UI"
/clone_lib="UI-E-CK1"
/tissue_type="Retina Foveal and Macular"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CK1 is a normalized cDNA library containing the
following tissue(s): Retina Foveal and Macular. The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand

cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_LIB=UI-E-CK1
TAG_TISSUE=Foveal and Macular Retina
TAG_SEQ=GTCC"

BASE COUNT 138 a 173 c 189 g 104 t 2 others
ORIGIN

Query Match 61.0%; Score 25; DB 14; Length 606;
Best Local Similarity 75.6%; Pred. No. 1.9e+02;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 GGGGGCACCAGCGCAGCCCAAGGCTGTGGCCCCGAGCG 41
|||||
Db 325 GGGGGCACCAGCGCAGCGCAGCCCGCTGGCGCAGAGGG 365

RESULT 9

LOCUS BI952735/c 793 bp mRNA linear EST 19-OCT-2001
DEFINITION HVS MEM007J12f Hordeum vulgare green seedling EST library
HVC DNA0014 (Blumeria infected) Hordeum vulgare cDNA clone
HVS MEM007J12f, mRNA sequence.
BI952735
BI952735.1 GI:16296792

VERSION BI952735
KEYWORDS EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
1 (bases 1 to 793)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons
J., Oates,R. and Main,D.

Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected Morex (compatible) seedling
cDNA library
Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
Total hg bases = 198
Seq primer: AATTACCCCTCACTAAAGG

JOURNAL

COMMENT

High quality sequence start: 22
High quality sequence stop: 590.
Location/Qualifiers
1..793
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVS MEM007J12f"
/clone_lib="Hordeum vulgare green seedling EST library
HVC DNA0014 (Blumeria infected)"
/tissue_type="green seedling leaf"
/lab_host="TJC121"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Morex (mla) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were infected with isolate 5874 of
Blumeria graminis f. sp. hordei, and leaves were harvested

FEATURES

Source


```

/db_xref="PANTOM_DB:4632419J12"
/db_xref="MGD:MGI:1899072"
/db_xref="taxon:10090"
/clone="4632419J12"
/tissue_type="skin"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
199.1440

```

/note="data source:SPTR, source key:P17475, evidence:ISS homolog to ALPHA-1-ANTIPROTEINASE PRECURSOR (ALPHA-1-ANTITRYPSIN) (ALPHA-1- PROTEINASE INHIBITOR) putative"

/codon_start=1

/protein_id="BAB29447.1"

/db_xref="GI:12852537"

/db_xref="MGI:1915304"

/translation="MTRMLDLGLFLAGLLTVKGLQDRDAPDMYDSPYRQEMRGKKDAROLARRNMEFGFLQLQRLASNSPGNIFLPLSISTAFMSLGAQNSITLEEIREGFNEKEMSNMVDVAHFYLLHLKLNQETEDTKMNLGNALFMDQKLRPQDFNLNAKNYYDADMLNFMQDLNTEOKDINRYISQKTHSRIRKNMWKSIDPQTVMLITNIFRGRMWYEDDPKQREEEFFIEKGTVKVPMMPQRLGYDMAYDSQLSCITLEIPRGNITATFVLPDNGKLKLEQGLQADIFAKWKLSTSKRYDVAVPKLRISSTYNMKKVLSRLGISKIFEEINGDLTRISSHRSRLKVGAEVHKAEKLKMDKEGMEGAAGSGAQTLPMTTPRHMKLDRPFILMIYENPMSMVELARIYDPSG"

polyA_signal	3670.	.3675			
	/note="putative"				
polyA_site	3689				
	/note="putative"				
BASE COUNT	966 a	955 c	910 g	857 t	1 others
ORIGIN					

Query Match	61.08;	Score 25;	DB 11;	length 3689;
Best Local Similarity	75.68;	Pred. No. 2.5e+02;		
Matches 31; Conservative	0;	Mismatches 10;	Indels 0;	Gaps 0;

Oy 1 GGGGCGACCGAGCGCGCAGGCCCAAGGGTCTGGGGCCCCGAGCG 41
||||||| | | | ||| ||| ||| | ||||
Db 2249 GGGGCGACCGAGCGCGCAGCCCATGTGTGGGCTTGAGCG 2289

RESULT	11
LOCUS	BI243119
DEFINITION	259 bp mRNA linear EST 12-JUL-2001 RE40676.5ptme RE Drosophila melanogaster normalized Embryo pf1c-1
ACCESSION	Drosophila melanogaster CDNA clone RE40676 5, mRNA sequence. BI243119
VERSION	BI243119.1 GI:14711973
KEYWORDS	EST.
SOURCE	fruit fly.

ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 259)

REFERENCE
AUTHORS

1 (bases 1 to 259)

Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S., Munnall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and Rubin, G. M.

TITLE	COMMENT
BDGP/HHMI RE Drosophila EST Project Unpublished (2001)	Contact: Stapleton, M. BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd., Berkeley, CA 94720, USA
Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
 Plate: RE.406 row: G column: 4
 High quality sequence stop: 258.

```

FEATURES
  source
    Location/Qualifiers
      1. 259
        /organism="Drosophila melanogaster"

```

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/db_xref="taxon:7227"
/clone="RE40676"
/clone_lib="RE Drosophila melanogaster normalized Embryo
pFlc-1"
/sex="male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DH5-alpha Tona"
/note="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_2
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."

```

Query Match	59.0%;	Score 24.2;	DB 13;	Length 259;
Best Local Similarity	78.4%;	Pred. No. 3e+02;		
Matches	29;	Conservative 0;	Mismatches 8;	Indels 0;
				Gaps 0;
Qy	3	GGGACCGAGCGAGGCCCAAGGTCTGGCCCCGAG	39	
Db	153	GGGAACCTGGGGGAGCCCCCAAGGTCAAGTACCCGAG	189	

RESULT 12				
BI482295				
LOCUS	BI482295	297 bp	mRNA	linear
DEFINITION	RE64967.5	prime RE	Drosophila melanogaster	normalized EST 27-AUG-2001

Drosophila melanogaster cDNA clone R64967 5 similar to CG6084: FBan006084 GO: [enzyme (GO: 0003824)] located on: 3L 68C9-68C9; ; 05/21/2001, mRNA sequence.

ACCESSION	BI482295	GI:15317308
VERSION	BI482295.1	
KEYWORDS	EST,	
SOURCE	fruit fly,	
ORGANISM	Drosophila melanogaster	
	Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;	
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
	Ephydroidea; Drosophilidae; Drosophila.	

REFERENCE
AUTHORS

1 (bases 1 to 297)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George
, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S.,
Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and Rubin
, G. M.

TITLE	COMMENT
BDGP/HHMI RE Drosophila EST Project Unpublished (2001)	Contact: Stapleton, M.

Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
 hit genomic AE003544: arm:3L [11370031,11651899]
 estimated-cyto:68C3-68C15: 05/21/2001
 Plate: RE.649 row: F column: 7
 High quality sequence stop: 260.
 Location/Qualifiers
 1..297

FEATURES	Source
Location/Qualifiers	1. .297
/organism="Drosophila melanogaster"	
/db_xref="taxon:7227"	
/clone="REG4967"	
/clone_1lb="RE Drosophila melanogaster normalized Embryo pF1C-1"	
/sex="male and female"	
/dev_stage="0-24 hours mixed stage embryonic"	
/lab_host="DH5-alpha Tona"	
/note="Organ: embryo; Vector: pF1C1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Ptero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."	
BASE COUNT	94 a 58 c 78 g 67 t
ORIGIN	

Query Match 59.0%; Score 24.2; DB 13; Length 297;
Best Local Similarity 78.4%; Pred. No. 3e+02;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 3 GGGCACCAGCGAGGCCCAAGGCTGTGGCCCCGAG 39
||| ||| | ||| ||||| || | |||||
Db 153 GGGAACTGGGCGAGCCCAAGGTCAGTCACCGAG 189

RESULT 13
BI589545
LOCUS 393 bp mRNA linear EST 06-SEP-2001
DEFINITION RH02982.5prime RH Drosophila melanogaster normalized Head p1c-1
Drosophila melanogaster cDNA clone RH02982 5 similar to CG6084;
FBan0006084 GO:[enzyme (GO:0003824)] located on: 3L 68C9-68C9;:
08/16/2001, mRNA sequence.

ACCESSION BI589545
VERSION BI589545.1 GI:15480967
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 393)
Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson
,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George
,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S.,
Mungall,C.J., Nunco,J., Pacleb,J., Paragas,V., Park,S.,
Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
,G.M.
BDGP/HMT RH Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003544: arm:3L [11370031,11651899]
estimated-cyto:68C3-68C15: 08/16/2001
Plate: RH.29 row: G column: 10
High quality sequence stop: 344.

FEATURES
source
1..393
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RH02982"
/clone_lib="RH Drosophila melanogaster normalized Head
p1c-1"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha Tona"
/note="Organ: head; Vector: p1c1; Site_1: XhoI; Site_2:
BamHI; Library was kindly generated by Plero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."

BASE COUNT 119 a 80 c 102 g 91 t 1 others

ORIGIN

Query Match 59.0%; Score 24.2; DB 13; Length 393;
Best Local Similarity 78.4%; Pred. No. 3.2e+02;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 3 GGGCACCAGCGAGGCCCAAGGCTGTGGCCCCGAG 39
||| ||| | ||| ||||| || | |||||
Db 154 GGGAACTGGGCGAGCCCAAGGTCAGTCACCGAG 190

RESULT 14
BI353926
LOCUS 438 bp mRNA linear EST 31-JUL-2001

DEFINITION GM25615.5prime GM Drosophila melanogaster ovary pot2 Drosophila
melanogaster cDNA clone GM25615 5 similar to CG6084: FBan0006084
GO:[enzyme (GO:0003824)] located on: 3L 68C9-68C9;: 05/18/2001,
mRNA sequence.

ACCESSION BI353926
VERSION BI353926.1 GI:15048368
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 438)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HMT Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003544: arm:3L [11370031,11651899]
estimated-cyto:68C3-68C15: 05/18/2001
Plate: GM.256 row: B column: 3
High quality sequence stop: 243.

FEATURES
source
1..438
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GM25615"
/clone_lib="GM Drosophila melanogaster ovary pot2"
/sex="female"
/dev_stage="newly eclosed females: germarium-stage 6"
/lab_host="X1 Blue"
/note="Organ: ovary; Vector: pot2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pot2. "

BASE COUNT 129 a 96 c 110 g 102 t 1 others

ORIGIN

Query Match 59.0%; Score 24.2; DB 13; Length 438;
Best Local Similarity 78.4%; Pred. No. 3.2e+02;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 3 GGGCACCAGCGAGGCCCAAGGCTGTGGCCCCGAG 39
||| ||| | ||| ||||| || | |||||
Db 125 GGGAACTGGGCGAGCCCAAGGTCAGTCACCGAG 161

RESULT 15
BI241551
LOCUS 448 bp mRNA linear EST 12-JUL-2001
DEFINITION RE38647.5prime RE Drosophila melanogaster normalized Embryo p1c-1
Drosophila melanogaster cDNA clone RE38647 5 similar to CG6084:
FBan0006084 'enzyme' located on: 3L 68C9-68C9;: 05/12/2001, mRNA
sequence.

ACCESSION BI241551
VERSION BI241551.1 GI:14710247
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 448)
Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson
,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George
,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S.,
Mungall,C.J., Nunco,J., Pacleb,J., Paragas,V., Park,S.,
Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
,G.M.

TITLE BDGP/HMI RE Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
hit genomic AE003544: arm:3L [11370031,11651899]
estimated-cyto:68C3-68C15: 05/12/2001
Plate: RE.386 row: D column: 11
High quality sequence stop: 411.
Location/Qualifiers

FEATURES

source
1..448
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RE38647"
/clone_lib="RE Drosophila melanogaster normalized Embryo
pFlc-1"
/sex="male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DH5-alpha Tona"
/note="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."

BASE COUNT 132 a 99 c 111 g 106 t
ORIGIN

Query Match 59.0%; Score 24.2; DB 13; Length 448;
Best Local Similarity 78.4%; Pred. No. 3.2e+02;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 3 GGGCACCGAGCGCGCCCAAGGGTCTGGGCCCCGAG 39
||| ||| | ||| ||||| || | |||||
Db 153 GGGAACTGGGGCAGCCCAAGGGTCAGTCAACCGAG 189

Search completed: February 15, 2003, 18:03:11
Job time : 86.5273 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 06:16:02 ; Search time 2.19024 Seconds
(without alignments)
5740.812 Million cell updates/sec

Title: US-09-636-259B-2_COPY_730_770

Perfect score: 41
Sequence: 1 gggggcaccgagcgagccgagcgc.....aagggtctggtgccccgagcg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_NA:*
2: /cgn2_6/ptodata/1/1na/5A_COMB.seq:*
3: /cgn2_6/ptodata/1/1na/5B_COMB.seq:*
4: /cgn2_6/ptodata/1/1na/6A_COMB.seq:*
5: /cgn2_6/ptodata/1/1na/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22.2	54.1	35060	3	US-08-814-095-7 Sequence 7, Appl1
2	21.4	52.2	4190	3	US-08-938-291A-2 Sequence 2, Appl1
3	21.6	51.7	1008	4	US-09-091-097-38 Sequence 38, Appl1
4	20.6	50.2	3164	1	US-08-188-228-49 Sequence 49, Appl1
5	20.6	50.2	3164	1	US-08-332-643-43 Sequence 43, Appl1
6	20.6	50.2	3164	1	US-08-332-638-49 Sequence 49, Appl1
7	20.4	49.8	1312	1	US-08-205-506A-1 Sequence 1, Appl1
8	20.4	49.8	1312	5	PCT-US94-02389-1 Sequence 1, Appl1
9	20.4	49.8	3318	4	US-09-593-589-3 Sequence 3, Appl1
10	20.4	49.8	9775	4	US-08-977-171-1 Sequence 1, Appl1
11	20.4	49.8	9934	4	US-08-977-171-2 Sequence 2, Appl1
12	20.2	49.3	1068	5	PCT-US91-00899-13 Sequence 13, Appl1
13	20.2	49.3	1215	5	PCT-US91-00899-5 Sequence 5, Appl1
14	20.2	49.3	1488	1	US-07-914-281-9 Sequence 9, Appl1
15	20.2	49.3	1488	1	US-08-393-246-9 Sequence 9, Appl1
16	20.2	49.3	1488	1	US-08-525-058A-9 Sequence 9, Appl1
17	20.2	49.3	1488	2	US-08-696-731-9 Sequence 9, Appl1
18	20.2	49.3	1488	4	US-09-042-531-9 Sequence 9, Appl1
19	20.2	49.3	2175	4	US-08-482-073-9 Sequence 9, Appl1
20	20.2	49.3	2861	4	US-08-482-073-10 Sequence 10, Appl1
21	20.2	49.3	3647	1	US-07-914-281-7 Sequence 7, Appl1
22	20.2	49.3	3647	1	US-08-393-246-7 Sequence 7, Appl1
23	20.2	49.3	3647	1	US-08-525-058A-7 Sequence 7, Appl1
24	20.2	49.3	3647	2	US-08-696-731-7 Sequence 7, Appl1
25	20.2	49.3	3647	4	US-09-042-531-7 Sequence 7, Appl1
26	20.2	49.3	3647	5	PCT-US91-00899-4 Sequence 4, Appl1
27	20.2	49.3	3854	2	US-08-720-484A-1 Sequence 1, Appl1

C 28	20.2	49.3	3854	3	US-08-953-823A-1	Sequence 1, Appl1
C 29	20.2	49.3	3854	4	US-09-398-239-1	Sequence 1, Appl1
C 30	20	48.8	141	4	US-08-943-731-8	Sequence 8, Appl1
C 31	20	48.8	225	1	US-08-136-993-6	Sequence 6, Appl1
C 32	20	48.8	1218	1	US-08-136-993-8	Sequence 8, Appl1
C 33	20	48.8	1322	1	US-08-136-993-12	Sequence 12, Appl1
C 34	20	48.8	4772	4	US-09-484-970B-133	Sequence 133, App
C 35	20	48.8	18609	4	US-08-943-731-1	Sequence 1, Appl1
C 36	19.8	48.3	51	1	US-07-690-983D-17	Sequence 17, Appl1
C 37	19.8	48.3	54	1	US-07-690-983D-27	Sequence 27, Appl1
C 38	19.8	48.3	748	4	US-08-998-416-434	Sequence 434, App
C 39	19.8	48.3	987	2	US-08-891-837B-1	Sequence 1, Appl1
C 40	19.8	48.3	1349	1	US-08-451-777A-4	Sequence 4, Appl1
C 41	19.8	48.3	1349	1	US-08-451-777A-5	Sequence 5, Appl1
C 42	19.8	48.3	1349	1	US-08-451-777A-6	Sequence 6, Appl1
C 43	19.8	48.3	1349	2	US-08-451-778A-4	Sequence 4, Appl1
C 44	19.8	48.3	1349	2	US-08-451-778A-5	Sequence 5, Appl1
C 45	19.8	48.3	1349	2	US-08-451-778A-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-814-095-7
Sequence 7, Application US/08814095
Patent No. 6025183
GENERAL INFORMATION:
APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: KOHN & ASSOCIATES
STREET: 30500 No. 6025183thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814, 095
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including ACHE
DESCRIPTION: Promotor, ACHE gene and ARS gene"
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7q22
FEATURE:

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NAME/KEY: promoter
LOCATION: 4089..22464
OTHER INFORMATION: /function= "ACHE Promotor"
FEATURE:
NAME/KEY: exon
LOCATION: 22465..22537
OTHER INFORMATION: /function= "non-translated"
OTHER INFORMATION: /gene= "ACHE"
FEATURE:
NAME/KEY: exon
LOCATION: 24090..25177
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "(translation start:
OTHER INFORMATION: 24110)"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
FEATURE:
NAME/KEY: exon
LOCATION: 25524..26009
IDENTIFICATION METHOD: experimental
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OTHER INFORMATION: /gene= "ACHE"
FEATURE:
NAME/KEY: exon
LOCATION: 27005..27274
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
FEATURE:
NAME/KEY: exon
LOCATION: 27255..28007
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
FEATURE:
NAME/KEY: terminator
LOCATION: 27385..27387
FEATURE:
NAME/KEY: exon
LOCATION: 28008..28129
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
FEATURE:
NAME/KEY: terminator
LOCATION: 28129..28131
FEATURE:
NAME/KEY: exon
LOCATION: complement (34528..34895)
OTHER INFORMATION: /function= "arsenite resistance
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 1
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NAME/KEY: exon
LOCATION: complement (34092..34358)
OTHER INFORMATION: /gene= "AR"
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NAME/KEY: exon
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OTHER INFORMATION: /gene= "AR"
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NAME/KEY: exon
LOCATION: complement (33493..33591)
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NAME/KEY: exon
LOCATION: complement (33297..33408)
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NAME/KEY: exon
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OTHER INFORMATION: /gene= "AR"
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NAME/KEY: exon
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OTHER INFORMATION: /gene= "AR"
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NAME/KEY: exon
LOCATION: complement (30816..31011)
OTHER INFORMATION: /gene= "AR"
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
FEATURE:
NAME/KEY: exon
LOCATION: complement (29945..30073)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
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NAME/KEY: exon
LOCATION: complement (29664..29856)
OTHER INFORMATION: /gene= "ARS"
OTHER INFORMATION: /number= 16
US-08-814-095-7
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Query Match 54.1%; Score 22.2; DB 3; Length 35060;
Best Local Similarity 77.1%; Pred. No. 25;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2 GGGCACCAGCGCAGGCCCAAGGCTCTGGGCC 36
Db 22583 GGGCACCAGCTGCGCTCCCGAGGGGTCCAGGCC 22617
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Thu Feb 20 09:21:37 2003

us-09-636-259b-2_copy_730_770.rml

RESULT 2
US-08-938-291A-2/C
Sequence 2, Application US/08938291A
Patent No. 6117673
GENERAL INFORMATION:
APPLICANT: Lev, Sime
APPLICANT: Plowman, Gregory D.
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: RDB PROTEINS AND RELATED
TITLE OF INVENTION: PRODUCTS AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938, 291A
FILING DATE: September 26, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,337
FILING DATE: October 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 228/172
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4190 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-938-291A-2

Query Match 52.2%; Score 21.4; DB 3; Length 4190;
Best Local Similarity 71.8%; Pred. No. 47;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 GGGCACCAGCGAGCCCAAGGCTCTGGCCCCGAGCG 41
11111 1 11111 11111 1111 11111
Db 98 GGGCAGGGCGCGCGCCGCGTGGGTGAGAGCCGAGCG 60

RESULT 3
US-09-091-097-38
Sequence 38, Application US/09091097
Patent No. 6432407
GENERAL INFORMATION:
APPLICANT: TAKESAKO, KAZUTOH
APPLICANT: OKADO, TAKASHI
APPLICANT: YAGIHARA, TOMOKO
APPLICANT: KURODA, MASANOBU
APPLICANT: ONISHI, YOSHIMI
APPLICANT: KATO, IKUNOSHIN
APPLICANT: AKIYAMA, KAZUO
APPLICANT: YASUEDA, HIROSHI
APPLICANT: YAMAGUCHI, HIDEYO
TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
TITLE OF INVENTION: MALASSEZIA

NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,097
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0346P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1008 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-09-091-097-38

Query Match 51.7%; Score 21.2; DB 4; Length 1008;
Best Local Similarity 76.5%; Pred. No. 56;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CACCGAGCGCAGGCCCAAGGCTCTGGCCCCGAG 39
11111 11 111111111 1 1 111
Db 657 CACCGAGGCGCTGCCCAAGGCTCTGACCGTGAG 690

RESULT 4
US-08-188-228-49/C
Sequence 49, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992

ATTORNEY/AGENT INFORMATION:
NAME: NO. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 3164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-188-228-49

Query Match
Best Local Similarity 50.2%; Score 20.6; DB 1; Length 3164;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 GGCACCGAGCGCAGGCCCAAGGCTGGGCCCG 37
Db 2131 GGGCGTCCAGCGCGCGCGGCGGCTTGGCCCCG 2097

RESULT 5
US-08-332-643-43/C
Sequence 43, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 3164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-332-643-43

Query Match

50.2%; Score 20.6; DB 1; Length 3164;

Best Local Similarity 74.3%; Pred. No. 86;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0,
QY 3 GGCACCGAGCGCAGGCCCAAGGCTGGGCCCG 37
Db 2131 GGGCGTCCAGCGCGCGCGGCGGCTTGGCCCCG 2097

RESULT 6
US-08-332-638-49/C
Sequence 49, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: NO. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 3164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-332-638-49

Query Match
Best Local Similarity 50.2%; Score 20.6; DB 1; Length 3164;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 3 GGCACCGAGCGCAGGCCCAAGGCTGGGCCCG 37
Db 2131 GGGCGTCCAGCGCGCGCGGCGGCTTGGCCCCG 2097

RESULT 7
US-08-205-506A-1
Sequence 1, Application US/08205506A
Patent No. 5545563
GENERAL INFORMATION:

APPLICANT: Darlington, Gretchen J.
APPLICANT: Wilson, Deborah R.
APPLICANT: Wilde, Margaret
TITLE OF INVENTION: THE HUMAN C/EBP GENE AND VECTORS FOR

```

; TITLE OF INVENTION: ITS EXPRESSION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 801 Pennsylvania Avenue, NW
; CITY: Washington, D.C.
; STATE:
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,506A
; FILING DATE: March 4, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Davis, Peter J.
; REGISTRATION NUMBER: 36,119
; REFERENCE/DOCKET NUMBER: 311.027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 662-0200
; TELEFAX: (202) 662-4643
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1312 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: C/EBP
; US-08-205-506A-1

Query Match          49.8%; Score 20.4; DB 1; Length 1312;
Best Local Similarity 71.1%; Pred. No. 1e+02;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 GGGCACCAGCGCAGCGCCCAAGGGTCTGGGCCCCGAGC 40
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RESULT 8
PCT-US94-02389-1
; Sequence 1, Application PC/TUS9402389
; GENERAL INFORMATION:
; APPLICANT: Darlington, Gretchen J.
; APPLICANT: Wilson, Deborah R.
; APPLICANT: Wilde, Margaret
; TITLE OF INVENTION: THE HUMAN C/EBP GENE AND VECTORS FOR ITS
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02389
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; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Auerbach, Jeffrey I.
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER: 225-107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1312 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: C/EBP
; PCT-US94-02389-1

Query Match          49.8%; Score 20.4; DB 5; Length 1312;
Best Local Similarity 71.1%; Pred. No. 1e+02;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 GGGCACCAGCGCAGCGCCCAAGGGTCTGGGCCCCGAGC 40
    ||||| 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 897 GGGCCCTGGCAGCGCGCTCAAGGGGCTGGCGCCGCCG 934

RESULT 9
US-09-593-589-3
; Sequence 3, Application US/09593589
; Patent No. 6306655
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP ALPHA EXPRESSION
; FILE REFERENCE: RTS-0119
; CURRENT APPLICATION NUMBER: US/09/593,589
; CURRENT FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 3
; LENGTH: 3318
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (592)...(1668)
; US-09-593-589-3

Query Match          49.8%; Score 20.4; DB 4; Length 3318;
Best Local Similarity 71.1%; Pred. No. 1e+02;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 GGGCACCAGCGCAGCGCCCAAGGGTCTGGGCCCCGAGC 40
    ||||| 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1332 GGGCCCTGGCAGCGCGCTCAAGGGGCTGGCGCCGCCG 1369

RESULT 10
US-08-977-171-1/c
; Sequence 1, Application US/08977171
; Patent No. 6232112
; GENERAL INFORMATION:
; APPLICANT: CATCHESIDE, DAVID E.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DIVERSIFICATION
; TITLE OF INVENTION: OF DNA
; NUMBER OF SEQUENCES: 2
```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6232112west Center, 90 South 7th Street
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,171
FILING DATE: 24-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Skoog, Mark T
REGISTRATION NUMBER: 40,178
REFERENCE/DOCKET NUMBER: 10552.13US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9775 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-977-171-1

Query Match      49.8%; Score 20.4; DB 4; Length 9775;
Best Local Similarity 71.1%; Pred. No. 97;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 GGGCACCAGCGCAGCCCAAGGCTGTGGCCCGAGC 40
Db 2547 GGGCACCAGCGCAGCAGCATGACTCGGCCCAACC 2510

RESULT 11
US-08-977-171-2/c
Sequence 2, Application US/08977171
Patent No. 6232112
GENERAL INFORMATION:
APPLICANT: CATCHESIDE, DAVID E.
TITLE OF INVENTION: REAGENTS AND METHODS FOR DIVERSIFICATION
TITLE OF INVENTION: OF DNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6232112west Center, 90 South 7th Street
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,171
FILING DATE: 24-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
```

```

ATTORNEY/AGENT INFORMATION:
NAME: Skoog, Mark T
REGISTRATION NUMBER: 40,178
REFERENCE/DOCKET NUMBER: 10552.13US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9934 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-977-171-2

Query Match      49.8%; Score 20.4; DB 4; Length 9934;
Best Local Similarity 71.1%; Pred. No. 97;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 GGGCACCAGCGCAGCCCAAGGCTGTGGCCCGAGC 40
Db 2651 GGGCACCAGCGCAGCAGCATGACTCGGCCCAACC 2614

RESULT 12
PCT-US91-00899-13/c
Sequence 13, Application PC/US9100899
GENERAL INFORMATION:
APPLICANT: Lowe, John B.
TITLE OF INVENTION: Method and Products for the Synthesis of
TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids,
TITLE OF INVENTION: or as Free Molecules, and for the Isolation of Cloned
TITLE OF INVENTION: Genetic Sequences That Determine These Structur
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00899
FILING DATE: 19910214
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye Ph.D., Jean-Paul
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-5940
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
PCT-US91-00899-13

Query Match      49.3%; Score 20.2; DB 5; Length 1068;
Best Local Similarity 75.8%; Pred. No. 1.2e+02;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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OY 7 ACCGAGCGCAGCCCAAGGCTCTGGCCCCGAG 39
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Db 356 ACCCAGCGCTGGCCCCGGGGCTGGGGCTGGAG 324

RESULT 13

PCT-US91-00899-5/c

; Sequence 5, Application PC/TUS9100899

; GENERAL INFORMATION:

; APPLICANT: Lowe, John B.

; TITLE OF INVENTION: Method and Products For the Synthesis of

; TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids,

; TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned

; TITLE OF INVENTION: Genetic Sequences That Determine These Structur

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 Jefferson Davis Highway, Suite 400

; CITY: Arlington

; STATE: Virginia

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US91/00899

; FILING DATE: 19910214

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Lavalleye Ph.D., Jean-Paul

; REGISTRATION NUMBER: 31,451

; REFERENCE/DOCKET NUMBER: 2363-021-55 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)521-5940

; TELEFAX: (703)486-2347

; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1215 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

; PCT-US91-00899-5

Query Match

Best Local Similarity 49.3%; Score 20.2; DB 5; Length 1215;

Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 7 ACCGAGCGCAGCCCAAGGCTCTGGCCCCGAG 39
||| ||||| ||||| ||| ||||| | |||

Db 503 ACCCAGCGCTGGCCCCGGGGCTGGGGCTGGAG 471

RESULT 14

US-07-914-281-9/c

; Sequence 9, Application US/07914281

; Patent No. 5324663

; GENERAL INFORMATION:

; APPLICANT: LOWE, JOHN B.

; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS

; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,

; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION

; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/914,281

; FILING DATE: 19920720

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Lavalleye, Jean-Paul M. P.

; REGISTRATION NUMBER: 31,451

; REFERENCE/DOCKET NUMBER: 2363-060-55

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)521-4500

; TELEFAX: (703)486-2347

; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1488 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

; US-07-914-281-9

Query Match

Best Local Similarity 49.3%; Score 20.2; DB 1; Length 1488;

Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 7 ACCGAGCGCAGCCCAAGGCTCTGGCCCCGAG 39
||| ||||| ||||| ||| ||||| | |||

Db 776 ACCCAGCGCTGGCCCCGGGGCTGGGGCTGGAG 744

RESULT 15

US-08-393-246-9/c

; Sequence 9, Application US/08393246

; Patent No. 5595900

; GENERAL INFORMATION:

; APPLICANT: LOWE, JOHN B.

; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS

; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,

; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION

; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 Jefferson Davis Highway, Fourth Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/393,246

; FILING DATE:

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/220,433

; FILING DATE: 30-MAR-1994

; APPLICATION NUMBER: US 07/914,281

; FILING DATE: 20-JUL-1992

; ATTORNEY/AGENT INFORMATION:

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; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1488 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-393-246-9

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Query Match          49.3%; Score 20.2; DB 1; Length 1488;
Best Local Similarity 75.8%; Pred. No. 1.2e+02;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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OY 7 ACCGAGCGCAGGCCCCAAGGGGTCTGGGCCCCCGAG 39
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Db 776 ACCCAGCGCTGGCCCGGGGGGCTGGGCTGAG 744

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Thu Feb 20 09:21:37 2003

us-09-636-259b-2_copy_730_770.rnpb

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 06:22:49 ; Search time 2.82052 Seconds
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Title: US-09-636-259B-2_COPY_730_770

Perfect score: 41
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

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Maximum Match 100%
Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	56.1	410	10	US-09-983-965-4927
2	22.2	54.1	155074	9	US-10-026-188-6
3	22	53.7	2622	10	US-09-815-242-7871
4	21.8	53.2	440	10	US-09-960-352-3868
5	21.8	53.2	967	10	US-09-764-877-2208
6	21.2	51.7	224	10	US-09-294-093B-3768
7	21.2	51.7	3667	9	US-09-974-298-64
8	20.8	50.7	487	10	US-09-864-761-1226
9	20.8	50.7	946	10	US-09-764-877-2858
10	20.8	50.7	2033	10	US-09-799-777-134
11	20.8	50.7	2033	10	US-09-947-316-3
12	20.8	50.7	2033	12	US-10-044-090-777
13	20.8	50.7	7521	9	US-09-819-104A-3
14	20.8	50.7	8686	9	US-09-819-104A-1
15	20.6	50.2	239	10	US-09-764-860-216
16	20.6	50.2	366	10	US-09-783-590-4787
17	20.6	50.2	2750	10	US-09-905-983-51
18	20.6	50.2	4000	10	US-09-954-456-2153
19	20.6	50.2	4000	10	US-09-880-107-3803

20	20.4	49.8	1698	10	US-09-815-242-7770	Sequence 7770, Ap
21	20.4	49.8	6143	10	US-09-880-107-1536	Sequence 1536, Ap
22	20.4	49.8	9775	10	US-09-751-962-1	Sequence 1, Appl1
23	20.4	49.8	9934	10	US-09-751-962-2	Sequence 2, Appl1
24	20.2	49.3	435	10	US-09-864-761-15679	Sequence 15679, A
25	20.2	49.3	967	10	US-09-764-877-2209	Sequence 2209, Ap
26	20.2	49.3	1488	10	US-09-863-475A-9	Sequence 9, Appl1
27	20.2	49.3	1966	9	US-09-764-868-152	Sequence 152, App
28	20.2	49.3	2466	12	US-10-044-090-251	Sequence 251, App
29	20.2	49.3	3387	10	US-09-789-481C-3	Sequence 3, Appl1
30	20.2	49.3	3647	10	US-09-863-475A-7	Sequence 7, Appl1
31	20.2	49.3	3900	10	US-09-789-481C-1	Sequence 1, Appl1
32	20	48.8	179	10	US-09-783-590-280	Sequence 280, App
33	20	48.8	491	9	US-09-854-133-305	Sequence 305, App
34	20	48.8	491	10	US-09-738-973-305	Sequence 305, App
35	20	48.8	1809	9	US-10-124-429-3	Sequence 3, Appl1
36	20	48.8	5597	10	US-09-895-072-4	Sequence 4, Appl1
37	20	48.8	5597	10	US-09-986-552-4	Sequence 4598, Ap
38	19.8	48.3	430	10	US-09-960-352-4598	Sequence 1603, Ap
39	19.8	48.3	463	10	US-09-764-869-1603	Sequence 9336, Ap
40	19.8	48.3	578	10	US-09-864-761-9336	Sequence 11, Appl
41	19.8	48.3	658	9	US-09-883-152-11	Sequence 1, Appl1
42	19.8	48.3	1002	9	US-09-995-225-1	Sequence 3, Appl1
43	19.8	48.3	1002	9	US-09-990-940-3	Sequence 1473, Ap
44	19.8	48.3	1051	10	US-09-917-800A-1473	Sequence 131, App
45	19.8	48.3	1436	9	US-09-975-719-131	

ALIGNMENTS

RESULT 1
US-09-983-965-4927
; Sequence 4927, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983, 965
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465, 231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113, 678
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 4927
; LENGTH: 410
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 25-LIB34-026-Q1-E1-G9
US-09-983-965-4927

Query Match 56.1%; Score 23; DB 10; Length 410;
Best local Similarity 74.4%; Pred. No. 16;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 GGGCACCAGCGACGCGCCCAAGGCTGCGCCCGAGC 40
||||| || ||| ||||| || ||||| |||||
Db 10 GGGGCCCCAAGCAGCAGGCTGGCAGGCGCTGGCCCTGAGC 48

RESULT 2
US-10-026-188-6/C
; Sequence 6, Application US/10026188
; Patent No. US20020164645A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.

```
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; TITLE OF INVENTION: Ion Channel
; FILE REFERENCE: 02307E-114910US
; CURRENT APPLICATION NUMBER: US/10/026,188
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/259,379
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 155074
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human genomic region containing ltrpc5
; OTHER INFORMATION: (Human Chromosome 11p15.5 PAC clone pDJ915f1
; OTHER INFORMATION: containing KVLQT1 gene)
; US-10-026-188-6
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Query Match          54.1%; Score 22.2; DB 9; Length 155074;
Best Local Similarity 77.1%; Pred. No. 29;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY 6 CACCGAGCGCAGGCCCAAGGCTCTGGCCCCCGAGC 40
    1 11111111111111111111111111111111
Db 51942 CTCCAGCCCGCAGCCAGGCTCTGCGCCCGCAGTGC 51908
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RESULT 3

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US-09-815-242-7871
; Sequence 7871, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7871
; LENGTH: 2622
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2622)
; US-09-815-242-7871
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Query Match          53.7%; Score 22; DB 10; Length 2622;
Best Local Similarity 73.7%; Pred. No. 34;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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    11111111111111111111111111111111
Db 1228 GCGCGCGACTCGAGGCCCAAGGGCTTGGCCCGAGCGCG 1265
```

RESULT 4

```
US-09-960-352-3868
; Sequence 3868, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 3868
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 17-LIB3058-018-Q1-K1-E9
; US-09-960-352-3868
```

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Query Match          53.2%; Score 21.8; DB 10; Length 440;
Best Local Similarity 70.7%; Pred. No. 40;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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```
QY 1 GGGGGCACCAGCGCGCAGGCCCAAGGCTCTGGCCCCCGAGCG 41
    11111111111111111111111111111111
Db 22 GGGGGCGCGCAGCGCGCAGCGCAGCGAGCGCGCGGCGCTGAGCG 62
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RESULT 5

```
US-09-764-877-2208/c
; Sequence 2208, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2208
; LENGTH: 967
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-877-2208
```

```
Query Match          53.2%; Score 21.8; DB 10; Length 967;
Best Local Similarity 78.8%; Pred. No. 39;
Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 8 CCGAGCGCAGGCCCAAGGCTCTGGCCCCCGAGCG 40
    11111111111111111111111111111111
Db 543 CCTCCTCAGACCGCAGGGGCTGTGGCCCCCGCAGC 511
```

RESULT 6

```
US-09-294-093B-3768
; Sequence 3768, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
```



```

; APPLICANT: Ialqudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294, 093B
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 3768
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700282543H2
; LOCATION: 2, 19, 27, 35, 46, 51-52, 57, 102, 119, 122, 124, 127, 131, 165, 185,
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-3768
```

```

Query Match          51.7%; Score 21.2; DB 10; Length 224;
Best Local Similarity 74.3%; Pred. No. 63;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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```

QY 7 ACCGAGCGCAGGCCCAAGGCTGTGGCCCGAGCG 41
    | | | | | | | | | | | | | | | | | |
Db 138 AGCTGGCGCAGGCCCAAGGCTATCGACNCCCGCG 172
```

```

RESULT 7
US-09-974-298-64
; Sequence 64, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Huel-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 64
; LENGTH: 3667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 234537.3
US-09-974-298-64
```

```

Query Match          51.7%; Score 21.2; DB 9; Length 3667;
Best Local Similarity 76.5%; Pred. No. 62;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```

QY 2 GGGGACCGAGCGCAGGCCCAAGGCTGTGGCCCG 35
    | | | | | | | | | | | | | | | | | |
Db 65 GGGGACCGAGCGCAGGCCCGCTAGCTGTGCCCC 98
```

```

RESULT 8
US-09-864-761-1226/c
; Sequence 1226, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
```

```

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1226
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006328.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 9.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 8.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.6
US-09-864-761-1226
```

```

Query Match          50.7%; Score 20.8; DB 10; Length 487;
Best Local Similarity 70.0%; Pred. No. 85;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```

QY 2 GGGGACCGAGCGCAGGCCCAAGGCTGTGGCCCGAGCG 41
    | | | | | | | | | | | | | | | | | |
Db 186 GGGGACCGAGCGCAGGCCCGTCAAGAGTCTGAGCCAGGTGAG 147
```

```

RESULT 9
US-09-764-877-2858
; Sequence 2858, Application US/09764877
```

```
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 2858
; LENGTH: 946
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-877-2858

Query Match          50.7%; Score 20.8; DB 10; Length 946;
Best Local Similarity 70.0%; Pred. No. 85;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      2 GGGGCACCGAGCGCGCCCAAGGCTCTGGCCCCGAGCG 41
        ||||| | | | | | | | | | | | | | | | | |
DB      185 GGGGCACCGAGCGCGCCCAAGAGTCTGAGCCAGGTGAG 224

RESULT 10
US-09-799-777-134/C
; Sequence 134, Application US/09799777
; Patent No. US20020091244A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; Hillman, Jennifer L.
; Corley, Neil C.
; Guegler, Karl J.
; Baugh, Mariah
; Sather, Susan
; Shah, Purvi
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/799,777
; FILING DATE: 06-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,485
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BILLINGS, LUCY J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0459 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 845-4166
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT21
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; CLONE: 2518547
; SEQUENCE DESCRIPTION: SEQ ID NO: 134 :
; US-09-799-777-134

Query Match          50.7%; Score 20.8; DB 10; Length 2033;
Best Local Similarity 70.0%; Pred. No. 85;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      1 GGGGCACCGAGCGCGCCCAAGGCTCTGGCCCCGAGC 40
        |||| | | | | | | | | | | | | | | | | |
DB      371 GGGGACACTGGCGCGGAATCAAGGCTGTGACACTGAGC 332

RESULT 11
US-09-947-316-3/C
; Sequence 3, Application US/09947316
; Patent No. US20020103339A1
; GENERAL INFORMATION:
; APPLICANT: Jennifer L. Hillman
; APPLICANT: Preeti Lal
; APPLICANT: Neil C. Corley
; APPLICANT: Karl J. Guegler
; APPLICANT: Chandra Paterson
; TITLE OF INVENTION: INTERFERON-RESPONSIVE PROTEIN
; FILE REFERENCE: PF-0459-1 CIP
; CURRENT APPLICATION NUMBER: US/09/947,316
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/157,091
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 2033
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 2518547
; US-09-947-316-3

Query Match          50.7%; Score 20.8; DB 10; Length 2033;
Best Local Similarity 70.0%; Pred. No. 85;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      1 GGGGCACCGAGCGCGCCCAAGGCTCTGGCCCCGAGC 40
        |||| | | | | | | | | | | | | | | | | |
DB      371 GGGGACACTGGCGCGGAATCAAGGCTGTGACACTGAGC 332

RESULT 12
US-10-044-090-777/C
; Sequence 777, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 777
; LENGTH: 2033
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 2518547CB1
; US-10-044-090-777

Query Match          50.7%; Score 20.8; DB 12; Length 2033;
Best Local Similarity 70.0%; Pred. No. 85;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

OY 1 GGGGGCACCAGCGAGCCCAAGGGTCTGGCCCCGAGC 40
||| ||| | | | | | | | | | | | | | | | |
Db 371 GGGGACACTGGCGCGGATCAAGGGTCTGGACACTGAGC 332

RESULT 13
US-09-819-104A-3/c

; Sequence 3, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 7521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7521)
US-09-819-104A-3

Query Match 50.7%; Score 20.8; DB 9; Length 7521;
Best Local Similarity 70.0%; Pred. No. 84;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 2 GGGGACCGAGCGCAGGCCCAAGGGTCTGGCCCCGAGCG 41
|| ||| ||| ||| ||| ||| | | | | | | | | | |
Db 4577 GGCTTACCCAGCTCAGGCACATGACCGGGCGCGCGCG 4538

RESULT 14
US-09-819-104A-1/c

; Sequence 1, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8686
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)..(7677)
US-09-819-104A-1

Query Match 50.7%; Score 20.8; DB 9; Length 8686;
Best Local Similarity 70.0%; Pred. No. 84;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 2 GGGGACCGAGCGCAGGCCCAAGGGTCTGGCCCCGAGCG 41
|| ||| ||| ||| ||| ||| | | | | | | | | | |
Db 4733 GGCTTACCCAGCTCAGGCACATGACCGGGCGCGCGCG 4694

RESULT 15
US-09-764-860-216

; Sequence 216, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-860-216

Query Match 50.2%; Score 20.6; DB 10; Length 239;
Best Local Similarity 74.3%; Pred. No. 99;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 5 GCACCGAGCGCAGGCCCAAGGGTCTGGCCCCGAG 39
||| ||| ||| ||| ||| | | | | | | | | | |
Db 72 GCACCGAGGTCAAGCAGAGGCCAGAGCGCCGAG 106

Search completed: February 13, 2003, 07:51:28
Job time : 54.8205 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 15, 2003, 13:41:57 ; Search time 47 Seconds

(without alignments)
1275.804 Million cell updates/sec

Title: US-09-636-259B-4

Perfect score: 2380
Sequence: 1 MGSLQPPAGNASWNGTEAPG.....HDFRRAFKKILCRGDRKRIV 450

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2380	100.0	450	22	AAM52123	Human alpha-2AAR v
2	2375	99.8	450	22	AAM52122	Human alpha-2AAR p
3	1553	65.3	324	10	AAP90552	Hamster beta-2 -ad
4	1537	64.6	330	15	AAR48700	G-protein coupled
5	1537	64.6	330	17	AAW02672	G-protein coupled
6	1523	64.0	334	15	AAR48701	G-protein coupled
7	1523	64.0	334	17	AAW02673	G-protein coupled
8	1454.5	61.1	307	22	AAU08334	Human alpha 2 adre
9	1171	49.2	458	15	AAR54834	Human derived adre
10	1159.5	48.7	461	22	AAM52124	Human alpha-2CAR p

11	1150.5	48.3	457	22	AAM52126	Human alpha-2CAR v
12	1126.5	47.3	450	22	AAM52117	Human alpha-2BAR t
13	1126.5	47.3	450	22	AAE00990	Human alpha2B-adre
14	1126	47.3	447	22	AAM52118	Human alpha-2BAR t
15	1094.5	46.0	487	12	AAE00989	Human alpha2B-adre
16	1094.5	46.0	487	18	AAW11804	Human alpha 2 beta
17	1094.5	46.0	487	18	AAW11804	Human alpha-2b adr
18	1046.5	44.0	330	15	AAR48698	G-protein coupled
19	1046.5	44.0	330	17	AAW02670	G-protein coupled
20	1029	43.2	330	15	AAR48699	G-protein coupled
21	1029	43.2	330	17	AAW02671	G-protein coupled
22	895	37.6	437	22	AAB99035	Sheep/guinea pig c
23	681.5	28.6	379	18	AAW33185	Corn barnacle G-pr
24	652	27.4	476	18	AAW24089	Balanus amphitrite
25	649	27.3	601	13	AAR21931	D.melanogaster oot
26	649	27.3	601	22	ABB63318	Drosophila melanog
27	649	27.3	601	23	AAG80701	D. melanogaster oc
28	649	27.3	601	23	AAE17036	Drosophila melano
29	627	26.3	414	12	AAR11800	Human retinal dopa
30	621.5	26.1	443	11	AAR05541	Human pituitary do
31	621.5	26.1	443	12	AAR11497	Human dopamine D2 r
32	621.5	26.1	443	20	AAV01600	Human D2 dopamine
33	621.5	26.1	443	22	AAU76292	Human dopamine rec
34	621.5	26.1	443	22	AAAB69075	Human D2 dopamine
35	621.5	26.1	443	23	AAM51019	Human D2 dopamine
36	618.5	26.0	415	11	AAR05539	Rat D2 dopamine re
37	618.5	26.0	415	20	AAV01598	Rat D2 dopamine re
38	617.5	25.9	415	17	AAW09388	Mouse dopamine D2
39	615.5	25.9	415	22	AAU08332	Rat D2 dopamine re
40	615.5	25.9	415	23	AAM51017	Rat D2 dopamine re
41	614.5	25.8	443	22	ABB56348	Non-endogenous hum
42	613	25.8	444	12	AAR10544	D2 dopamine recept
43	613	25.8	444	17	AAW09387	Mouse dopamine D2
44	590	24.8	422	22	AAB70249	HTR1A protein. Ho
45	589	24.7	637	20	AAV13445	Invertebrate octop

ALIGNMENTS

RESULT 1	
AAM52123	
ID	AAM52123 standard; Protein; 450 AA.
XX	
AC	AAM52123;
XX	
DT	18-FEB-2002 (first entry)
XX	
DE	Human alpha-2AAR variant protein.
XX	
KW	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW	polymorphic site; allelic variant; cardiovascular disease;
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW	phosphorylation; inositol phosphate; alpha-2AAR.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Misc-difference 251
XX	
PN	WO200179561-A2.
XX	
PD	25-OCT-2001.
XX	
PF	17-APR-2001; 2001WO-US12575.
XX	
PR	17-APR-2000; 2000US-0551744.
PR	10-AUG-2000; 2000US-0636259.
PR	19-OCT-2000; 2000US-0692077.
XX	
PA	(LIGG/) LIGGETT S B.
PA	(SMAL/) SMALT K M.

XX Liggett SB, Small KM;
PI WPI; 2001-611728/70.
XX N-PSDB; AAI99918.
DR
DR
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
PS Claim 48; Page 154-155; 163pp; English.

The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising: (a) obtaining a sample having a polynucleotide encoding an alpha-2B, alpha2A or alpha2C or fragment or complement of; and (b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (II) or a site comprising (A) (ggggcgggccg) or (B) (ggggcggtgag) at positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the human alpha-2AAR variant protein.

..... SQ Sequence 450 AA;

Query Match	100.0%;	Score 2380;	DB 22;	Length 450;
Best Local Similarity	100.0%;	Pred. No. 3.3e-172;		
Matches 450;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MSLQPDAGNASWNGTEAPGGGARATPYSLOVTLTLVCLAGLMLLTFEGNVLIIAVFT	60
Db	1	MSGLQPDAGNASWNGTEAPGGGARATPYSLOVTLTLVCLAGLMLLTFEGNVLIIAVFT	60
QY	61	SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFGKAWCEIYLALDVLFTSS	120
Db	61	SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFGKAWCEIYLALDVLFTSS	120
QY	121	IYHLCALSLDRYWSITQALIEYNLKRTPRIRAKIITVWVISAVISFPPLISIEKKGGGGG	180
Db	121	IYHLCALSLDRYWSITQALIEYNLKRTPRIRAKIITVWVISAVISFPPLISIEKKGGGGG	180
QY	181	POPAPRCEINDOKWYIYSSCIGSFAPCLIMILYVRIOIAKRRTRVPPSRGPDAYA	240
Db	181	POPAPRCEINDOKWYIYSSCIGSFAPCLIMILYVRIOIAKRRTRVPPSRGPDAYA	240
QY	241	APPGTERRPKGLGPERSAAGPGAFAEPLPTOLNGAPGEPAPAGPRDLDLDESSSSD	300
Db	241	APPGTERRPKGLGPERSAAGPGAFAEPLPTOLNGAPGEPAPAGPRDLDLDESSSSD	300
QY	301	HAERPPGPRRPERGPRGCKAKARASQVKPGDSLBRGPGATGIGTPAGPGEEERVGAAKAS	360
Db	301	HAERPPGPRRPERGPRGCKAKARASQVKPGDSLBRGPGATGIGTPAGPGEEERVGAAKAS	360
QY	361	RWRGQNRKREKRTFVLAVVIGVFVVCWPFPEFTYTLTAVGCSVPRLTEKFFWFYGCNSS	420
Db	361	RWRGQNRKREKRTFVLAVVIGVFVVCWPFPEFTYTLTAVGCSVPRLTEKFFWFYGCNSS	420
QY	421	LNPLYTIFENHDFRAAFKKLICRGDRKRIV	450

Db 421 LNPVIYTIENHDFRAFKKILCRGDKRIV 450

RESULT 2	
AAM52122	
ID	AAM52122 standard; Protein; 450 AA.

AC AAM52122;

DT 18-FEB-2002 (first entry)

Human alpha-2AAR protein.

AA Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW phosphorylation; inositol phosphate; alpha-2AAR.

... Homo sapiens.

PN WO200179561-A2

PD 25-OCT-2001.

PF 17-APR-2001; 2001WO-US12575.

PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.

PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.

PI Liggett SB, Small KM;

DR WPI; 2001-611728/70.

DR N-PSDB; AAI99917.

aa Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -

PS Claim 48; Page 152-154; 163pp; English.

The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising:
(a) obtaining a sample having a polynucleotide encoding an alpha-2B, alpha-2A or alpha-2C or fragment or complement of; and
(b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (II) or a site comprising (A) (ggggcggggcg) or (B) (ggggcgctgag) at positions 961-972 of (III). The method may be used for genotyping an alpha-2B, alpha-2A or alpha-2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha-2B, alpha-2A or alpha-2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha-2B, alpha-2A, or alpha-2C agonist (e.g. ephedrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the human alpha-2AAR protein.

... SQ Sequence 450 AA;

Query Match	99.8%;	Score 2375;	DB 22;	Length 450;
Best Local Similarity	99.8%;	Pred. No. 8e-172;		
Matches 449; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

```
OY      1  MGSIQPDAGNASWNGTEAPGGGARATPYSLOVTLTLVCLAGLMLLTVEGNVLIIVFT  60
      1  |||||||
Db      1  MGSIQPDAGNASWNGTEAPGGGARATPYSLOVTLTLVCLAGLMLLTVEGNVLIIVFT  60
OY      61  SRAIKAPQNLFLVSLASADILVATLVIPFSLANEVWGMYFGKAWCEIYLADVLCTSS  120
      1  |||||||
Db      61  SRAIKAPQNLFLVSLASADILVATLVIPFSLANEVWGMYFGKAWCEIYLADVLCTSS  120
OY      121  IVHLCAISLDRYWSITQAI EYNLKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGG  180
      1  |||||||
Db      121  IVHLCAISLDRYWSITQAI EYNLKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGG  180
OY      181  PQPAEPRCEINDQKWYVISSCIGSFAPCLIMLVVRIYQIAKRRTVPSPRRGPDAVA  240
      1  |||||||
Db      181  PQPAEPRCEINDQKWYVISSCIGSFAPCLIMLVVRIYQIAKRRTVPSPRRGPDAVA  240
OY      241  APPGCTERRPKGLGPERGAGPGAEAEPLPTQLNGAPGEPAPAGPRDTDALDLESSSSD  300
      1  |||||||
Db      241  APPGCTERRPKGLGPERGAGPGAEAEPLPTQLNGAPGEPAPAGPRDTDALDLESSSSD  300
OY      301  HAERPPGPRRPERGPRGKGKARASQVKPGDSLPRRGPGATGIGTPAAGPGEERVGAAKAS  360
      1  |||||||
Db      301  HAERPPGPRRPERGPRGKGKARASQVKPGDSLPRRGPGATGIGTPAAGPGEERVGAAKAS  360
OY      361  RWRGRONREKRTFVLAVVIGVFVVCWPFPEFTYTLTAVGCSVPRTLKFFWFGYCNS  420
      1  |||||||
Db      361  RWRGRONREKRTFVLAVVIGVFVVCWPFPEFTYTLTAVGCSVPRTLKFFWFGYCNS  420
OY      421  LNPVIYTIENHDFRRAFKKILCRGDRKRIY  450
      1  |||||||
Db      421  LNPVIYTIENHDFRRAFKKILCRGDRKRIY  450
```

```
RESULT 3
AAP90552
ID      AAP90552 standard; protein; 324 AA.
XX
AC      AAP90552;
XX
DT      16-FEB-1990 (first entry)
XX
DE      Hamster beta-2 -adrenergic receptor.
XX
KW      Alpha-2 -adrenergic receptor; 5HT1c receptor.
OS      Homo sapiens.
XX
FH      Key
FT      Domain
FT      /label=I
FT      /note="transmembrane domain"
FT      70..90
FT      /label=II
FT      /note="transmembrane domain"
FT      107..128
FT      /label=III
FT      /note="transmembrane domain"
FT      148..172
FT      /label=IV
FT      /note="transmembrane domain"
FT      192..215
FT      /label=V
FT      /note="transmembrane domain"
FT      249..271
FT      /label=VI
FT      /note="transmembrane domain"
FT      281..303
FT      /label=VII
FT      /note="transmembrane domain"
FT      227
FT      /note="125 bp cytoplasmic loop"
XX
```

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PN      W08918149-A.
XX
PD      08-SEP-1989.
XX
PF      28-FEB-1989; 89WO-US00808.
XX
PR      29-FEB-1988; 88US-0162654.
XX
PA      (UYCO-) COLUMBIA UNIVERSITY.
XX
PI      Axel R, Jessell TM;
XX
DR      WPI; 1989-278308/38.
XX
PT      DNA encoding serotonin 5HT1c receptor - used for producing protein,
PT      antibodies and probes for studying receptor binding and screening drugs.
XX
PS      Disclosure; Fig 11; 84pp; English.
XX
CC      Sequence codes for human alpha 2 adrenergic receptor.
CC      See also AAP90549-P90554, AAP92111 and AAN90955.
XX
SQ      Sequence 324 AA;
```

Query Match 65.3%; Score 1553; DB 10; Length 324;
Best Local Similarity 70.4%; Pred. No. 9.8e-110;
Matches 317; Conservative 0; Mismatches 7; Indels 126; Gaps 4;

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OY      1  MGSIQPDAGNASWNGTEAPGGGARATPYSLOVTLTLVCLAGLMLLTVEGNVLIIVFT  60
      1  |||||||
Db      1  MGSIQPDAGNASWNGTEAPGGGARATPYSLOVTLTLVCLAGLMLLTVEGNVLIIVFT  60
OY      61  SRAIKAPQNLFLVSLASADILVATLVIPFSLANEVWGMYFGKAWCEIYLADVLCTSS  120
      1  |||||||
Db      61  SRAIKAPQNLFLVSLASADILVATLVIPFSLANEVWGMYFGKTWCEIYLADVL-CTSS  119
OY      121  IVHLCAISLDRYWSITQAI EYNLKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGG  180
      1  |||||||
Db      120  IVHLCAISLDRY-SITQAI EYNLKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGG  178
OY      181  PQPAEPRCEINDQKWYVISSCIGSFAPCLIMLVVRIYQIAKRRTVPSPRRGPDAVA  240
      1  |||||||
Db      179  PQPAEPRCEINDQKWYVISSCIGSFAPCLIMLVVRIYQIAKRRT-
OY      241  APPGCTERRPKGLGPERGAGPGAEAEPLPTQLNGAPGEPAPAGPRDTDALDLESSSSD  300
      1  |||||||
Db      227  -----
OY      301  HAERPPGPRRPERGPRGKGKARASQVKPGDSLPRRGPGATGIGTPAAGPGEERVGAAKAS  360
      1  |||
Db      227  -----XSGIDPRRRAGA----- 237
OY      361  RWRGRONREKRTFVLAVVIGVFVVCWPFPEFTYTLTAVGCSVPRTLKFFWFGYCNS  420
      1  |||||||
Db      238  ---GGQNRKERTFVLAVVIGVFVVCWPFPEFTYTLTAVGCSVPRTLKFFWFGYCNS  294
OY      421  LNPVIYTIENHDFRRAFKKILCRGDRKRIY  450
      1  |||||||
Db      295  LNPVIYTIENHDFRRAFKKILCRGDRKRIY  324
```

```
RESULT 4
AAR48700
ID      AAR48700 standard; Protein; 330 AA.
XX
AC      AAR48700;
XX
DT      05-JUN-1996 (first entry)
XX
DE      G-protein coupled human alpha-2 C10 adrenergic receptor protein.
KW      G-protein coupled receptor; ligand binding assay; transmembrane domain;
KW      psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin;
```

KW	muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
KW	rhodopsin; opsin; odorant; cytomegalovirus.
OS	Homo sapiens.
XX	
PN	WO9405695-A1.
XX	
PD	17-MAR-1994.
XX	
PF	09-SEP-1993; 93WO-US08528.
XX	
PR	10-SEP-1992; 92US-0943236.
XX	
PA	(UYNY) UNIV NEW YORK STATE.
XX	
PI	Murphy RB, Schuster DI;
XX	
DR	WPI; 1994-101120/12.
PT	Polypeptides of G-coupled receptor proteins (GPRs) - useful for
PT	binding GPR ligands or modulating GPR binding
XX	
PS	Disclosure; Page 73-74; 160pp; English.
XX	
CC	Proteins AAR48685-R48758 represent a range of G-protein coupled receptor
CC	proteins selected from CAMP, adenosine, muscarinic acetylcholine,
CC	adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
CC	odorant, cytomegaloviral and other G-protein coupled receptors. The
CC	receptor proteins were used to design polypeptides, pref. based on the
CC	transmembrane domains, for use in G-protein coupled receptor ligand
CC	binding assays. The polypeptide fragments retain biological activity
CC	such as binding a GPR ligand or modulating GPR ligand binding to a GPR
CC	(see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples
CC	of polypeptide fragments). The polypeptide fragments can be used in
CC	compositions for treating subjects suffering from a pathology related to
CC	a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
XX	
SQ	Sequence 330 AA;
Query Match	64.6%; Score 1537; DB 15; Length 330;
Best Local Similarity	74.2%; Pred. No. 1.6e-108;
Matches 310; Conservative	7; Mismatches 13; Indels 88; Gaps 6;
QY	33 TLTLVCLAGLLMLLTVEGNVLVITAVFTSRALKAPQNLFVLSASADILVATLVIPFSLA 92
DB	1 TLTLVCLAGLLMLLTVEGNVLVITAVFTSRALKAPQNLFVLSASADILVATLVIPFSLA 58
QY	93 NEVMGWYEGKAWCEIYALDVLCTSSIVHLCAISLDRYWSITQALEYNLKRTPRIKA 152
DB	59 NEVMGWYEGKAWCEIYALDVLCTSSIVHLCAISLDRYWSITQALEYNLKRTPRIKA 117
QY	153 IITVWVISAVISFPLISIEKKGGGGPQPAEPRCEINDQKWYVSISSCIGSFAPCLIM 212
DB	118 IITVWVISAVISFPLISIEKKGGGGPQPAEPRCEINDQKWYVSISSCIGSFAPCLIM 177
QY	213 ILVYVRIYQIAKRRTRVPPSRGPDVAAPPGTERRPKGLGPERSAGPGGAELPLPTQ 272
DB	178 ILVYVRIYQIAKRRTRVPPSRGPDVAAPPGTERRPKGLGPERSAGPGGAELPLPTQ 227
QY	273 LINGAPGEPAAPGPRDTALDLESSSSDHAERPPGPRRPERGPRGKGARASQVKPGDSL 332
DB	228 LINGAPGEPAAPGPRDTALDLESSSSDHAERPPGPRRPERGPRGKGARASQVKPGDSL 236
QY	333 PRRGPATGIGTPAAGGGEERVGAAKASRRRGQRNREKRTFVLAVVIGVFWCWPPEFF 392
DB	237 PRRRAGA-----GGQNRKRTFVLAVVIGVFWCWPPEFF 272
QY	393 TYTLFAVGSVPRTLKFFFWFGYCNSSINPVIYTIENHDFRAAFKKILCRGDRKRIV 450
DB	273 TYTLFAVGSVPRTLKFFFWFGYCNSSINPVIYTIENHDFRAAFKKILCRGDRKRIV 330

AAW02672	ID	AAW02672 standard; peptide; 330 AA.
XX	AC	AAW02672;
XX	DT	12-NOV-1996 (first entry)
XX	DE	G-protein coupled human alpha-2 C10 adrenergic receptor.
KW	KM	G-protein coupled receptor; ligand binding assay; transmembrane domain; schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin; muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin; odorant; cytomegalovirus; serotonergic.
OS	OS	Homo sapiens.
PN	PN	US508384-A.
PD	PD	16-APR-1996.
PF	PF	10-SEP-1992; 92US-0943236.
PR	PR	09-SEP-1993; 93US-0118270. 10-SEP-1992; 92US-0943236.
PA	PA	(UYNV) UNIV NEW YORK STATE.
PI	PI	Murphy RB, Schuster DI;
DR	DR	WPI; 1996-208785/21.
PT	PT	New dopamine receptor peptide - useful as antipsychotic agent, e.g. for treating schizophrenia
PS	PS	Disclosure; Column 71-74; 184pp; English.
CC	CC	Proteins AAW02657-W02720 represent a range of G-protein coupled receptor (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endothelin, bombesin, rhodopsin, opsin, odorant, cytomegaloviral and other GPR proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. CC The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAW02747-W02999 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
Seq	Seq	Sequence 330 AA;
Query Match	Query Match	64.6%; Score 1537; DB 17; Length 330;
Best Local Similarity	Best Local Similarity	74.2%; Pred. No. 1.6e-108;
Matches 310; Conservative	Matches 310; Conservative	7; Mismatches 13; Indels 88; Gaps 6;
QY	QY	33 TLTVLCIAGLLMLLTVEGNVLIIAVFTSRALKAPONLFLVSLASADILVATLVIPESLA 92 : :
Db	Db	1 TLTVCIA--CLSLTFEGNVLIIAVFTSRALKAPONLFLVSIASADILVATLVIPESLA 58
QY	QY	93 NEVMGYWEKAMCEIYLALDVLFCTSSIVHLCAISLDRYWSITQAIEYNLKRTPRIKA 152
Db	Db	59 NEVNGWYFGK-WCEIYLLADVLFCTSSIVHLCALSIDRYWSITQAIEYNLKRTPRIKA 117
QY	QY	153 IITVWVISAVISFPPLISIEKKGGGGGPQPAEPRCEINDQKWYVISSCTGSFFAPCLIM 212
Db	Db	118 IITVWVISAVISFPPLISIEKKGGGGGPQPAEPRCEINDQKWYVISSCTGSFFAPCLIM 177
QY	QY	213 ILVVYRIQIAKRTRVPSPRRGPDVAVAPPGETERRPKGLGPERSAAGAEAPLPQTQ 272
Db	Db	178 -LVYVRIQIAKRTRVPSPRRGPDVAVAPPGETERRPGLGPERSAAGPG----- 227
QY	QY	273 LMGAPGEAPDAGPRDTDLLEESSSSSDHAERPPGRPRPERGPRGKGARASQVKPGDSL 332 :: :


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Db      228  -----GRGRS-----ASGL 236

QY      333  PRPGGATGIGTPAAGPGEERVGAKAASRWGRONREKRETFVLAVIGVFVWCWEPPEF 392
      |||  ||  |  |||||:|||||
Db      237  PRRRAGA-----GGONREKRETFVLAVIGVFVWCWEPPEF 272

QY      393  TYTLTAVGGSVPRTLKFEFFWFGCNSSLNPVIYTIENHDFRAAFKKILCRGDRKRIV 450
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      273  TYTLTAVGGSVPRTLKFEFFWFGCNSSLNPVIYTIENHDFRAAFKKILCRGDRKRIV 330

```

RESULT 6
AAR48701
ID AAR48701 standard; Protein; 334 AA.

DT	05-JUN-1996	(first entry)
XX		
DE	G-protein coupled rat alpha-2 adrenergic receptor R20 protein.	

KW G-protein coupled receptor; ligand binding assay; transmembrane domain;;
 KW psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin;;
 KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
 KW rhodopsin; opsin; odorant; cytomegalovirus.

05 Rattus rattus.

PN W09405695-A1

PD 17-MAR-1994.

PF 09-SEP-1993; 93WO-US08528.

PR 10-SEP-1992; 92US-0943236.

PA (UYNY) UNIV NEW YORK STATE.

PI Murphy RB, Schuster DI;

DR WPI; 1994-101120/12.

PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for
PT binding GPR ligands or modulating GPR binding

PS Disclosure; Page 74-75; 160pp; English.

Proteins AAR48685-R48758 represent a range of G-protein coupled receptor proteins selected from cAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomegaloviral and other G-protein coupled receptors. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.

50 Sequence 334 AA;

Query Match	64.0%;	Score 1523;	DB 15;	Length 334;
Best Local Similarity	71.6%;	Pred. NO. 1.9e-107;		
Matches 300;	Conservative 10;	Mismatches 23;	Indels 86;	Gaps 3;

QY	33	TLTVCLAGLMLLTVFEGNVLIIVAFSTRALKAPQNLFFVSLASADILVATLVIPESLA	92
	:		
Ddb	1	TLTVLCIAGLIMLTFVEGNVLIIVAFSTRALKAPQNLFFVSLASADILVATLVIPESLA	60

```
OY      93 NEVMGYWFGKAMCEIYLALDVLECTSSIVHLCAISLDRWYSITQAIENLNKRTPRTKA    152
        ||||| ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Ddb     61 NEVM-YWFEKGWVCEIYLALDVLECTSSIVHLCAISLDRWYSITQAIENLNKRTPRRRKA    119
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OY	153	IITWVWISAVISFPP-LISIEKKGCGGQPDPAEPRCEINDQKWVISSICIGSFAPCLI	211
	120	IIVTWVISAVISFPPLISIEKKAGAGGGQDPAEPSCKINDQKWVISSISIGSFAPCLI	179
OY	212	MILVVRIYQIAKRRTRVPPSRRGPDAVAABPGCTERRRPGLGPERSAGPGAELPT	271
Dd	180	NHLVYVRITYQIAKRRTRVPPSRRGPDACSAPBGADRRPNVAVGERGATAG-----	231
OY	272	QLNGAPEPAPAGPRDTDALDLSESSSDHAERPPGPRRPERGPRGCKARASQVKPGDS	331
Dd	232	-----	231

Db 180 NHTLVYVRIYQIAKRRTRVPPSRRGPDACSAPPGGADRRPNAVGPARGAGTAG----- 231

QY 272 QLINGGEPAPAGPRDLDLESSSDHAERPGRPRPERGPRGKGKARASQVKPGDS 331

Db 232 231

QY 332 LPRGPGATGIGTPAAGPGEERVGAAKASRWRGRQNRKREFTVLAVVIGVFVVCWEPFF 391

Db 232 -----GQGERAGGAKASRWGRGRNREREKRTFVIAVIGVFVVCWEPFF 275

QY 392 FTYTLTAVGCSVPRTLEKFFFWGCGCNSSLNPVIYTIENHDFRAFKKILCRGDRKRIY 450

Db 276 ETTYTLIAGCPVYQLENEFFWEGCNSLNPIYTIENHDFRAFKKILCRGDKRIV 334

RESULT 7	
AAW02673	
ID	AAW02673 standard; peptide; 334 AA.

AC AAW02673;

DT 12-NOV-1996 (first entry)

DE G-protein coupled rat alpha-2 adrenergic receptor.

KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW schizophrenia; dopamine; CAMP; adenosine; thrombin; adrenergic; opsin;
 KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
 KW odorant; cytomegalovirus; serotonergic.

OS *Rattus rattus*.

PN US5508384-A.

PD 16-APR-1996.

PF 10-SEP-1992; 92US-0943236.

PR 09-SEP-1993; 93US-0118270.

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NEW YORK STATE
STATE OF NEW YORK
COUNTY OF NEW YORK
IN SENATE
January 11, 1911.
REPORT
OF THE
COMMISSIONERS OF THE
LAND OFFICE
IN RESPONSE TO A
RESOLUTION PASSED
BY THE SENATE
MAY 11, 1909.
ALBANY:
J. B. LIPPINCOTT
PRINTERS.
1911.

XXI multiply AB, scissilel DL,

XX
DA
XX
WFL; 1930-2087-21.

new dopamine receptor peptide - useful as antipsychotic agent, e.g. for treating schizophrenia

Disclosure: Column 73-76: English

Proteins AAW02657-W02730 represent a range of G-protein coupled receptor (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomegaloviral and other GPR proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAW02747-W02999 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.

SQ Sequence 334 AA;

Query Match		64.0%;	Score 1523;	DB 17;	Length 334;
Best Local Similarity		71.6%;	Pred. No. 1.9e-107;		
Matches 300;		Conservative 10;	Mismatches 23;	Indels 86;	Gaps 3;
OY	33	TLTIVCLAGLMLLTFVGNVLVIATVTSRALKAPQNLFLVSLASADILVATLVIPESLA	92		
Db	1	TLTIVCLAGLIMLTFVEGNVLVIATVTSRALKAPQNLFLVSIASADILVATLVIPESLA	60		
OY	93	NEVMGYWYFGKAWCEIYLALDVLFCSTSSIVHLCAISLDRWSTIQAIIEYNLKRTPRIKA	152		
Db	61	NEVM-YWYFGKAWCEIYLADVLFCSTSSIVHLCAISLDRWSTIQAIIEYNLKRTPRIKA	119		
OY	153	IIITVWVISAVISFPP-LISIEKKGGGGPQPAEPCEINDQKWYVIVSSICGSFFAPCLI	211		
Db	120	IIITVWVISAVISFPPLLISIEKKGAGGGOQPAEPSCKINDQKWYVIVSSIGSFFAPCLI	179		
OY	212	MILVYVRIQIAKRRTRVPPSRRGPDAAVAPPGGTERRPKGLGPERSAGPGAFAEPLPT	271		
Db	180	NHLVYVRIQIAKRRTRVPPSRRGPDACAPPGADRRPNNAVGPBERGAGTAG-----	231		
OY	272	QLNGAPGEPADGPRDLDLESSSSSDHAERPPGPRRPERGPRGKGKARASQVKPGDS	331		
Db	232	-----	231		
OY	332	LPRRGPATGIGTPAAGPEERVGAAKASRWGRQNRKRETFEVLAVVIGVFVWCWEPFF	391		
Db	232	-----GQGERAGGAKASRWGRQNRKRETFEVLAVVIGVFVWCWEPFF	275		
OY	392	FTYTLTAVGCSVPRTLKFFEFWFGYCNSLNPVITYTIFNHDFFRAFKKILCRGDRKRIV	450		
Db	276	FTYTLTAVGCPVPYQLNFEEFWFGYCNSLNPVITYTIFNHDFFRAFKKILCRGDRKRIV	334		
RESULT 8					
ID	AAU08334				
XX	AAU08334 standard; Protein; 307 AA.				
XX	AC	AAU08334;			
XX	DT	21-MAY-2002 (first entry)			
XX	DE	Human alpha 2 adrenergic receptor.			
XX	KW	Human; D2 dopamine receptor; RGB-2; antiparkinsonian; hormone secretion;			
KW	KW	G-protein coupled receptor; schizophrenia; drug addiction;			
KW	KW	Parkinson's disease; Tourette syndrome; Tardive dyskinesia;			
XX	XX	receptor; neuroleptic.			
OS	Homo sapiens.				
XX	Key	Location/Qualifiers			
FH	Domain	37..59			
FT		/note= "Transmembrane domain I"			
FT	Domain	71..96			
FT		/note= "Transmembrane domain II"			
FT	Domain	108..129			
FT		/note= "Transmembrane domain III"			
FT	Domain	151..173			
FT		/note= "Transmembrane domain IV"			
FT	Domain	190..213			
FT		/note= "Transmembrane domain V"			
FT	Domain	238..261			
FT		/note= "Transmembrane domain VI"			
FT	Domain	269..292			
FT		/note= "Transmembrane domain VII"			
XX	PN	US6277591-B1.			
XX	PD	21-AUG-2001.			
XX	PF	07-JUN-1995; 95US-0480390.			
XX	XX				

PR 20-NOV-1989; 89US-0438544.
PR 09-NOV-1992; 92US-0973588.
PR 18-NOV-1988; 88US-0273373.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Clivelli O, Bunzow JR, Grandy DK, Machida CA;
XX
DR WPI; 2001-540405/60.

PT New isolated mammalian G-protein coupled D2 dopamine receptor
PT polynucleotide, useful in gene therapy and for treating schizophrenia,
PT drug addiction, Parkinson's disease, Tourette syndrome and Tardive
PT dyskinesia -
XX

PS Claim 1; Fig 2; 71pp; English.

CC This invention relates to the nucleotide and polypeptide sequences of an
CC isolated mammalian G-protein coupled D₂ dopamine receptor. This protein
CC binds to G proteins to inhibit cyclic AMP generation and hormone
CC secretion. The nucleotide sequences of the invention are useful as
CC oligonucleotide probes and to screen nucleic acid libraries containing
CC dopamine receptor nucleic acid sequences. These probes are also useful
CC in hybridisation methods to locate the dopamine gene positions in
CC various mammalian chromosomal maps or to determine the levels of mRNA or
CC receptor concentrations in a sample. The nucleic acid sequences can also
CC be used to identify dopamine receptor gene disorders (defective or
CC aberrant genes) and for in vitro diagnostic procedures on DNA samples in
CC given patients. A composition comprising the nucleic acid may be used
CC for increasing the concentration of the receptor or its gene in a
CC sample, or for in vivo uses such as gene therapy to render a defective
CC gene or gene product inactive or to provide an increased concentration
CC of dopamine receptor in a given location. The nucleotide sequences are
CC useful for treating disease conditions associated with abnormalities in
CC the structure, expression or concentration of the dopamine receptor or
CC its gene, where the disease conditions are selected from neurological
CC and other disorders, including schizophrenia, drug addiction, The
CC Parkinson's disease, Tourette syndrome, and Tardive dyskinesia. The
CC nucleotide sequence is also useful for preparing the corresponding
CC transgenic animals, in particular nonhuman mammals and to inject
CC oocytes from frogs, which can then be conventionally used in binding or
CC second messenger analyses. This sequence represents the human alpha 2
CC adrenergic receptor which has homology to the rat D2 dopamine
CC receptor of the invention.

XX SQ Sequence 307 AA;

Query Match 61.1%; Score 1454.5; DB 22; Length 307;
Best Local Similarity 65.7%; Pred. No. 2.7e-102;
Matches 291; Conservative 7; Mismatches 8; Indels 137; Gaps 1;

OY	1	MGSLQPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLLTFEGNVLIIVFT	60		
Db	1	MGSLQPDQAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLLTFEGNVLIIVFT	60		
OY	61	SRATKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWYFGKAWCEIYLALDVLFCSTSS	120		
Db	61	SRATKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWYFGKTWCEIYLALDVLFCSTSS	120		
OY	121	IVHLCAISLDRWSTIQAIIEYNLKRTPRIKAIITVWVISAVISFPPLLISIEKKGGGG	180		
Db	121	IVHLCAISIQRYWSTIQAIIEYNLKRTPRIKAIITVWVISAVISFPPLLISIEKKGGGG	180		
OY	181	PQPAEPCEINDQKWYVIVSSICGSFFAPCLIMILVYVRIQIAKRTRVPPSRGPDAAV	240		
Db	181	PQPAEPCEINDQKWYVIVSSICGSFFAPXIIMILVYVRIQIAKRTRVP-----	230		
OY	241	APPGTERRPKGLGPERSAAGPGAFAEPLPTQLNGAPGEPAPGPRDTALDLESSSSSD	300		
Db	231	-----	230		
OY	301	HAERPPGPRRPERGPRGKGKARASQVKGDSLPRRGPATGIGTPAAGPEERVGAAKAS	360		

Db 231 ----- 230

QY 361 RWRGRONREKFTFVLAVVIGVFVVCWPEPPEFTYTLTAVGCSVPRTLEKFEFWEFGYCNSS 420

Db 231 -----REKRTFVIADVIGMEFVVCWPEPPEFTYTLTAVGCSVPRTLEKFEFWEFGYCNSS 283

QY 421 LNPVIYTIENHDFRRRAFKILCR 443

Db 284 LNPVIYTIENHDFRRRAFKILCR 306

RESULT 9

AAR54834

ID AAR54834 standard; Protein; 458 AA.

XX

AC AAR54834;

DT 01-FEB-1995 (first entry)

XX

DE Human derived adrenaline alpha 2CII receptor.

XX

KW adrenaline receptor; alpha CII; screening; detection; pharmacology;

KM drugs.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "may or may not be present, but is only present if amino acid residues 2-17 are present"

FT Peptide 2..17

FT /label= "N-terminal_peptide

FT /note= "may or may not be present"

XX

PN JP06121686-A.

XX

PD 06-MAY-1994.

XX

PF 12-OCT-1992; 92JP-0272744.

XX

PR 12-OCT-1992; 92JP-0272744.

XX

PA (ASAH) ASAMI KASEI KOGYO KK.

XX

DR WPI; 1994-185923/23.

DR N-PSDB; AA064890.

XX

PT Adrenaline receptor gene encoding alpha 2CII receptor - for

PT screening drugs reactive to the alpha 2CII receptor

XX

PS Claim 1; Page 9-11; 13pp; Japanese.

XX

CC AA064890 encodes the amino acid sequence of a polypeptide

CC (AAR54834) that constitutes human derived adrenaline alpha 2CII

CC receptor. The DNA can be used for the study of the pharmacological

CC importance of the gene expression in humans.

XX

SQ Sequence 458 AA;

Query Match 49.28; Score 1171; DB 15; Length 458;

Best Local Similarity 52.3%; Pred. No. 1.2e-80;

Matches 252; Conservative 38; Mismatches 102; Indels 90; Gaps 9;

QY 10 NASWNGTEAPGGARAT-----PYSLOYTLTLVCLAGLMLTLVFGNVLIYAVFT 60

Db 19 NASGAGERGSGGVANASGASWGPARGYSAGAVAGLAAVGFLIVETVGNVLVIAYLT 78

QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFGKAWCEIYLALDVLCCTSS 120

Db 79 SRALRAPQNLFLVSLASADILVATLVIPFSLANEIMAYWYFGQVWCGVYLALDVLCCTSS 138

QY 121 IVHLCAISLDRYWSITQAIEYNLKRTPRIKAIITTVWVISAVISFPPLISIEKKGGGG 180

Db 139 IVHLCAISLDRYWSVTQAIVEYNLKRTPRRVKATIVAWLISAVISFPPLVSLYRQPDGA- 197

QY 181 PQPAEPRCEINDOKWYVVISGIGSEFAPCLIMILYVRIYQIAKRRTRVPPSRGPDAVA 240

Db 198 --AYPOGLNDETWYILSSGIGSEFAPCLIMGLVYARIYRAKLRTRITLSEKRAP---V 251

QY 241 APPGCTERRPKGLGPERASGPGGAEAEPPLPTQLNGAPGEPAPAGPRDTDALDUESSSD 300

Db 252 GPDGASPTTENGIGAAGAGENGHCA-----PPPA-----DVEPDESSA 290

QY 301 HAERPPGPRRPERGPRGKARASQVKKPGDSLPRRGPGATGCTPAAGPGEERVGAAKAS 360

Db 291 AAE-----RRRRRGALRRG-----GRRRAGAEGGAGGADGGAESGALTAS 332

QY 361 RWRG-----RQREKFTFVLAVVIGVFVVCWF 388

Db 333 RSPGPGRLSRASSRSVVEFLSRRRARRASSVCRKVAQAAREKRTFVLAVVMGVFLCMF 392

QY 389 PFEFTYTLTAV--GCSVPRTLEKFEFWEFGYCNSSLNPVIYTIENHDFRRRAFKILCRGD 445

Db 393 PFEFYSLYGICREACQVPGPLKFEFWEFGYCNSSLNPVIYTIENHDFRRSEFKILFRRR 452

QY 446 RK 447

Db 453 RR 454

RESULT 10

AAM52124

ID AAM52124 standard; Protein; 461 AA.

XX

AC AAM52124;

XX

DT 18-FEB-2002 (first entry)

XX

DE Human alpha-2CAR protein.

XX

KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;

KW polymorphic site; allelic variant; cardiovascular disease;

KW central nervous system disease; adenylyl cyclase; MAP kinase activity;

KW phosphorylation; inositol phosphate; alpha-2CAR.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 205..409

FT /note= "featured in figure 12"

FT Domain 208..231

FT /label= transmembrane_domain

FT Region 321..324

FT /label= polymorphic_site

FT /note= "Polymorphic site absent in the variant protein

FT Domain 383..406

FT /label= transmembrane_domain

XX

PN WO200179561-A2.

XX

PD 25-OCT-2001.

XX

PF 17-APR-2001; 2001WO-US12575.

XX

PR 17-APR-2000; 2000US-0551744.

PR 10-AUG-2000; 2000US-0636259.

PR 19-OCT-2000; 2000US-0692077.

XX

PA (LIGG/) LIGGETT S B.

PA (SMAL/) SMALL K M.

XX

PI Liggett SB, Small KM;

XX

DR WPI; 2001-611728/70.

DR N-PSDB; AA199931.

PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -

Claim 78; Page 158-160; 163pp; English.

The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising:
(a) obtaining a sample having a polynucleotide encoding an alpha-2B, alpha2A or alpha2C or fragment or complement of; and
(b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (IIV) or a site comprising (A) (ggggcgggcg) or (B) (ggggcgctgag) at positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. ephrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauvolsicine, idazoxan, tolazoline, phenolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the human alpha-2CAR protein, the sequence includes a 4 amino acid polymorphic site at residues 321-324 (GAG), absent in the alpha-2CAR variant protein (AAM52126).

SQ Sequence 461 AA;

Query Match	48.7%;	Score 1159.5;	DB 22;	Length 461;
Best Local Similarity	51.7%;	Pred. No. 9.1e-80;		
Matches 254;	Conservative 37;	Mismatches 95;	Indels 105;	Gaps 12;

[illegible]

Db 447 FKHTLERRRR 457

RESULT 11
AAM52126
ID AAM52126 standard; Protein; 457 AA.

AC AAM52126;

DT 18-FEB-2002 (first entry)

Human alpha-2CAR variant protein.

AA Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW phosphorylation; inositol phosphate; alpha-2CAR.

OS Homo sapiens.

Key	Location/Qualifiers
-----	---------------------

Domain	label= transmembrane_domain
FT	
FT	

FT	Domain	/label= transmembrane_domain
11	Domain	

PN WO200179561-A2.

PD 25-OCT-2001.

PF 17-APR-2001; 2001WO-US12575.

PR 17-APR-2000; 2000US-0551744.

PR 19-OCT-2000; 2000US-0692077.

PA (LIGG/) LIGGETT S. B.

LIQUETT SB, Small KM;

DR WPI; 2001-611728/70.

DR N-PSDB; AA199933.

PT Genotyping an alpha-

PT disease associate

XX Claim 78; Page 160-162; 163pp; English.
PS

The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising:
(a) obtaining a sample having a polynucleotide encoding an alpha-2B, alpha2A or alpha2C or fragment or complement of; and
(b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (II) or a site comprising (A) (ggggcggggcg) or (B) (ggggcgctgag) at positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BH933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate

QY	206	FAPCLIMLVVVRITQIAKRRTRVPSSRGGPDVAAPPGGIERRPKGGLPERSAGPGAE	265
		: : : :	:
Dd	182	FAPCLIMLVYLRIYLIAKR----	SNRRGPRAKGGPGGESHKÖPR--PDHGALASAK 233
QY	266	AEPPLPT-----QLNG--APGEPAIPA-GPRDLDLDEES-----SS	298
		: :: :	
Dd	234	LPALASVASAREVNNGHSKSTGEKEGETPEDTGTRALPPSWAALPNSGÖGQKEGYCASP	293
QY	299	SDHAERPBGRPRPERGPRGKGKARASÖVKPGD--SLPRRGH-----ATGIGTPAAGPE	351
		: : :	
Dd	294	EDEAE-----EEEEEEECPEQAVPVSPASACSPLOQPQGSRLVATLRGÖVLIRG-	348
QY	352	ERVGAAKASRMWRGRQ--NREKRFTFLAVVIGVFVCWCPPEFTYTLLTAV--GCSPRT	406
			:
Dd	349	--VGAIQGOWMRRRAQLTREKRFTFLAVVIGFVLCWFPEFFESSYLGATICPKHKCVPHG	406
QY	407	LKFKEFWFCYCNSLNPIVITYTFNHDFRAFKILCR	443
		:	:
Dd	407	LFOEFEWICYNSSLNPVIYTIENÖDFRRAFRIILCR	443

CC	XX	RESULT 13
CC	XX	AAE00990
CC	XX	AAE00990 standard; Protein; 450 AA.
CC	XX	AAE00990;
CC	XX	04-JUL-2001 (first entry)
CC	XX	Human alpha2B-adrenoceptor (alpha2B-AR) protein.
CC	XX	Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
CC	XX	glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
CC	XX	norepinephrine; epinephrine; therapy; vascular contraction;
CC	XX	coronary artery; coronary heart disease; CHD; chronic angina pectoris;
CC	XX	acute myocardial infarction; AMI; Prinzmetal's variant.
CC	XX	Homo sapiens.
CC	XX	Key Location/Qualifiers
CC	XX	Region 298..309
CC	XX	/note="Glutamic acid repeat"
CC	XX	WO200129082-A1.
CC	XX	26-APR-2001.
CC	XX	20-OCT-2000; 2000WO-FI00913.
CC	XX	22-OCT-1999; 99US-0422985.
CC	XX	(JUVA-) JUVANTIA PHARMA LTD OY.
CC	XX	Snapiir A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
CC	XX	Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Nyssönen K;
CC	XX	Salonen R, Kaahane J, Valkonen V;
CC	XX	WPI; 2001-300318/31.
CC	XX	N-PSDB; AAD04762.
CC	XX	New DNA molecule encoding variant specific adrenoceptor protein with
CC	XX	deletion of specific amino acids located in the third intracellular
CC	XX	loop of the polypeptide, for treating vascular contraction of coronary
CC	XX	arteries -
CC	XX	Disclosure; Page 29-31; 37pp; English.
CC	XX	The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) protein
CC	XX	Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of
CC	XX	12 glutamates, in an acidic stretch of 18 amino acids (amino acids
CC	XX	294-311), located in the third intracellular loop of the receptor
CC	XX	polypeptide Alpha2B-AR gene is located on chromosome 2. Alpha2-AR

mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries which is clinically expressed as coronary heart disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in gene therapy.

SQ Sequence 450 AA;

Query Match	47.38;	Score 1126.5;	DB 22;	Length 450;
Best Local Similarity	53.28;	Pred. No. 2.8e-77;		
Matches 243; Conservative	50;	Mismatches 105;	Indels 59;	Gaps 14;

QY	27	PYSLOVITLLVCLAGLMLLTVEGNVLIIAVFTSRALKAPONLFLVSLASADITVATLV	86
		: : : : : : :	
Db	6	PYSVOATAIAAAITFLILFTIFGNALVILAVLTSTRSLRAFONLFLVSLAAADILVATLI	65
QY	87	IPFSLANEVWGYYFGKAWCEIYALDVLCTSSIVHLCAISLDRYWSITQAIENYMKRT	146
		: : : : : : :	
Db	66	IPFSLANEILGWYFRRTWCEYVYALDVLCTSSIVHLCAISLDRYWAVSRALEXMKRT	125
QY	147	PRRIKAIITWVVISAVISFPPLISIEKKGGGGGPOP-AEPCEINDOKWYVSSICISGF	205
		: : : :	
Db	126	PRRIKCIITLWVLIAAVISLPLI----YKGDQGPQFRGRPQCKLQEWAYILASSIGSF	181
QY	206	FAPCLIMILVVRITYQIAKRRTRVPSRRGPDAAVAPGGETERRPKGLGPERSAGPGAE	265
		:	
Db	182	FAPCLIMILVYLRITYLIAKR-----SNRRGPRAKGGPGQGESKQPR--PDHGALASAK	233
QY	266	AEPLPT-----QLNG--APGEPA-PGPRDTALDLES-----SS	298
		: : :	
Db	234	LPALASVASAREVNGHKSSTGEKEGETPEDTGTRALPPSNALLPNSGGQKEGVCGASP	293
QY	299	SDHAERPPGPRRPERGPRGKGKARASQVKPGD--SLPRRPG-----ATGIGTPAAGPE	351
Db	294	EDEAE-----EEEEEEECPEQAVPVSPASACSPLOQPGSRVLATLRGQVLLGRG-	348
QY	352	ERVGAAKASRMKRGRO--NREKRFTEVLAVVIGVFVVCWPEPFETTYLTAV--GCSVPRT	406
Db	349	--VGAIGGQWWRRAQLTREKRFTVLAVVIGVFVLCWPEPFETTSYSLGAICPKHCKVPHG	406
QY	407	LKKEFFWFGYCNSSLNPVITYTTFNHDFRAFKILCR	443
Db	407	LFOEFFWFGYCNSSLNPVITYTTFNODERRAFRILCR	443

	RESULT	14
ID	AAM52118	
	AAM52118 standard; Protein; 447 AA.	
AC	AAM52118;	
XX		
DT	18-FEB-2002	(first entry)
DE	Human alpha-2BAR third intracellular loop variant	
XX		
KW	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; alpha-2D; polymorphic site; allelic variant; cardiovascular central nervous system disease; adenylyl cyclase; phosphorylation; inositol phosphate; alpha-2BAR.	
KW		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Domain	170..193
FT		/label= transmembrane_domain
FT	Region	307..309
FT		/label= polymorphic_site
FT	Domain	370..393
FT		/label= transmembrane_domain

CC	vascular contraction of coronary arteries which is clinically expressed
CC	as coronary heart disease (CHD), unstable chronic angina pectoris which is
CC	clinically expressed as Prinzmetal's variant form or acute myocardial
CC	infarction (AMI). Alpha2B-AR gene is used in gene therapy.
XX	
SQ	Sequence 447 AA:

... SQ Sequence 447 AA:

Query Match	Score	DB	Length
47.38;	1126;	22;	447;

Best Local Similarity 53.28; Pred. No. 3e-77;

Matches	243;	Conservative	50;	Mismatches	102;	Indels	62;	Gaps	14;
---------	------	--------------	-----	------------	------	--------	-----	------	-----

27 PYSLOYTITVCLAGLMLTFEGNVLIIAVETSRALKAPONLEFVSLASADILVATLV 86

Db 6 PYSVQATAIAAAITFLIFTIEGNALVILAVTSRSLRAPQNLFLVSLAADIVATLI 65

QY 87 IPESLANEVMGYWYFGKAMCEIYLALDVLFCCTSSIVHLCAISLDKRWYSITQAI EYNL KRT 146
 |||||::||| : |||:||||| ||||| |||||:::|:| | ||
 Db 66 IPESLANELGWIYFRTWCEVYLALDVLFCCTSSIVHLCAISLDKRWAVSRAL EYNS KRT 125

Db 66 IPFSLANELGYFRRTWCEVYLALDVLCTSSIVHLCAISLDRYWAVSRALEYNSKRT 125

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QY      147  PRRIKAIITVWVISAIVSFPPPLISIEKKGGGGGPQP-AEPRCEINDQKWYVISSCIGSF 205
        ||||| ||:|:|:|:|:|:| |||||      | |||||  |:|:|:|:|:|:| |||||
Db      126  PRRIKCIITVWVIAAIVSLPPLI---YKGGDGPQPRGRPQCKLNDQAWYILASSIGSF 181

```

Db 126 PRIKCIITWLIAAVISPLI --- YKGDQGPQPRGRQCKLNQEAWTILASSIGSF 181

```
QY      206 FAPCLIMILVVRITYLAKRTRVPSPSRGPDVAAPGGTERRPXGLGPERSAGPGCAE 265  
        ||||| | :||| | | :| :| :| :  
Db     182 FAPCLIMILVLRITLYIAKR-----SNRRGPRRAKGGPQGSGSKQPR---PDHGALASAK 233
```

Db 182 FAPCLIMLVYLRILAKR-----SNRRGPRAKGPGGESKQPR---PDHGALASAK 233

```
QY      266 AEDPPT-----QLNG--APGEPA-P-GPRDTALDLEES-----SS 298  
        | :||| :||| ||| |  
Db      234 LPALASVASAREVNGHSHKSTGEKEGETPEDTGTALLPPSWAALPNSGQGQKEGVCGASP 293
```

Db 234 LPALASVASAREVNGHSGSTGEKEGETPEDTGTALPPSWALPNSGQGQKEGVCASP 293

```

Oy 299 SDHAERPPGPRRPERGPRKGKARASQVKPGD--SLPRRPG-----ATGIGTPAAGPGE 351
    | | | : : | | | : | | | |
Db 294 EDEAEE-----EEEEEECEPQAVPVSPASACSPPLQQPQGSRLVATLRGQVLLGRG- 345

```

```
Db 294 EDEAEE-----EEEEEECEPQAVPVSPASACSPPLQQPQGSRLATLRLRGVLLRG- 34
```

```
OY      352 ERVGLAKASRWGRQ--NRKRFTEVLAVIGVFVCWMPFFFTYTTLFV---GCSVPRT   406
```

||||| |
DB 346 --VGAI GGQWMRRRAQLTRERKFTEFLAVIGVFVCWFPEFFTSLSGAICPKHKCVPHG 403

Db 346 --VGAIGGQWRRRAQLTREKRFTEVLAVIGFVLCWFPEFFSYSLGALCPNHCKVPHG 400

```

QY      407 LEKFEFFWEGYCNSLNPIVYITFENHDFRRAFKILCR 443
         ||::||| | ||||| ||||| ||||| ||||| ::||| |
Db      404 LEQFEFFWIGYCNSLNPIVYITFENODERRAERILCR 440

```

Dd 404 LEQFFFWNLGYCNSLNPIYILFNQDKRAKFRILCK 440

Search completed: February 15, 2003, 18:04:25
Job time : 49 secs

Job time : 49 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 15, 2003, 16:56:00 ; Search time 24.5 Seconds
(without alignments)
1765.734 Million cell updates/sec

Title: US-09-636-259B-4
Perfect score: 2380
Sequence: 1 MGSLQPDAGNASWNGTEAPG.....HDFRRAFKKILCRGDRKRIV 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2221	93.3	450	2 A38316	alpha-2-adrenergic
2	2216	93.1	450	2 A34169	alpha-2A-adrenergic
3	2193	92.1	450	2 I49481	alpha-2 adrenergic
4	2126	89.3	450	2 B40392	alpha-2-adrenergic
5	2105	88.4	450	2 JH0190	alpha-2-adrenergic
6	1173	49.3	458	2 I49480	alpha-2 adrenergic
7	1169	49.1	458	2 A40392	alpha-2-adrenergic
8	1167	49.0	458	2 A48392	alpha 2C4 adrenoce
9	1167	49.0	458	2 A37869	alpha-2B-adrenergic
10	1160.5	48.8	461	2 A31237	alpha-2C-adrenergic
11	1127.5	47.4	450	2 A37223	alpha-2B-adrenergic
12	1126.5	47.3	432	2 I50829	alpha-2-adrenocept
13	1121.5	47.1	455	2 S28221	alpha-2-C2 adrener
14	1111.5	46.7	448	2 I51883	alpha-2B-adrenergic
15	1100.5	46.2	453	2 A35642	alpha-2B-adrenergic
16	693.5	29.1	484	2 S58868	G protein-coupled
17	681.5	28.6	379	2 JC6178	serotonin receptor
18	652	27.4	476	2 JC5042	G protein-coupled
19	649	27.3	601	2 SI2004	tyramine receptor
20	649	27.3	601	2 JH0170	octopamine recepto
21	624	26.2	444	1 DYBOD2	dopamine receptor
22	621.5	26.1	443	1 DYHUD2	dopamine receptor
23	617	25.9	511	2 C56849	dopamine receptor
24	613	25.8	444	1 DYMSD2	dopamine receptor
25	613	25.8	444	1 S08146	dopamine receptor
26	611	25.7	377	2 B30341	G protein-coupled
27	608.5	25.6	442	1 DXXLD2	dopamine receptor
28	594.5	25.0	430	2 T16079	hypothetical prote
29	590	24.8	422	2 I38209	serotonin receptor

30	587	24.7	421	2 I49375	serotonin receptor
31	586.5	24.6	377	2 S68423	serotonin receptor
32	585.5	24.6	377	2 A53279	serotonin receptor
33	579.5	24.3	514	2 D56849	dopamine receptor-
34	578	24.3	422	2 JH0315	serotonin receptor
35	577.5	24.3	390	2 JN0268	serotonin receptor
36	573.5	24.1	517	2 A45121	alpha-1B adrenergic
37	564	23.7	374	2 I77467	serotonin receptor
38	562	23.6	564	2 A38271	serotonin receptor
39	561.5	23.6	389	2 S68422	serotonin receptor
40	560	23.5	387	1 DYHUD4	dopamine receptor
41	560	23.5	515	2 A40491	alpha-1-adrenergic
42	559.5	23.5	390	2 S58126	serotonin receptor
43	558.5	23.5	501	2 T18863	hypothetical prote
44	558	23.4	386	2 A42688	serotonin receptor
45	556.5	23.4	515	2 JC1525	alpha-1B-adrenergic

ALIGNMENTS

RESULT 1									
A38316									
alpha-2-adrenergic receptor - pig									
C:Species: Sus scrofa domestica (domestic pig)									
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999									
C:Accession: A38316									
R:Guyer, C.A.; Horstman, D.A.; Wilson, A.L.; Clark, J.D.; Cragoe Jr., E.J.; Limbird, J. Biol. Chem. 265, 17307-17317, 1990									
A:Title: Cloning, sequencing, and expression of the gene encoding the porcine alpha-2									
A:Reference number: A38316; MUID:91009167; PMID:2170371									
A:Accession: A38316									
A:Molecule type: DNA									
A:Residues: 1-450 <GUY>									
A:Cross-references: GB:J05652; MID:g164303; PIDN:AAA30984.1; PID:g164304									
C:Superfamily: vertebrate rhodopsin									
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein									
Query Match									
Best Local Similarity 93.3%; Score 2221; DB 2; Length 450;									
Matches 422; Conservative 3; Mismatches 25; Indels 0; Gaps 0;									
QY	1	MGSLQPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLLTVFGNVLTAVFT	60						
DB	1	MGSLQPEAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLLTVFGNVLTAVFT	60						
QY	61	SRALKAPQNLFLVSLASADILVATLVIIPFSLANEVMGYFGKAWCEIYALDVLFC	120						
DB	61	SRALKAPQNLFLVSLASADILVATLVIIPFSLANEVMGYFGKAWCEIYALDVLFC	120						
QY	121	IVHLCAISLDKRWYSITQAIIEYNLKRTPRRIKAIITVWVISAVISFPPLISIEKGGG	180						
DB	121	IVHLCAISLDKRWYSITQAIIEYNLKRTPRRIKAIITVWVISAVISFPPLISIEKGGG	180						
QY	181	PQPAEPKCEINDQKWYVSSCISGFAPCLIMILVYVRIYQIAKRTRVPPSRGPD	240						
DB	181	QQPAEPKCEINDQKWYVSSCISGFAPCLIMILVYVRIYQIAKRTRVPPSRGPD	240						
QY	241	APPGGTERRPKGLGPERSAGPGCAEAEPPLQTLNGAPGEPAPGPRDTDALDESS	300						
DB	241	ALPGGAERPNGLGPERGVGRVGAEAEPPLVQNLGAPGEPAPGPRDADGLDESS	300						
QY	301	HAERPPGRRPERGPRGKGAKARASQVKGPSLPRRPGATGIGTPAAGPGEEYGA	360						
DB	301	HAERPPGRRSERGPRAKSKARASQVKGPSLPRRPGAPGAPATGAGEERGVA	360						
QY	361	RWRGRONREKRTFVLAVVIGVEVVCWPEPFETTYTLTAVGCSVPRTLKFFFW	420						
DB	361	RWRGRONREKRTFVLAVVIGVEVVCWPEPFETTYTLTAVGCSVPRTLKFFFW	420						
QY	421	LNPVITYTFNHDFRRAFKKILCRGDRKRIV	450						
DB	421	LNPVITYTFNHDFRRAFKKILCRGDRKRIV	450						

OY 241 APPGTERRRPKGLGPERGAGAEAPLPTQLNG--APGEPAPAGPRDTDALDLEESS 297
Db 251 -----AGPDGAS---PTTENGLGKAAGENGHCAPPRTE-VEPDESS 287
OY 298 SSDHAERPPGRRPERGPRGKGKARASOVKPGDSLPRRGPGATGIGTPAAGPEERVGAA 357
Db 288 AAERRRRRGALRRGRRREGAEGDTSADGPGGLAAEQGARTASRSP--GPGGRLSRAS 345
OY 358 KAS-----RWRGR-----QNRKRTFVLAVVIGVFVVCWPFPEFFTYTLTAV-- 399
Db 346 SRSVEFFLSRRRRARSSVCRKKAQAAREKRTFVLAVVMGVFLVCWPFPEFFSYSLYGICR 405
OY 400 -GCSVPTLKFKEFFWFGYCNSSLNPVITYTFNHDFRAAFKILCRGDRK 447
Db 406 EACQLPEPLKFFFWIGYCNSSLNPVITYTFVNQDFRRSFKHILFRRRRR 454

RESULT 7

A40392
alpha-2-adrenergic receptor (clone RG10) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
C:Accession: A40392
R;Lanier, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.
J. Biol. Chem. 266, 10470-10478, 1991
A:Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic rec
A:Reference number: A40392; MUID:91244823; PMID:1645350
A:Accession: A40392
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-458 <LAN>
A:Cross-references: GB:M62371; NID:g206612; PIDN:AAA42033.1; PID:g206613
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 49.1%; Score 1169; DB 2; Length 458;
Best Local Similarity 53.9%; Pred. No. 2.6e-67;
Matches 251; Conservative 48; Mismatches 105; Indels 62; Gaps 12;

OY 14 NGTEA----PGGARAT-----PYSLOVTLTVCLAGLMLLTVEGNVLIATVFT 60
Db 19 NGSDAGEWGSGGGANASGTDWGPPEGQYSAGAVAGLAAVGFLIVFTVGNVLIATVLT 78
OY 61 SRALKAPQNLFLVSLASADILVATLVPESLANEVMGYWFGKAWCEIYLALDVLCTSS 120
Db 79 SRALRAPQNLFLVSLASADILVATLVPESLANELMAYWYFGQVWCVVYALDVLFCCTSS 138
OY 121 IVHLCAISLDRYWSITQAI EYNLKRTPRRRIKAIITVWVISAVISFPPLISIEKKGGGG 180
Db 139 IVHLCAISLDRYWSVTQAVEYNLKRTPRRVKATIVAVWLISAVISFPPLVSFYRRPDGA- 197
OY 181 PQPAEPRCEINDQKWYVISSCIGSFAPCLIMILVYVRIYQIAKRRTRVPPSRRGPDAVA 240
Db 198 ---AYPQGLNDETWYILSSCIGSFAPCLIMGLVYARIVAKLRTLSEKRGF---A 251
OY 241 APPGTERRRPKGLGPERGAGAEAPLPTQLNGAPGEPAPAGPRDTDALDLEESSSD 300
Db 252 RPDGASPTTENG LG--KAAGENGHCAPR-RTEV-----EP-----DESSAAE 290
OY 301 HAERPPGRRPERGPRGKGKARASQVYKPGDSLPRRGPGATGIGTPAAGPEERVGAAKAS 360
Db 291 RRRRRGAVRGRGRREGAEGDTSADGPGGLAAEQGARTASRSP--GPGGRLSRASRS 348
OY 361 -----RWGR-----QNRKRTFVLAVVIGVFVVCWPFPEFFTYTLTAV---GC 401
Db 349 VEFPLSRRRARRSSVCRKKAQAAREKRTFVLAVVMGVFLVCWPFPEFFSYSLYGICREAC 408
OY 402 SVPTLKFKEFFWFGYCNSSLNPVITYTFNHDFRAAFKILCRGDRK 447
Db 409 QLPEPLKFFFWIGYCNSSLNPVITYTFVNQDFRRSFKHILFRRRRR 454

RESULT 8

A48392
alpha 2C4 adrenoceptor subtype - mouse
N:Alternate names: alpha 2C4 isoceptor
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C:Accession: A48392
R;Chang, Y.H.; Chang, N.C.; Chen, W.M.; Chang, A.C.
Biochem. Mol. Biol. Int. 29, 467-474, 1993
A:Title: Molecular characterization of a murine homologue of alpha 2C4 adrenoceptor s
A:Reference number: A48392; MUID:93250567; PMID:8387367
A:Accession: A48392
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-458 <CHA>
A:Cross-references: GB:M97516; NID:q191728; PIDN:AAA37183.1; PID:q191729
A:Experimental source: DBA/2, liver
A:Note: sequence extracted from NCBI backbone (NCBIN:131475, NCBI P:131476)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 49.0%; Score 1167; DB 2; Length 458;
Best Local Similarity 53.4%; Pred. No. 3.4e-67;
Matches 251; Conservative 46; Mismatches 103; Indels 70; Gaps 12;

OY 14 NGTEA----PGGARAT-----PYSLOVTLTVCLAGLMLLTVEGNVLIATVFT 60
Db 19 NGSDAGEWGSGGGANASGTDWVPPPGQYSAGAVAGLAAVGFLIVFTVGNVLIATVLT 78
OY 61 SRALKAPQNLFLVSLASADILVATLVPESLANEVMGYWFGKAWCEIYLALDVLCTSS 120
Db 79 SRALRAPQNLFLVSLASADILVATLVPESLANELMAYWYFGQVWCVVYALDVLFCCTSS 138
OY 121 IVHLCAISLDRYWSITQAI EYNLKRTPRRRIKAIITVWVISAVISFPPLISIEKKGGGG 180
Db 139 IVHLCAISLDRYWSVTQAVEYNLKRTPRRVKATIVAVWLISAVISFPPLVSFYRR----- 193
OY 181 PQ-PAEPRCEINDQKWYVISSCIGSFAPCLIMILVYVRIYQIAKRRTRVPPSRRGPDAY 239
Db 194 PDVAAYPQGLNDETWYILSSCIGSFAPCLIMGLVYARIVAKLRTLSEKRGF--- 250
OY 240 AAPGTERRRPKGLGPERGAGAEAPLPTQLNG--APGEPAPAGPRDTDALDLEES 296
Db 251 -----AGPDGAS---PTTENGLGKAAGENGHCAPPRTE-VEPDES 286
OY 297 SSDHAERPPGRRPERGPRGKGKARASQVYKPGDSLPRRGPGATGIGTPAAGPEERVG 356
Db 287 SAAERRRRAAVRGRGRREGAEGDTSADGPGGLAAEQGARTASRSP--GPGGRLSRA 344
OY 357 AKAS-----RWGR-----QNRKRTFVLAVVIGVFVVCWPFPEFFTYTLTAV- 399
Db 345 SRSVEFFLSRRRRARSSVCRKKAQAAREKRTFVLAVVMGVFLVCWPFPEFFSYSLYGIC 404
OY 400 -GCSVPTLKFKEFFWFGYCNSSLNPVITYTFNHDFRAAFKILCRGDRK 447
Db 405 REACQLPEPLKFFFWIGYCNSSLNPVITYTFVNQDFRRSFKHILFRRRRR 454

RESULT 9

A37869
alpha-2B-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C:Accession: A37869; S13023
R;Flordellis, C.S.; Handy, D.E.; Bresnahan, M.R.; Zannis, V.I.; Gavras, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 1019-1023, 1991
A:Title: Cloning and expression of a rat brain alpha-2B-adrenergic receptor.
A:Reference number: A37869; MUID:91126047; PMID:1704126
A:Accession: A37869
A:Molecule type: mRNA
A:Residues: 1-458 <FLO>
A:Cross-references: GB:M58316; NID:g202585; PIDN:AAA40634.1; PID:g202586
A:Note: the authors translated the codon ACC for residue 69 as Asn and GCG for residu
R;Voigt, M.M.; McCune, S.K.; Kanterman, R.Y.; Felder, C.C.

FEBS Lett. 278, 45-50, 1991

A;Title: The rat alpha(2)-C4 adrenergic receptor gene encodes a novel pharmacological su

A;Reference number: S13023; MUID:91130596; PMID:1704314

A;Accession: S13023

A;Molecule type: DNA

A;Residues: 1-39,'G','41-68','N','70-154','E','156-244','S','246-458 <VOI>

A;Cross-references: GB:X57659; NID:g288044; PIDN:CAA40861.1; PID:g288045

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match

Best Local Similarity 49.0%; Score 1167; DB 2; Length 458;

Matches 250; Conservative 46; Mismatches 105; Indels 68; Gaps 11;

14 NGTEA----PGGARAT-----PYSLOVTLTVCLAGLMLLTVEGNLVIIAVFT 60

19 NSDAGEWSSGGANASGTDWAPPQGYSGAVAGLAAVGFLIVFTVGVTVLVIAVLT 78

61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWYFGKAWCEIYLALDVLCTSS 120

79 SRALRAPQNLFLVSLASADILVATLVMPFSLANELMAWYFGQVWCQVYLLADVLCTSS 138

121 IVHLCAISLDRYWSITQAIENLKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGG 180

139 IVHLCAISLDRYWSVTQAVEYNLKRTPRKATIVAVWLISAVISFPPLVSFYRRPDGA- 197

181 POPAEPCEINDQKWYVSSCIGSFAPCLIMILVYVRIYQIAKRTRVPPSRGPDVA 240

198 ---AYPOGLENDETMYILSSCIGSFAPCLIMGLVYARIYRAKLRTLTLEKRG- 250

241 APPGTERRPKGLGPERSAGPGAEAELPTQLNG--APGEPAPAGPRDTALDLEES 297

251 -----AGPDGAS---PTTENGGLKAGENGHCAPPRTE-VEPDESS 287

298 SSDHAERPPGRRPERGPRGKGARASQVKGDSLPRRPGATGCTPAAGPGEERYGAA 357

288 AAEERRRRGALRRGRRREGAEGDGTGSADGPGPLAAEQGARTASRSP--GPGRLSRAS 345

358 KAS-----RWRGR-----QNRKRTFVLAVVIGVFVVCWFPFFFTYTLTAV-- 399

346 SRSVEFFLSRRRRARSSVCRKKAQAAREKRTFVLAVVMGVFVLCWFPFFFSYSLYICR 405

400 -GCSVPRTLKFFFWFGYCNSSLNPVIYTFNHDFRRAFKILCRGDRK 447

406 EACQLPEPLFKFFFWIGYCNSSLNPVIYTFVNODFRRSFKHLFRRRR 454

RESULT 10

A31237

alpha-2C-adrenergic receptor - human

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Aug-1999

C;Accession: A31237; S14309; S14310

R;Regan, J.W.; Kobilka, T.S.; Yang-Feng, T.L.; Caron, M.G.; Lefkowitz, R.J.; Kobilka, B.

Proc. Natl. Acad. Sci. U.S.A. 85, 6301-6305, 1988

A;Title: Cloning and expression of a human kidney cDNA for an alpha-2-adrenergic recepto

A;Reference number: A31237; MUID:88320430; PMID:2842764

A;Accession: A31237

A;Molecule type: mRNA

A;Residues: 1-461 <REG>

A;Cross-references: GB:J03853; NID:g178193; PIDN:AAA35513.1; PID:g178194

R;Chhajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.

FEBS Lett. 280, 241-244, 1991

A;Title: Identification of an additional gene belonging to the alpha(2) adrenergic recep

A;Reference number: S14308; MUID:91192139; PMID:1849485

A;Accession: S14309

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 95-223 <CHH>

A;Accession: S14310

A;Molecule type: DNA

A;Residues: 95-223 <CH2>

C;Genetics:

A;Gene: GDB:ADRA2C; ADARL2; ADRA2L2; ADRA2RL2

A;Cross-references: GDB:120540; OMIM:104250

A;Map position: 4p16.3-4p15

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 48.8%; Score 1160.5; DB 2; Length 461;

Matches 254; Conservative 38; Mismatches 94; Indels 105; Gaps 12;

10 NASWNGTEAPGGARAT-----PYSLOVTLTVCLAGLMLLTVEGNLVIIAVFT 60

19 NASGAGERSSGGVANASGASWGP RP RGYSAGAVAGLAAVGFLIVFTVGVNLVIAVLT 78

61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWYFGKAWCEIYLALDVLCTSS 120

79 SRALRAPQNLFLVSLASADILVATLVMPFSLANELMAWYFGQVWCQVYLLADVLCTSS 138

121 IVHLCAISLDRYWSITQAIENLKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGG 180

139 IVHLCAISLDRYWSVTQAVEYNLKRTPRKATIVAVWLISAVISFPPLVSLYRQPDGA- 197

181 POPAEPCEINDQKWYVSSCIGSFAPCLIMILVYVRIYQIAKRTRVPPSRGPDVA 240

198 ---AYPOGLENDETMYILSSCIGSFAPCLIMGLVYARIYRAKLRTLTLEKRG- 250

241 APPGTERRPKGLGPERSAGPGAEAELPTQLNG--APGE--PAPAGPRDTALDLEE 295

251 -----VGPDGAS---PTTENGGLGAAAGEARTGTARPR- 282

296 SSSSDHAERP---PGRRRPERGPRGKGARASQVKGDSLPRRPGATGCTPAAGPGE 351

283 WSRTTRAQRP RGAPBLR--RGRRRAGAEG-----GAGGADGGGAGPGA 326

352 ERVGAAKASRWG-----RQNRKRTFVLAVV 379

327 AQSGALTASRSPGPGRLSRASSRSVEFFLSRRRRARSSVCRKKAQAAREKRTFVLAVV 386

380 IGVEFVVCWFPFFFTYTLTAV--GCSVPRTLKFFFWFGYCNSSLNPVIYTFNHDFRRA 436

387 MGVEFVLCWFPFFFTYSLYIGICREACQVPGLKFFFWIGYCNSSLNPVIYTFVNODFRPS 446

437 FKKILCRGDRK 447

447 FKHLFRRRR 457

RESULT 11

A37223

alpha-2B-adrenergic receptor - human

N;Alternate names: alpha-2C2-adrenergic receptor

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 29-Oct-1999

C;Accession: A37223; I39407; S14308; A36158

R;Weinshank, R.L.; Zgombick, J.M.; Macchi, M.; Adham, N.; Lichtblau, H.; Branchek, T

Mol. Pharmacol. 38, 681-688, 1990

A;Title: Cloning, expression, and pharmacological characterization of a human alpha-2

A;Reference number: A37223; MUID:91042469; PMID:2172775

A;Accession: A37223

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-450 <WEI>

R;Lomasney, J.W.; Lorenz, W.; Allen, L.F.; King, K.; Regan, J.W.; Yang-Feng, T.L.; Ca

Proc. Natl. Acad. Sci. U.S.A. 87, 5094-5098, 1990

A;Title: Expansion of the alpha 2-adrenergic receptor family: cloning and characteriz

A;Reference number: I39407; MUID:90311349; PMID:2164221

A;Accession: I39407

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-450 <LOM>

A;Cross-references: GB:M34041; NID:g178197; PIDN:AAE51666.1; PID:g178198

R;Chhajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.

FEBS Lett. 280, 241-244, 1991

A:Title: Identification of an additional gene belonging to the alpha(2) adrenergic recep
A:Reference number: S14308; MUID:91192139; PMID:1849485
A:Accession: S14308
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 56-185 <CHH>
A:Cross-references: GB:X59684; NID:g28635
A:Note: this translation is not annotated in GenBank entry HSALPH218, release 111.0
R:Chang, A.C.; Ho, T.F.; Chang, N.C.
Biochem. Biophys. Res. Commun. 172, 817-823, 1990
A:Title: In vitro amplification by polymerase chain reaction of a partial gene encoding
A:Reference number: A36158; MUID:91054503; PMID:2173582
A:Accession: A36158
A:Molecule type: DNA
A:Residues: 95-361, 'QL', 364-389 <CHA>
A:Cross-references: GB:M38742; NID:g177867; PIDN:AAA62823.1; PID:g177868
C:Genetics:
A:Gene: GDB:ADRA2B; ADRARL1; ADRA2L1; ADRA2RL1
A:Cross-references: GDB:120539; OMIM:104260
A:Map position: 2p13-2q13
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match	47.4%;	Score 1127.5;	DB 2;	Length 450;
Best Local Similarity	53.2%;	Pred. No. 1.1e-64;		
Matches 243; Conservative	51;	Mismatches 104;	Indels 59;	Gaps 14;

OY	27	PYSLOVTLTVLVLGLMLLTVEGNLVIIAFTSRALAKPQNLFLVSLASADILVATLV	86
		: : : : : : : :	
Dd	6	PYSQATAAIAAITFLILETFEGNALVILAVALTSRSTRAPQNLEVLVSLAADILVATLI	65
OY	87	IPESLANEVMGYWYFGKAWCEIYLALDVLCTSSIVHLCAISLDRYWSITQAIEYNLKRT	146
		: : : : : : : : :	
Dd	66	IPESLANELLGWYFRFRCWEYXIALDVLCETSSIVHLCATSIDRYWAVSRALEYNSKRT	125
OY	147	PRRIKAIITVWVISAVISFPDLISIEKKGGGQPQ-AEPDCEINDQKWYVISSCIGSF	205
		: : : : : : :	
Dd	126	PRRIKIITVWLIAAVISLPPLI---YKGDOGQPPGRGPQCKLNQEAWYILASSIGSF	181
OY	206	FAPCLIMILVVYRIQIARTRRVPSRRGPDVAAPPGTERRRPKGLGPERSAGPGAEE	265
		: : : : : :	
Dd	182	FAPCLIMILVYLRITYLIAKR-----SNRRGPRAKGGPQGGESEKQPR--PDHGALASAK	233
OY	266	AEPPLPT----QLNG--APGEDAPA-GPRDTALDLEES-----SS	298
		: : :	
Dd	234	LPALASVASAREVNHGSHSKSTGEKEGETPEDTGTRALPPSMALPNSGOGQKEGVCGASP	293
OY	299	SDHAERPPGPRRPERGPRGCKAKARASQVKPGD--SLPRRGPG-----ATGIGTPAAGPGE	351
		: :	
Dd	294	EDEAFE----EEEEEEEECEFEQOAVPVSPASACSPPLQQPOGSRVLATLRGBVLLGRG-	348
OY	352	ERYGAKAASRWGRON--REKRTFVLAVVIGVFVVCWFEPFFTYTTLTAV--GCSVPRT	406
		: : :	
Dd	349	--VGAIGGQWMRRRAHVTREREFTFVLAVVIGVFVLCWFEPFFSYSLSGAICPKHKCVPHG	406
OY	407	LKFEFFWEGYCNSSLNPVITYTIHNHDFRRAFKILCR	443
		: :	
Dd	407	LKQEFFWICYCNSSLNPVITYTIENODERRAFRRLCR	443

RESULT 12
I50829
alpha 2-adrenoceptor - cuckoo wrasse
C;Species: *Labrus ossifagus* (cuckoo wrasse)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C;Accession: I50829
R;Svensson, S.P.; Bailey, T.J.; Pepperl, D.J.; Grundstrom, N.; Ala-Uotila, S.; Scheinin
B.; J. Pharmacol. 110, 54-60, 1993
A;Title: Cloning and expression of a fish a2-adrenoceptor.
A;Reference number: I50829; MUID:94035926; PMID:7693288
A;Accession: I50829
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

A;Residues: 1-432 <SVE>
A;Cross-references: EMBL:U07743; NID:g467287; PIDN:AAA17386.1; PID:g467288
C;Superfamily: vertebrate rhodopsin

Query Match	47.3%;	Score 1126.5;	DB 2;	Length 432;
Best Local Similarity	53.0%;	Pred. No. 1.2e-64;		
Matches 240;	Conservative 50;	Mismatches 108;	Indels 55;	Gaps 11;

QY	10	NASWNGTEABEGGARATPYSLQVTLTLLVCLAGLMLLTVEGNVLVTIAVFTSRALKAPÖN	69
		: :: :	
Db	18	NASWS---ADSG-----YSTAAIASIALAVSFLIFTVGNILVIAVITSRAALKAPÖN	68
QY	70	LFLVSLASADILIVATLVIPFESLANEVMGYWF GKANCEIYLALDVLCTSSIVHLC AISL	129
		:	
Db	69	LFLVSLATADILIVATLVMPFESLANELMGYWF GKVMCGIYLALDVLCTSSIVHLC AISL	128
QY	130	DRYWSITQAEIXNLKRTPRRIKAITITVVVISAVISFPPLISIEKKGGGQPÖAPERCE	189
		: : : : : : : : : : :	
Db	129	DRYWSVTQAVEYNLKRTPKRVKCILIVWLISAFISSPPLSID---SNNYISSQÖCM	184
QY	190	INDÖKWYVISSCIGSEFAPCLIMILVYVRIOÄAKRRTRVPPSRRGPDAVAAPPGTERR	249
		: : : :	
Db	185	LNDDTWYILSSMASFEAPCLIMILYIRIQYÖAKTRER-----SMGKEPR	231
QY	250	PKGL----GPERASGP-----GGAEAEPPTÖLNGARPGEPA PAPAGRDTDALDL EESS	297
		: : : : : : : : : : : : : : : :	
Db	232	PDGV TÖTENGLNKANS PCHGDRENGHCÖPPTPSQRTVITIGÖ-----QTDDADMDESE	284
QY	298	SSDHAERP PGPRBERG PRGKGKARASÖVKPGDSLPRRGPGATGICTPA GPEERVGA A	357
		: : : : : : : : : : : : : : : :	
Db	285	SSEGGKHKPÖRÖDSÖRAKR -PGLKXSSISKÖSARISRVSNNKSVDLFASRRKRRRSSIAEK	343
QY	358	KASRWGRÖNREREKFTFVLAVVIGVFVVCWPFEEFFTYLTAV--GC SVPRLLKF FFWF	414
Db	344	KVS----QAREKRFTFVLAVVMGVFVVCWPFEEFFSYSLHAVCRDYCKIPDILFK-FFWI	397
QY	415	GYCNSSLNPVIYITFNHDFRRAFKKILCRGDRK 447	
		:	
Db	398	GYCNSSLNPAYITFNHRDFRRAFÖKITLCKSWKK 430	

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RESULT 13
S28221
alpha-2-C2 adrenergic receptor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 13-Aug-1999
C/Accession: S28221; JH0693
R/Chen, W.M.; Chang, A.C.; Shie, B.J.; Chang, Y.H.; Chang, N.C.A.
Biochim. Biophys. Acta 1171, 219-223, 1992
A/Title: Molecular cloning and characterization of a mouse alpha(2)C2 adrenoceptor su
A/Reference number: S28221; MUID:93129625; PMID:1336396
A/Accession: S28221
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-455 <CHE>
A/Cross-references: EMBL:M94583
A/Note: the authors translated the codon CCA for residue 161 as Phe, ACT for residue
R;Chruscinski, A.J.; Link, R.E.; Daunt, D.A.; Barsh, G.S.; Kobilka, B.K.
Biochem. Biophys. Res. Commun. 186, 1280-1287, 1992
A/Title: Cloning and expression of the mouse homolog of the human alpha2-C2 adrenergic
A/Reference number: JH0693; MUID:92378586; PMID:1354956
A/Accession: JH0693
A/Molecule type: DNA
A/Residues: 6-228, 231-455 <CHR>
A/Cross-references: GB:U00979; NID:g191547; PIDN:AAA37131.1; PID:g191548
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein
F:18-43/Domain: transmembrane #status predicted <TM1>
F:55-81/Domain: transmembrane #status predicted <TM2>
F:90-115/Domain: transmembrane #status predicted <TM3>
F:134-158/Domain: transmembrane #status predicted <TM4>
F:173-199/Domain: transmembrane #status predicted <TM5>
F:377-402/Domain: transmembrane #status predicted <TM6>

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Db 411 FQFFWIGYCNSSLNBPVYTVFNODFRRAFRRLCR 446

Search completed: February 15, 2003, 18:08:04
Job time : 25.5 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 15, 2003, 14:30:52 ; Search time 50 Seconds
(without alignments)
1854.424 Million cell updates/sec

Title: US-09-636-259B-4

Perfect score: 2380

Sequence: 1 MGSLQPDAGNASWNGTEAPG.....HDFRRAFKKILCRGDRKRIV 450

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2380	100.0	450	4 Q9BZK1	Q9bzk1 homo sapien
2	1305.5	54.9	388	13 Q90WY4	Q90wy4 brachydanio
3	1174.5	49.3	432	13 Q90WY6	Q90wy6 brachydanio
4	1132	47.6	510	13 Q90WY5	Q90wy5 brachydanio
5	1126	47.3	447	4 Q9BZK0	Q9bzk0 homo sapien
6	1116.5	46.9	448	11 Q925K7	Q925k7 mus musculu
7	1113.5	46.8	448	11 Q925K6	Q925k6 mus musculu
8	1112.5	46.7	453	11 Q925E4	Q925e4 rattus norv
9	969.5	40.7	393	11 Q9JYW2	Q9jyw2 cavia porce
10	943	39.6	392	6 Q95N90	Q95n90 tadarida br
11	940	39.5	390	6 Q9GL19	Q9gl19 cynocephalu
12	939.5	39.5	391	6 Q8SQA0	Q8sga0 emballonura
13	938.5	39.4	389	6 Q9GKZ5	Q9gkz5 tupaiata tana
14	938.5	39.4	395	6 Q9GL12	Q9gl12 manis sp. a
15	938	39.4	390	6 Q9GKZ6	Q9gkz6 trichechus
16	937.5	39.4	379	6 Q9GL13	Q9gl13 macropus ru

17	935.5	39.3	393	6 Q9GL11	Q9gl11 nycticebus
18	933.5	39.2	395	6 Q95N91	Q95n91 tonatia bid
19	933	39.2	388	6 Q9GL18	Q9gl18 diceros bic
20	932.5	39.2	389	6 Q9GL07	Q9gl07 phoca vitul
21	932	39.2	390	6 Q95N89	Q95n89 taphozous s
22	931.5	39.1	387	6 Q9GL17	Q9gl17 felis silve
23	929.5	39.1	393	6 Q95N92	Q95n92 myotis daub
24	928.5	39.0	383	6 Q9GL20	Q9gl20 cynopterus
25	928.5	39.0	393	6 Q9GL15	Q9gl15 macrotus ca
26	928	39.0	392	6 Q9GL35	Q9gl35 balaenopter
27	925.5	38.9	393	6 Q9GL16	Q9gl16 hippopotamu
28	924.5	38.8	391	6 Q9GL06	Q9gl06 sus scrofa
29	923.5	38.8	385	6 Q9GL14	Q9gl14 micropotamo
30	922.5	38.8	389	6 Q95N94	Q95n94 hipposidero
31	922	38.7	388	6 Q8SQ91	Q8sq91 nycteris th
32	921.5	38.7	385	6 Q9GKZ7	Q9gkz7 tenrec ecau
33	920.5	38.7	391	6 Q8SQB3	Q8sqb3 antrozous p
34	919	38.6	388	6 Q8SQ93	Q8sq93 nycteris gr
35	919	38.6	396	6 Q8SQ87	Q8sq87 rhogeessa t
36	914.5	38.4	395	6 Q8SQ94	Q8sq94 noctilio al
37	913	38.4	392	6 Q95N95	Q95n95 megaderma l
38	910.5	38.3	383	6 Q9GL28	Q9gl28 bradypus tr
39	910	38.2	394	6 Q8SQA1	Q8sqa1 desmodus ro
40	910	38.2	398	6 Q8SQ92	Q8sq92 natalus str
41	909.5	38.2	389	6 Q8SQ95	Q8sq95 nyctimene a
42	907.5	38.1	383	6 Q95N93	Q95n93 pteropus ra
43	904	38.0	365	6 Q8SQ88	Q8sq88 rhinopoma h
44	900.5	37.8	389	6 Q8SQ89	Q8sq89 rhinolophus
45	684.5	28.8	419	5 Q77254	Q77254 boophilus m

ALIGNMENTS

RESULT 1
Q9BZK1 PRELIMINARY; PRT; 450 AA.
ID Q9BZK1
AC Q9BZK1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha 2A adrenergic receptor.
GN ADRA2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20556293; PubMed=10948191;
RA Small K.M., Forbes S.L., Brown K.M., Liggett S.B.;
RT "An asn to lys polymorphism in the third intracellular loop of the
RT human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted
RT Gi coupling.";
RL J. Biol. Chem. 275:38518-38523(2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF316894; AAK01634.1; -.
DR HSSP; P29274; 1MH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT VARIANT 251 K -> N.
SQ SEQUENCE 450 AA; 48970 MW; 94E02E227CE5ECFE CRC64;

Query Match 100.0%; Score 2380; DB 4; Length 450;
Best Local Similarity 100.0%; Pred. No. 5.8e-165;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSLQPDAGNASWNGTEAPGCGARATPYSLQVTLTVLCIAGLIMLTLTVFGNVLTITAVFT 60

|||||
Db 1 MGSLOPDAGNASWNGTEAPGGARATPYSLQVTLTLVCLAGLMLLTVFGNVLVIIVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVWGMYFGKAWCEIYLALDVLCTSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVWGMYFGKAWCEIYLALDVLCTSS 120
QY 121 IVHLCAISLDRWYSITQAIENYLNKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGG 180
Db 121 IVHLCAISLDRWYSITQAIENYLNKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGG 180
QY 181 PQPAEPRCEINDQKWYVIVSSCIGSEFAPCLIMILVYVRIYQIAKRRTVPPSRKGPDAVA 240
Db 181 PQPAEPRCEINDQKWYVIVSSCIGSEFAPCLIMILVYVRIYQIAKRRTVPPSRKGPDAVA 240
QY 241 APPGTERRPKGLGPERSAGPGAEAEPLPTQLNGAPGEPAPAGPRDTDALDESSSSSD 300
Db 241 APPGTERRPKGLGPERSAGPGAEAEPLPTQLNGAPGEPAPAGPRDTDALDESSSSSD 300
QY 301 HAERPPGPRPERGPRGKARASQVKPGDSLPRRPGATGIGTPAAGPGEERVGAAKAS 360
Db 301 HAERPPGPRPERGPRGKARASQVKPGDSLPRRPGATGIGTPAAGPGEERVGAAKAS 360
QY 361 RWRGRQNRKERTFVLAVVIGVFWCWFPEFFTYTLTAVGCSVPRTLKFEFFWGYCNS 420
Db 361 RWRGRQNRKERTFVLAVVIGVFWCWFPEFFTYTLTAVGCSVPRTLKFEFFWGYCNS 420
QY 421 LNPVITYTFNHDFRAFKKILCRGDKRRIY 450
Db 421 LNPVITYTFNHDFRAFKKILCRGDKRRIY 450

RESULT 2

Q90WY4 PRELIMINARY; PRT; 388 AA.
ID Q90WY4;
AC Q90WY4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha2A-adrenergic receptor.
GN ADRA2A.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Ruuskanen J., Xhaard H., Marjamaki A., Salaneck E., Salminen T.,
RA Yan Y.L., Postlethwait J.H., Johnson M.S., Larnhammar D., Scheinin M.;
RT "Origin of Alpha2-Adrenergic Receptor Subtypes as Revealed by Cloning
RT and Mapping of Three Receptor Subtype Genes in the Zebrafish (Danio
RT rerio).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY048971; AAL07510.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 388 AA; 43996 MW; 431965A04E1986DD CRC64;

Query Match 54.9%; Score 1305.5; DB 13; Length 388;
Best Local Similarity 60.5%; Pred. No. 4.6e-87;
Matches 266; Conservative 37; Mismatches 78; Indels 59; Gaps 8;

QY 15 GTEAPGGARATPYSLQVTLTLVCLAGLMLLTVFGNVLVIIVFTSRALKAPQNLFLVS 74
Db 4 GANATNGTNATKEITLLVALLPLSTIAVGLLILITFGNVLVIIVFTSRALKAPQNLFLVS 63
QY 75 LASADILVATLVIPFSLANEVWGMYFGKAWCEIYLALDVLCTSSIVHLCAISLDRWYS 134
Db 64 LASADILVATLVIPFSLANEVWGMYFGKAWCEIYLALDVLCTSSIVHLCAISLDRWYS 123

QY 135 ITQAIENYLNKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGGPQPAEPRCEINDQ 194
Db 124 ITQAIENYLNKRTPRRIKAIITVWVISAVISFPPLITMKSEG-----DICDINKEK 175
QY 195 WYIVSSCIGSEFAPCLIMILVYVRIYQIAKRRTVPPSRKGPDAVAAPPGTERRPKGLG 254
Db 176 WYIVSSCIGSEFAPCLIMILVYVRIYQIAKRTRAP-----G 213
QY 255 PERSAGPGAEAEPLPTQLNGAPGEPAPAGPRDTD--ALDESSSSSDHAERPPGPRRP 311
Db 214 DHRKNEVGKENDP-HEKLNIGQN---AEPDDKDEINGVMESSSSSDHKVSNDCSLKK 268
QY 312 ERGPRGKARASQVKPGDSLPRRPGATGIGTPAAGPGEERVGAAKASRWGRQNRK 371
Db 269 K--SSKGTKLSQIKPGD-----GDKTEACQTTKASRWKGRQNRK 308
QY 372 FTFVLAVVIGVFWCWFPEFFTYTLTA-VGCSVPRTLKFEFFWGYCNSLNPTVTFN 430
Db 309 FTFVLAVVIGVFWCWFPEFFTYTLTAFCDCVPETLKFEFFWGYCNSLNPTVTFN 368
QY 431 HDFRAFKKILCRGDKRRIY 450
Db 369 NDFRRSEKILCRDKRRV 388

RESULT 3

Q90WY6 PRELIMINARY; PRT; 432 AA.
ID Q90WY6;
AC Q90WY6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha2C-adrenergic receptor.
GN ADRA2C.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Ruuskanen J., Xhaard H., Marjamaki A., Salaneck E., Salminen T.,
RA Yan Y.L., Postlethwait J.H., Johnson M.S., Larnhammar D., Scheinin M.;
RT "Origin of Alpha2-Adrenergic Receptor Subtypes as Revealed by Cloning
RT and Mapping of Three Receptor Subtype Genes in the Zebrafish (Danio
RT rerio).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY048969; AAL07508.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 432 AA; 49137 MW; 1A52F0283C663DA7 CRC64;

Query Match 49.3%; Score 1174.5; DB 13; Length 432;
Best Local Similarity 56.4%; Pred. No. 1.6e-77;
Matches 242; Conservative 45; Mismatches 113; Indels 29; Gaps 8;

QY 20 GGGARATPYSLQVTLTLVCLAGLMLLTVFGNVLVIIVFTSRALKAPQNLFLVSLASAD 79
Db 22 GNSTNSTSYSPATITIGLAVSEFLIFTIVGNVLVIAVLTSRALKPQNLFLVSLASAD 81
QY 80 ILVATLVIPFSLANEVWGMYFGKAWCEIYLALDVLCTSSIVHLCAISLDRWYSITQAI 139
Db 82 ILVATLVIPFSLANEVWGMYFGECWNCNITLADVLCTSSIVHLCAISLDRWYSITQAV 141
QY 140 EYNLKRTPRIKAIITVWVISAVISFPPLISIEKKGGGGPQPAEPRCEINDQKWYVIS 199
Db 142 EYNLKRTPRIKAIITVWVISAVISFPPLISIMDR---NTVDERRRPMQQLNDHTWYILY 197
QY 200 SCIGSEFAPCLIMILVYVRIYQIAKRTR-VPFSRRGPDVAAPPGTERRPKGLPERS 258

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Db 198 SSIGSFAPCVIMILVYIRIYQVAKTRTRNMSEKRRDPDG-----GSGTPRLLENGLSREDS 253
Qy 259 AGPGAEAEPLPTQLNGAPGEPAPGPRDLDLLESSSSSDH-AERPPGPRPERGPRG 317
Db 254 RRENG-----HCSSSPGERKPA--EDNPADADLEDDSSSDEKAKRSQNETAPSKDRR 303
Qy 318 KGKARASQVKGPDSLPRRPGATGIGTPAAGPGEERVGAAKASRWGRGRONREKRTFYLA 377
Db 304 SSRKNSSSSKHSSRKSRASSKSLDFS-----SRKRRTISRKKISQAREKRTFYLA 357
Qy 378 VVIGVFVVCWPFPEFTYTLTAV---GCSVPRTLKFEFEWEGYCNSSLNPVIYTFNHDFR 434
Db 358 VVMGVFVVCWPFPEFSYSLYGCRCPCALPDPLKFEFEWIGYCNSSLNPVIYTFNQDFR 417
Qy 435 RAFKKILCR 443
Db 418 RAFQKILCK 426
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RESULT 4

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Q90WY5 PRELIMINARY; PRT; 510 AA.
ID Q90WY5 AC Q90WY5:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha2B-adrenergic receptor.
GN ADRA2B.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Ruuskanen J., Xhaard H., Marjamaki A., Salaneck E., Salminen T.,
RA Yan Y.L., Postlethwait J.H., Johnson M.S., Larhammar D., Scheinin M.;
RT "Origin of Alpha2-Adrenergic Receptor Subtypes as Revealed by Cloning
RT and Mapping of Three Receptor Subtype Genes in the Zebrafish (Danio
RT rerio).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY048970; AAL07509.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM Receptor.
SQ SEQUENCE 510 AA; 55971 MW; 1CB07C0AFC6DE3D3 CRC64;
```

Query Match 47.6%; Score 1132; DB 13; Length 510;
Best Local Similarity 48.5%; Pred. No. 2.4e-74;
Matches 249; Conservative 58; Mismatches 104; Indels 102; Gaps 15;

```
Qy 14 NCTEAPGGGARAT-----PYSLOVTLTVCLAGLLMLLTVFGNVLIIVAVTSRAL 64
Db 16 NGT---GGTSSPTCNSMIKLAPYSPEATAFAITAITLMLLITIVGNLVIIVLTSRSL 72
Qy 65 KAPQNLFLVSLASADILVATLVIPFSLANVWGYWFGKAWCEIYALDVLCTSSIVHL 124
Db 73 RGPQNLFLVSLAADIIVATLIIPFSLANELMGWYFRSWCEIYALDVLCTSSIVHL 132
Qy 125 CAISLDRYWSTQAIENLKRTPRIKAITTVWVISAVISFPPLISIEKGGGGGPQPA 184
Db 133 CAISLDRYMSISRAVYTGPKTRPKIKCAILVWVLISAVISFPPLISM-NKNKGGESGA 191
Qy 185 EPRCEINDQKWYVSSCIGSFAPCLIMILVYVRIYQIAKRTRVPPS---RRGPDAAVA 241
Db 192 LPQCQLNDERWYILYSTIGSFAPCLIMILVYMRITYQIAKQRTCPGEPKREAPANAT 251
Qy 242 P-----PGTER--RPKGLPERSAGPGAEAEPLPTQLNGAPGE----- 279
Db 252 PQHKIQNGRGDETFGLQKKARPPTLAVSQVESVQQAANTPIANNLLQAPSTTLTPTTPC 311
```

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Qy 280 PAPAGPRDLDLLESSSSSDHAERPPGPRRPERGPRGKGKARASQV-----PGDS 331
Db 312 PSFS-----PSNSSEVA-----PSKSKEGKKEKKKKNNKNNKKEPDNNNGES 355
Qy 332 L-----PRRPGATGIGTP-----AAGPGEERV-----GA 356
Db 356 MSSDSDTEQGRGLEVPCTPTMT--SGIHSPTMQKYRDMIAATAKAKLVARAKQDGT 413
Qy 357 AKASRWGRGRONREKRTFYLAIVIGVFVVCWPFPEFTYTLTAV---GCSVPRTLKFEFW 413
Db 414 PMSARKAMVNREKRTFYLAIVIGVFVVCWPFPEFSYSLQAVCPSCALPEPLKFEFW 473
Qy 414 EGYCNSSLNPVIYTFNHDFRAFAKKILCRGDR 446
Db 474 IGYCNSSLNPVIYTFNKNDFRAFAKKILCKMTK 506
```

RESULT 5

```
Q9BZK0 PRELIMINARY; PRT; 447 AA.
ID Q9BZK0 AC Q9BZK0:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha 2B adrenergic receptor.
GN ADRA2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21265012; PubMed=11056163;
RA Small K.M., Brown K.M., Forbes S.L., Liggett S.B.;
RT "Polymorphic Deletion of Three Intracellular Acidic Residues of the
RT alpha 2B-Adrenergic Receptor Decreases G Protein-coupled Receptor
RT Kinase-mediated Phosphorylation and Desensitization.";
RL J. Biol. Chem. 276:4917-4922(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF316895; AAK01635.1; -.
DR HSSP; P29274; 1MHM.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT VARIANT 298 300 EEE->KRR.
SQ SEQUENCE 447 AA; 49566 MW; B33D4B5B719C1C45 CRC64;
```

Query Match 47.3%; Score 1126; DB 4; Length 447;
Best Local Similarity 53.2%; Pred. No. 5.6e-74;
Matches 243; Conservative 50; Mismatches 102; Indels 62; Gaps 14;

```
Qy 27 PYSLOVTLTVCLAGLLMLLTVFGNVLIIVAVTSRALKAPQNLFLVSLASADILVATLV 86
Db 6 PYSVQATTAIAAATFTLFTFGNALVILLAVLTSRSLRAPQNLFLVSLAADIIVATLI 65
Qy 87 IPFSLANVWGYWFGKAWCEIYALDVLCTSSIVHLCAISLDRYWSTQAIENLKR 146
Db 66 IPFSLANELLGYWYFRRTWCEYVIALDVLCTSSIVHLCAISLDRYWAVSRALEYNKRT 125
Qy 147 PRRKAITTVWVISAVISFPPLISIEKGGGGGPQ-AEPRCEINDQKWYVSSCIGSF 205
Db 126 PRRKICILTVWLIAAVISLPLI---YKGDQGPQPRGRPQCKLNOEAWYILASSIGSF 181
Qy 206 FAPCLIMILVYVRIYQIAKRTRVPPSRRGPDAAVAPPGCTERRPKGLPERSAGPGAE 265
Db 182 FAPCLIMILVYLRILYIAKR-----SNRRGPRAKGGPGQGESKQPR--PDHGALASAK 233
Qy 266 AEPLPT-----QLNG---APGEPAPA-GPRDLDLLEES-----SS 298
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Db 234 LPALASVASAREVNGHSHKSTGKEGETPEDTGTTRALPPSWAALPNSGGQKEGVCASP 293
QY 299 SDHAERPPGRRPREGPRGKGARASQVKPGD--SLPRRPG----ATGIGTPAAGPGE 351
Db 294 EDEAEE-----EEEEEECEQAVPVPSPASACSPPLQDPQGSRLATLRGQVLLGRG- 345
QY 352 ERVGAAKASRWGRQ--NREKRTFVLAVVIGVFVWCWPEPFETTYTLTAV--GCSVPRT 406
Db 346 --VGAIGGQWRRRAQLTREKRTFVLAVVIGVFVLCWPEPFEEFSSYSLGAICPKHKVPHG 403
QY 407 LFKFFFWGCGYCNSSLNPVITYITFNHDFRRAFKKILCR 443
Db 404 LFOFFFWGCGYCNSSLNPVITYITFNODFRRAFRILCR 440
RESULT 6
Q925K7 PRELIMINARY; PRT; 448 AA.
AC Q925K7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Adrenergic receptor alpha 2B.
GN ADRA2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT "High-Throughput Sequence Identification of Gene Coding Variants
RT within Alcohol-Related QTLs."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332049; AAK56078.1; -
DR MGD; MGI:87935; Adra2b.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 448 AA; 50018 MW; 1B5ED9456C0B2B73 CRC64;
Query Match 46.9%; Score 1116.5; DB 11; Length 448;
Best Local Similarity 52.7%; Pred. No. 2.8e-73;
Matches 241; Conservative 50; Mismatches 105; Indels 61; Gaps 14;
QY 27 PYSLOVTLTVCLAGLMLLTVEGNLVITIAVFTSRALKAPQNLFLVSLASADILVATLV 86
Db 6 PYSVQATAIASAITFLILFTIFGNALVILAVLTSRLAPQNLFLVSLAADIIVATLI 65
QY 87 IPESLANEVMGYWFGKAWCEIYALDVLFCSTSIVHLCAISLDRYWSITQAIENLKRT 146
Db 66 IPESLANELLGYWFWRAWCEVYALDVLFCSTSIVHLCAISLDRYWAVSRALEYNSKRT 125
QY 147 PRRIKAIITVWVISAVISFPPLISIEKKGGGGPQP-AEPRCEINDQWYVYSSCIGSF 205
Db 126 PRRIKCIITVWLIAAVISLPLI---YKGDQRPPEPHGLPQCELNQEAWYILASSIGSF 181
QY 206 FAPCLIMILVYVRIYQIAKRRTRVPPSRRGPDVAAPPGTERRPKGLGPERSAGPGGAE 265
Db 182 FAPCLIMILVYLRIVYIAKR-----SHCRGLGAKRSGEGESKKPR---PAAGVPASAK 233
QY 266 AEPLPTQLNG---APGEPAPAGPRDTALDLESSSSSDHAER---PPG---PRRPERGP 315
Db 234 VPTLVSPSSVGEANGHPK--PREK-----EEGETPEDPEARALPPNWSALLPRSVQDQK 286
QY 316 RGKGKARASQVKPGD-----SLPRRPGATGIGTPAAGPGEER----- 353
Db 287 KGTSGATAEKGAEDEEEVEECEPQTLT--ASPASVFNPLQOPQTSRYLATLRGQVLLS 344

QY 354 --VGAAKASRWGRQ--NREKRTFVLAVVIGVFVWCWPEPFETTYTLTAV--GCSVPRT 406
Db 345 KNVGVASGQWRRRTQLSREKRTFVLAVVIGVFVWCWPEPFEEFSSYSLGAICPQHKVPHG 404
QY 407 LFKFFFWGCGYCNSSLNPVITYITFNHDFRRAFKKILCR 443
Db 405 LFOFFFWGCGYCNSSLNPVITYITFNODFRRAFRILCR 441
RESULT 7
Q925K6 PRELIMINARY; PRT; 448 AA.
AC Q925K6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Adrenergic receptor alpha 2B.
GN ADRA2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ILS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT "High-Throughput Sequence Identification of Gene Coding Variants
RT within Alcohol-Related QTLs."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332050; AAK56079.1; -
DR MGD; MGI:87935; Adra2b.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 448 AA; 49998 MW; B37E5E21B0EC4625 CRC64;
Query Match 46.8%; Score 1113.5; DB 11; Length 448;
Best Local Similarity 52.7%; Pred. No. 4.6e-73;
Matches 241; Conservative 49; Mismatches 106; Indels 61; Gaps 14;
QY 27 PYSLOVTLTVCLAGLMLLTVEGNLVITIAVFTSRALKAPQNLFLVSLASADILVATLV 86
Db 6 PYSVQATAIASAITFLILFTIFGNALVILAVLTSRLAPQNLFLVSLAADIIVATLI 65
QY 87 IPESLANEVMGYWFGKAWCEIYALDVLFCSTSIVHLCAISLDRYWSITQAIENLKRT 146
Db 66 IPESLANELLGYWFWRAWCEVYALDVLFCSTSIVHLCAISLDRYWAVSRALEYNSKRT 125
QY 147 PRRIKAIITVWVISAVISFPPLISIEKKGGGGPQP-AEPRCEINDQWYVYSSCIGSF 205
Db 126 PRRIKCIITVWLIAAVISLPLI---YKGDQRPPEPHGLPQCELNQEAWYILASSIGSF 181
QY 206 FAPCLIMILVYVRIYQIAKRRTRVPPSRRGPDVAAPPGTERRPKGLGPERSAGPGGAE 265
Db 182 FAPCLIMILVYLRIVYIAKR-----SHCRGLGAKRSGEGESKKPH---PAAGVPASAK 233
QY 266 AEPLPTQLNG---APGEPAPAGPRDTALDLESSSSSDHAER---PPG---PRRPERGP 315
Db 234 VPTLVSPSSVGEANGHPK--PREK-----EEGETPEDPEARALPPNWSALLPRSVQDQK 286
QY 316 RGKGKARASQVKPGD-----SLPRRPGATGIGTPAAGPGEER----- 353
Db 287 KGTSGATAEKGAEDEEEVEECEPQTLT--ASPASVFNPLQOPQTSRYLATLRGQVLLS 344
QY 354 --VGAAKASRWGRQ--NREKRTFVLAVVIGVFVWCWPEPFETTYTLTAV--GCSVPRT 406
Db 345 KNVGVASGQWRRRTQLSREKRTFVLAVVIGVFVWCWPEPFEEFSSYSLGAICPQHKVPHG 404
QY 407 LFKFFFWGCGYCNSSLNPVITYITFNHDFRRAFKKILCR 443

Db 405 LFOFFFWIGYCNSSLNPVITYTIFNODFRRAFRILCR 441

RESULT 8

0925E4 PRELIMINARY; PRT; 453 AA.
AC Q925E4; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE Alpha2B-adrenergic receptor.
GN Rng.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Schaak S., Cussac D., Paris H.;
RT "Cloning and characterization of the rat alpha2B-adrenergic receptor
RT gene promoter.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF366899; AAK53388.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 453 AA; 50369 MW; CBA69CE23EACB511 CRC64;

Query Match 46.7%; Score 1112.5; DB 11; Length 453;
Best Local Similarity 52.5%; Pred. No. 5.4e-73;
Matches 240; Conservative 51; Mismatches 105; Indels 61; Gaps 14;

QY 27 PYSLOYTLVLVCLAGLMLLVFEGNVLTITAVFTSRALKAPQNLFLVSLASADILVATLV 86
Db 11 PYSVOATAIASAITFLILFTFGNALVTLAVLTSRSLRAPQNLFLVSLAADILVATLI 70
QY 87 IPFSLANEVMGYWYFGKAWCEIYLALDVLFCTSSIVHLCALISLDRYWSTQAIENLKR 146
Db 71 IPFSLANELGYWYFWRAWCEYLLALDVLFCTSSIVHLCALISLDRYWAVSRALEYNKRT 130
QY 147 PRRIKAITTVWVISAVISFPLISIEKKGGGQPP-AEPRCEINDQKWYVISCIGSF 205
Db 131 PRRIKCIITLWVLIAAVISLPLI---YKGDQRPERRGLPQCELNGEAWYILASSIGSF 186
QY 206 FAPCLIMILVYVRIYQIAKRRTRVPPSRGPDVAADPGGTERPKGLGPERGAGPGAE 265
Db 187 FAPCLIMILVYLRIVIAKR-----SHCRGLGAKRSGEGESKKPQ---PVAGVPTSAK 238
QY 266 AEPLPTQLNG---APGEPAPAGPRDLDLLESSSSDHAER---PPG---PRRPERGP 315
Db 239 VPTLVSPSSVGEANGHPRP---PREK-----EEGETPEDPEARALPPTWSALPRSGQGOK 291
QY 316 RKGKARASQVKKPGD-----SLPRKPGATGIGTPAAGPEER----- 353
Db 292 KGTSGATAEEGDEDEVEECEPQTLR-ASPASVCPNPLOQPOTSRLVLAFLRGQVLLG 349
QY 354 --VGAASRWRGRQ--NREKRTFVLAVVIGVVCWPEFFFTYTLTAV---GCSVPRT 406
Db 350 KNVGVASGQWRRRTQISREKRTFVLAVVIGVVCWPEFFFTYSIGALCPQHCKVPHG 409
QY 407 LKFEFFWFGYCNSSLNPVITYTIFNHDFFRAFKILCR 443
Db 410 LFOFFFWIGYCNSSLNPVITYTIFNODFRRAFRILCR 446

RESULT 9
09JTW2 PRELIMINARY; PRT; 393 AA.
AC Q9JTW2;
OX Q9JTW2;

DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX NCBI_Taxid=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Madsen O.;
RT "Molecular evolution of alpha adrenergic receptor 2B.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ271336; CAB66895.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 393 AA; 42921 MW; 5399B7175A53BD48 CRC64;

Query Match 40.7%; Score 969.5; DB 11; Length 393;
Best Local Similarity 52.2%; Pred. No. 1.1e-62;
Matches 214; Conservative 42; Mismatches 85; Indels 69; Gaps 13;

QY 43 LMLTVFEGNVLTITAVFTSRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFG 102
Db 9 LILFTIFGNALVTLAVLTSRSLRAPQNLFLVSLAADILVATLIIPFSLANELGYWYFW 68
QY 103 KAWCEIYLALDVLFCTSSIVHLCALISLDRYWSTQAIENLKRTPRIKAITTVWISA 162
Db 69 RTWCEVYLALDVLFCTSSIVHLCALISLDRYWAVSRALEYNKRTPRIKCIITLWVLI 128
QY 163 VISFPLISIEKKGGGQPP-AEPRCEINDQKWYVISCIGSFAPCLIMILVYVRIYQ 221
Db 129 VISLPLI---YKGDQGPQPRGSPQCKINOEAWYILASSIGSFAPCLIMILVYLRITL 184
QY 222 IAKRTRVPPSRGPDVAADPGGTERPKGLGPERGAGPGAE---PLPTQLNG-- 275
Db 185 IAKR-----SNRGRPRAKGGPGEGQSKSRPL-----PGAPASAKVPPPLASPLSTG 232
QY 276 -APGEPAPAGPRDLDLLESSSSDHAERPPGPRRPERGPRGKARASQVKP----- 328
Db 233 EANGHPKPTGEKE-----EGETSEDPARTLPSPWALPTSGQGOKKAVVLAPAEAEAE 286
QY 329 -----GDSL-PRRPG-----ATGIGTPAAGPEERVGAAKASRWR 363
Db 287 EEEEGDECEQAAAPGLPASMCSPSIQPOGSRVLATLRGQVLLGRG---VGAVDQWWR 343
QY 364 GR-QNREKRTFVLAVVIGVVCWPEFFFTYTLTAV---GCSVPRTL 408
Db 344 RRTQMTREKRTFVLAVVIGVVCWPEFFFTYSIGALCPQHCKVPHGLF 393

RESULT 10
095N90 PRELIMINARY; PRT; 392 AA.
AC Q95N90;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha adrenergic receptor 2B (Fragment).
GN AAR2B.
OS Tadarida brasiliensis (Brazilian free-tailed bat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Molossidae; Tadarida.
OX NCBI_Taxid=9438;

Db 69 RTWCEVYLALDVLECTISSIVHLCAISLDRYMAVSRALEYNSKRTPRRIKCIILLTWLIAA 128
QY 163 VISFPPLISIEKKGGGGPQPAEPRCEINDQKVVYISSCIGSFAPCLIMILVYVRIYQI 222
Db 129 VISLPPLI---YKGDQGSQPRGRPOCKLNQEAWYILASSIGSFAPCLIMILVYLRITYL 185
QY 223 AKRRTRVPPSRRGPDAAVAPPGGTERRPKGLGSPERSAGPGGAEAEPPLT-----QLN 274
Db 186 AKR-----SHRRGPRAKWGPREGESKQPCWV-----PGASA-TLPTLASLASGEAN 232
QY 275 G-----APGEP-APAGPRDTDAL-----DLEESSS 298
Db 233 GHSKPIGEKREGETPEDPGTIPALPPSWSALPNSGQONEGVCGASPEEEAEHEEEEEE 292
QY 299 SDHAER--PPGPRR---PERGPRGKGKARASQVKGDSLPRRGPGATGIGTPAAGPGEE 352
Db 293 EDHEPQALPASPASVCSPLRQPOG---SRVLATLRGQVLLGRGVGAA----- 337
QY 353 RVGAAKASRWGRQNRREKRTFVLAVVIGVFVVCWPEFFFTYTLTAV---GCSVPRTL 408
Db 338 -VSGGQWWRRAQLTREKRTFVLAVVIGVFVLCWPEFFFTSYSLSGAICPQHCKVPHGLF 395

RESULT 15

Q9GKZ6 PRELIMINARY; PRT; 390 AA.
ID Q9GKZ6
AC Q9GKZ6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE Alpha adrenergic receptor, subtype 2B (Fragment).
GN AAR2B.
OS Trichechus manatus (Caribbean manatee) (West Indian manatee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Sirenia; Trichechidae; Trichechus.
OX NCBI_TaxID=9778;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., Madsen O., Catzefflis F., Stanhope M., de Jong W.W.;
RT "Probing 1the protein sequence support for the 'African clade' of
RT mammals.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ251109; CAC16418.1; -.
DR HSSP; P29274; 1MMH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 390
SQ SEQUENCE 390 AA; 42713 MW; 06D90A8D1CE912A3 CRC64;

Query Match 39.4%; Score 938; DB 6; Length 390;

Best Local Similarity 52.5%; Pred. No. 2.1e-60;

Matches 212; Conservative 36; Mismatches 96; Indels 60; Gaps 14;

QY 43 LMLLTVEGNAVLIIVAVTSRALKAPQNLFLVSLASADILVATLVIIPSLANEVMGYWYFG 102
Db 9 LILFTIEGNSLVILAVLTSRLAPQNLFLVSLAAADILVATLIIIPSLANELLGWYFW 68
QY 103 KAWCEIYLALDVLECTSSIVHLCAISLDRYWSITQAI EYNLKRTPRRIKALITTWVISA 162
Db 69 RTWCEVYLALDVLECTSSIVHLCAISLDRYMAVSRALEYNSKRTPRRIKRIITVWLIAA 128
QY 163 VISFPPLISIEKKGGGGPQPAEPRCEINDQKVVYISSCIGSFAPCLIMILVYVRIYQ 221
Db 129 AISLPPLI---YKGDQGPQPRGRPOCKLNQEAWYIILSSSIGSFAPCLIMILVYLRITYL 184

QY 222 IAKRRTRVPPSRRGPDAAVAPPGGTERRPKGL--GPERSAAGPGGAEAEPPLTQING---- 275
Db 185 IAKR-----SHRRGPGAKGAPRKGESKQPHSLDSCPSALAN-----LPTLASSLAVA 231
QY 276 --APGEPAPAGPRDTDALDLEESSSSDHAERPPG-PRRPERGPRGK-GKARASQVKGDS 331
Db 232 GEADGHSMPPEKER-----ETSEDPGTPTLPSPWPVLPNSGQQKEGVCGASLEEEADK 286
QY 332 LPRR--GP-----GATGIGTPAAGPGEER-----VGAAKASRWGRQ--N 367
Db 287 EEEEECGPPAVPASPATACSPPLQQPQGSRLATLRGQVFLGRGVGAAGGQWWRRAQLT 346
QY 368 REKRTFVLAVVIGVFVVCWPEFFFTYTLTAV---GCSVPRTL 408
Db 347 REKRTFVLAVVIGVFVLCWPEFFFTSYSLSGAICPQHCKVPHGLF 390

Search completed: February 15, 2003, 18:07:01

Job time : 51 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 12:02:49 ; Search time 15.5 Seconds
(without alignments)
854.214 Million cell updates/sec

Title: US-09-636-259B-4
Perfect score: 2380
Sequence: 1 MGSLQPDAGNASWNGTEAPG.....HDFRRAFKKILCRGDRKRIV 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2205	92.6	450	1	US-08-444-734A-8
2	2164	90.9	450	1	US-08-194-338-5
3	1665	70.0	358	2	US-08-465-971B-4
4	1537	64.6	330	1	US-08-118-270-21
5	1537	64.6	330	5	PCT-US93-08528-21
6	1523	64.0	334	1	US-08-118-270-22
7	1523	64.0	334	5	PCT-US93-08528-22
8	1465	61.6	450	1	US-08-196-989B-11
9	1465	61.6	450	2	US-08-760-936-11
10	1140.5	47.9	461	1	US-08-194-338-4
11	1046.5	44.0	330	1	US-08-118-270-19
12	1046.5	44.0	330	5	PCT-US93-08528-19
13	1029	43.2	330	1	US-08-118-270-20
14	1029	43.2	330	5	PCT-US93-08528-20
15	649	27.3	601	1	US-07-676-174A-2
16	623.5	26.2	443	1	US-07-626-618A-18
17	623.5	26.2	443	1	US-08-333-977-18
18	617.5	25.9	415	1	US-08-194-338-10
19	615	25.8	444	1	US-07-626-618A-19
20	615	25.8	444	1	US-08-333-977-19
21	613	25.8	444	1	US-07-781-254A-1
22	590	24.8	422	1	US-07-817-920-3
23	590	24.8	422	1	US-08-370-542-3
24	590	24.8	422	1	US-08-117-006-3
25	590	24.8	422	1	US-08-216-594-3
26	590	24.8	422	1	US-08-542-358-3
27	590	24.8	422	2	US-08-157-185-13

28	590	24.8	422	3	US-08-281-526B-13	Sequence 13, Appl
29	590	24.8	422	3	US-09-018-351-3	Sequence 3, Appl1
30	590	24.8	422	4	US-09-332-837-13	Sequence 13, Appl
31	590	24.8	422	5	PCT-US93-00149-3	Sequence 3, Appl1
32	586.5	24.6	443	1	US-08-444-734A-3	Sequence 2, Appl1
33	585.5	24.6	377	2	US-08-461-812-2	Sequence 14, Appl
34	585.5	24.6	377	2	US-08-157-185-14	Sequence 14, Appl
35	585.5	24.6	377	3	US-08-281-526B-14	Sequence 14, Appl
36	585.5	24.6	377	4	US-09-450-790A-14	Sequence 14, Appl
37	585.5	24.6	377	4	US-09-332-837-14	Sequence 14, Appl
38	585	24.6	375	1	US-08-370-542-5	Sequence 5, Appl1
39	585	24.6	375	1	US-08-542-358-5	Sequence 5, Appl1
40	585	24.6	375	3	US-09-018-351-5	Sequence 5, Appl1
41	585	24.6	376	1	US-07-817-920-5	Sequence 5, Appl1
42	585	24.6	376	1	US-08-117-006-5	Sequence 5, Appl1
43	585	24.6	376	1	US-08-216-594-5	Sequence 5, Appl1
44	585	24.6	376	5	PCT-US93-00149-5	Sequence 5, Appl1
45	583	24.5	467	1	US-08-056-051-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-444-734A-8
; Sequence 8, Application US/08444734A
; Patent No. 5610282
; GENERAL INFORMATION:
; APPLICANT: Sibley, David R.
; APPLICANT: Monma, Frederick J.
; APPLICANT: Mahan, Lawrence C.
; APPLICANT: Mcvittie, Loris D.
; TITLE OF INVENTION: CDNA encoding the rat D1 dopamine
; TITLE OF INVENTION: receptor linked to adenylyl cyclase activation and
; TITLE OF INVENTION: expression of the receptor protein in plasmid-transfected
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,734A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,917
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/548,714
; FILING DATE: 06-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: NIH065.001FW1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 760-0404
; TELEFAX: (714) 760-9502
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-444-734A-8

Query Match 92.6%; Score 2205; DB 1; Length 450;
Best Local Similarity 93.6%; Pred. No. 7.5e-119;
Matches 421; Conservative 2; Mismatches 27; Indels 0; Gaps 0;

QY 1 MGSLOPDAGNASWNGTEAPGGGARATPYSLQVTLTVCLAGLMLTVFNGNVLIIAVFT 60
Db 1 MGSLOPDAGNASWNGTEAPGGGARATPYSLQVTLTVCLAGLMLTVFNGNVLIIAVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPESLANEVMGYWFGKAWCEIYLADLVFCTSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVIPESLANEVMGYWFGKTWCEIYLADLVFCTSS 120
QY 121 IYHLCALISLDRYWSITQATIEYNLKRTPRIKAIITVWVISAVISFPPLISIEKKGGGGG 180
Db 121 IYHLCALISLDRYWSITQATIEYNLKRTPRIKAIITVWVISAVISFPPLISIEKKGGGGG 180
QY 181 PQPAERCEINDQKWYVVISCSGFEAPCLIMILVYVRIYQIAKRTRVPPSRGPDVA 240
Db 181 PQPAERCEINDQKWYVVISCSGFEAPCLIMILVYVRIYQIAKRTRVPPSRGPDVA 240
QY 241 APPGTERRPKGLGPERSAGPGGAEAEPPLTQNLGAPGEPAPAGPRDTALDLESSSSD 300
Db 241 APPGTERRPKGLGPERSAGPGGAEAEPPLTQNLGAPGEPAPAGPRDTALDLESSSSD 300
QY 301 HAERPPGRRPERGPRGKGKARASQVKGPSLPRRGPGATGIGTPAGPGGEERVGAAKAS 360
Db 301 HAERPPGRRPERGPRGKGKARASQVKGPSLPRRGPGATGIGTPAGPGGEERVGAAKAS 360
QY 361 RWRGRQNEKRFTFVLAVVIGVVCWPFPEFTYTLTAVGCSVPRTLKFEFFWFGYCNSS 420
Db 361 RWRGRQNEKRFTFVLAVVIGVVCWPFPEFTYTLTAVGCSVPRTLKFEFFWFGYCNSS 420
QY 421 LNPVITYTIFNHDFRRAFKKILCRGDRKRIV 450
Db 421 LNPVITYTIFNHDFRRAFKKILCRGDRKRIV 450

RESULT 2
US-08-194-338-5
Sequence 5, Application US/08194338
Patent No. 5474898
GENERAL INFORMATION:
APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: McCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.

REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH101.001DV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-194-338-5

Query Match 90.9%; Score 2164; DB 1; Length 450;
Best Local Similarity 92.6%; Pred. No. 1.6e-116;
Matches 415; Conservative 3; Mismatches 30; Indels 0; Gaps 0;

QY 3 SLOPDAGNASWNGTEAPGGGARATPYSLQVTLTVCLAGLMLTVFNGNVLIIAVFTSR 62
Db 3 SLOPDAGNASWNGTEAPQQQARATPYSLQVTLTVCLAGLMLTVFNGNVLIIAVFTSR 62
QY 63 ALKAPQNLFLVSLASADILVATLVIPESLANEVMGYWFGKAWCEIYLADLVFCTSSIV 122
Db 63 ALKAPQNLFLVSLASADILVATLVIPESLANEVMGYWFGKTWCEIYLADLVFCTSSIV 122
QY 123 HLCAISLDRYWSITQATIEYNLKRTPRIKAIITVWVISAVISFPPLISIEKKGGGGG 182
Db 123 HLCAISLDRYWSITQATIEYNLKRTPRIKAIITVWVISAVISFPPLISIEKKGGGGG 182
QY 183 PAEPCEINDQKWYVVISCSGFEAPCLIMILVYVRIYQIAKRTRVPPSRGPDVAAP 242
Db 183 PAEPCEINDQKWYVVISCSGFEAPCLIMILVYVRIYQIAKRTRVPPSRGPDVAAP 242
QY 243 PGTERRPKGLGPERSAGPGGAEAEPPLTQNLGAPGEPAPAGPRDTALDLESSSSDHA 302
Db 243 PGTERRPKGLGPERSAGPGGAEAEPPLTQNLGAPGEPAPAGPRDTALDLESSSSDHA 302
QY 303 ERPPGRRPERGPRGKGKARASQVKGPSLPRRGPGATGIGTPAGPGGEERVGAAKASRW 362
Db 303 ERPPGRRPERGPRGKGKARASQVKGPSLPRRGPGATGIGTPAGPGGEERVGAAKASRW 362
QY 363 RGRQNEKRFTFVLAVVIGVVCWPFPEFTYTLTAVGCSVPRTLKFEFFWFGYCNSSLN 422
Db 363 RGRQNEKRFTFVLAVVIGVVCWPFPEFTYTLTAVGCSVPRTLKFEFFWFGYCNSSLN 422
QY 423 PVITYTIFNHDFRRAFKKILCRGDRKRIV 450
Db 423 PVITYTIFNHDFRRAFKKILCRGDRKRIV 450

RESULT 3
US-08-465-971B-4
Sequence 4, Application US/08465971B
Patent No. 5942414
GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
TITLE OF INVENTION: Human G-protein Receptor HIBEF51
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,971B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-465-971B-4

Query Match 70.0%; Score 1665; DB 2; Length 358;
Best Local Similarity 74.0%; Pred. No. 3.4e-88;
Matches 339; Conservative 4; Mismatches 7; Indels 108; Gaps 7;

OY 1 MGSLOPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLTVFNGNLVIAVFT 60
Db 1 MGSLOPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLTVFNGNLVIAVFT 60
OY 61 SRALKAPQNLFLV-SLASADILVA--TLVIPESLANEVMGYEGKAWCEIYALDVLFC 117
Db 61 SRALKAPQNLFLVXSLASADILVAXXTLVIPESLANEVMGYEGKAWCEIYALDVLFC 120
OY 118 TTSIVHLCAISLDRYWSITQAIIEYNLKRTPRIKAITTVWISAVISFPPLISIEKKG- 176
Db 121 TTSIVHLCAISLDRYWSITQAIIEYNLKRTPRIKAITTVWISAVISFPPLISIEKKGX 180
OY 177 -GGGQPAPAEPRCEINDQKWYISSICGSFFAPCLIMLVYVRITYQIAKRTRVPPSRRG 235
Db 181 XGGGPQAPAEPRCEINDQKWYISSICGSFFAPCLIMLVYVRITYQIAKRTRVPPSRRG 240
OY 236 PDAVAAPPGCTERRPKGLGERSAGPGCAEAEPPTQINGAPGEPAPAGPRDTDALDLEE 295
Db 241 PDAVAAPPGGLQ----- 252
OY 296 SSSSHAERPPGRRPERGPRGKGAKARASQVKGDSLPRRGPGATGIGTPAAGPEERVG 355
Db 253 -----GGRGS-----ASGLPRRRAGA----- 268
OY 356 AAKASRWGRONREKRFTEVLAVVIGVFVVCWPEPFFFTYTLTAVGCSVPRTLKFEFFWEG 415
Db 269 -----GGONREKRFTEVLAVVIGVFVVCWPEPFFFTYTLTAVGCSVPRTLKFEFFWEG 320
OY 416 YCNSSLNPVIYTIFFNHDFRRAFKKI--LCRGDRKRIV 450
Db 321 YCNSSLNPVIYTIFFNHDFRRAFKKIXXXLCRGDRKRIV 358

RESULT 4
US-08-118-270-21
Sequence 21, Application US/08118270
Patent No. 5508384

GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-21

Query Match 64.6%; Score 1537; DB 1; Length 330;
Best Local Similarity 74.2%; Pred. No. 6.2e-81;
Matches 310; Conservative 7; Mismatches 13; Indels 88; Gaps 6;

OY 33 TLTVCLAGLMLTVFNGNLVIAVFTSRALKAPQNLFLVSLASADILVATLVIPESLA 92
Db 1 TLTVLCIA--CLSLTVFNGNLVIAVFTSRALKAPQNLFLVSLASADILVATLVIPESLA 58
OY 93 NEVMGYWYEGKAWCEIYALDVLFTCTSSIVHLCAISLDRYWSITQAIIEYNLKRTPRIKA 152
Db 59 NEVMGYWYEGKAWCEIYALDVLFTCTSSIVHLCAISLDRYWSITQAIIEYNLKRTPRIKA 117
OY 153 IITVWISAVISFPPLISIEKKGCGGQPAPAEPRCEINDQKWYISSICGSFFAPCLIM 212
Db 118 IITVWISAVISFPPLISIEKKGCGGQPAPAEPRCEINDQKWYISSICGSFFAPCLIM 177
OY 213 ILVYVRITYQIAKRTRVPPSRGPDVAAPPGCTERRPKGLGERSAGPGCAEAEPPTQ 272
Db 178 -LVYVRITYQIAKRTRVPPSRGPDVAAPPGCTERRPKGLGERSAGPGG----- 227
OY 273 LINGAPGEPAPAGPRDTDALDLESSSSSHAERPPGRRPERGPRGKGAKARASQVKGDSL 332
Db 228 -----GGRGS-----ASGL 236
OY 333 PRRPGATGIGTPAAGPEERVGAAKASRWGRONREKRFTEVLAVVIGVFVVCWPEPFF 392
Db 237 PRRRAGA-----GGONREKRFTEVLAVVIGVFVVCWPEPFF 272
OY 393 TYTLTAVGCSVPRTLKFEFFWEGYCNSSLNPVIYTIFFNHDFRRAFKKILCRGDRKRIV 450
Db 273 TYTLTAVGCSVPRTLKFEFFWEGYCNSSLNPVIYTIFFNHDFRRAFKKILCRGDRKRIV 330

RESULT 5
PCT-US93-08528-21
Sequence 21, Application PC/TUS9308528

GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-21

Query Match 64.6%; Score 1537; DB 5; Length 330;
Best Local Similarity 74.2%; Pred. No. 6.2e-81;
Matches 310; Conservative 7; Mismatches 13; Indels 88; Gaps 6;
QY 33 TLTLLVCLAGLMLLTVEGNVLVITIAVFTSRALKAPQNLFVLSASADILVATLVIPFSLA 92
Db 1 TLTLLVCLAGLMLLTVEGNVLVITIAVFTSRALKAPQNLFVLSASADILVATLVIPFSLA 58
QY 93 NEVMGYWYFGKAWCEIYALDVLFTCTSSIVHLCAISLDRYWSITQAI EYNLKRTPRRIKA 152
Db 59 NEVMGYWYFGK-WCEIYALDVLFTCTSSIVHLCAISLDRYWSITQAI EYNLKRTPRRIKA 117
QY 153 IITVWVISAVISFPPLISIEKKGGGGQPAPAEPRCEINDQKWYVSISSIGSFAPCLIM 212
Db 118 IITVWVISAVISFPPLISIEKKGGGGQPAPAEPRCEINDQKWYVSISSIGSFAPCLIM 177
QY 213 ILVYVRIYQIAKRRTRVPPSRGPDAAVAPPGGTERRPKGLGPERSAGPGGA EAEPLPTQ 272
Db 178 -LVYVRIYQIAKRRTRVPPSRGPDAAVAPPGGTERRPNGLGPERSAGPGG----- 227
QY 273 LINGAPGEPAPAGPRDTDALDLESSSSDHAERPPGPRRPERGPRGKAKARASQVKPGDSL 332
Db 228 -----GGRGRS-----ASGL 236
QY 333 PRRGPGATGIGTPAAGPGGEERVGAAKASRWGRQNRKRTFVLA VVIGVFVVCWPFPEF 392
Db 237 PRRRAGA-----GGQNRKRTFVIA VVIGVFVVCWPFPEF 272
QY 393 TYTLTAVGCSVPRTLKFFFWEGYCNSSLNPVIYTI FNHDFRAAFKKILCRGDRKRIY 450
Db 273 TYTLTAVLCSPRTLKFFFWEGYCNSSLNPVIYTI FNHDFRAAFKKILCRGDRKRIY 330

RESULT 6
US-08-118-270-22
; Sequence 22, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.

APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-22

Query Match 64.0%; Score 1523; DB 1; Length 334;
Best Local Similarity 71.6%; Pred. No. 3.9e-80;
Matches 300; Conservative 10; Mismatches 23; Indels 86; Gaps 3;
QY 33 TLTLLVCLAGLMLLTVEGNVLVITIAVFTSRALKAPQNLFVLSASADILVATLVIPFSLA 92
Db 1 TLTLLVCLAGLMLLTVEGNVLVITIAVFTSRALKAPQNLFVLSASADILVATLVIPFSLA 60
QY 93 NEVMGYWYFGKAWCEIYALDVLFTCTSSIVHLCAISLDRYWSITQAI EYNLKRTPRRIKA 152
Db 61 NEVM-YWYFGKAWCEIYALDVLFTCTSSIVHLCAISLDRYWSITQAI EYNLKRTPRRIKA 119
QY 153 IITVWVISAVISFPPLISIEKKGGGGQPAPAEPRCEINDQKWYVSISSIGSFAPCLIM 211
Db 120 IITVWVISAVISFPPLISIEKKGGGGQPAPAEPRCEINDQKWYVSISSIGSFAPCLIM 179
QY 212 MLVYVRIYQIAKRRTRVPPSRGPDAAVAPPGGTERRPKGLGPERSAGPGGA EAEPLPT 271
Db 180 NMLVYVRIYQIAKRRTRVPPSRGPDACAPPGADRPNNAVGP ERGAGTAG----- 231
QY 272 QLINGAPGEPAPAGPRDTDALDLESSSSDHAERPPGPRRPERGPRGKAKARASQVKPGDS 331
Db 232 ----- 231
QY 332 LPRRPGATGIGTPAAGPGGEERVGAAKASRWGRQNRKRTFVLA VVIGVFVVCWPFPEF 391
Db 232 -----GGGERAGGAAKASRWGRQNRKRTFVIA VVIGVFVVCWPFPEF 275
QY 392 FTYTLTAVGCSVPRTLKFFFWEGYCNSSLNPVIYTI FNHDFRAAFKKILCRGDRKRIY 450
Db 276 FTYTLTAVGCPVPYQLNFNFWEGYCNSSLNPVIYTI FNHDFRAAFKKILCRGDRKRIY 334

RESULT 7

PCT-US93-08528-22
; Sequence 22, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-08528-22

Query Match 64.0%; Score 1523; DB 5; Length 334;
Best Local Similarity 71.6%; Pred. No. 3.9e-80;
Matches 300; Conservative 10; Mismatches 23; Indels 86; Gaps 3;

QY 33 TLTVCLAGLMLLTVEGNLVIIAVFTSRALKAPQNLFLVSLASADILVATVTPESLA 92
DB 1 TLTVCIAGLIMLFTVEGNLVIIAVFTSRALKAPQNLFLVSIASADILVATVTPESLA 60
QY 93 NEVNGIWFEGKAWCEIYLADVLEFCTSSIVHLCAISLDRWVSITQAIIEYNLKRTPRIKA 152
DB 61 NEVW-YWYFGKWCEIYLADVLEFCTSSIVHLCAISLDRWVSITQAIIEYNLKRTPRIKA 119
QY 153 IITVWVISAVISFPP-LISIEKKGCGGQPAEPCEINDQKWYVSSICISFFAPCLI 211
DB 120 IITVWVISAVISFPPPLISIEKKGAGGQPAEPSCKINDQKWYVSSISGFFAPCLI 179
QY 212 MILVYVRIYQIAKRRTRVPPSRGPDAAVAPPGTERPKGLGPERSAFGAEAPLPT 271
DB 180 NMLVYVRIYQIAKRRTRVPPSRGPDACAPPGADRRPNVAVPERAGTAG----- 231
QY 272 QLNGAPGEPAPAGPRDTDALDLESSSSDHAERPPGPRRPERGPRGKGKARASQVKPGDS 331
DB 232 ----- 231
QY 332 LPRRGATGIGTPAGPGEERVGAKASRWGRONREKRTFVLAVVIGVFWCWPFF 391
DB 232 -----GQGEERAGAKAKASRWGRONREKRTFVIAVIGVFWCWPFF 275
QY 392 FTYTLTAVGCSVPRTLKFFFWFGYCNSSLNPIYTTIFNHFRRRAFKILCRGDRKRIY 450
DB 276 FTYTLTAVGCSVPRTLKFFFWFGYCNSSLNPIYTTIFNHFRRRAFKILCRGDRKRIY 334

RESULT 8
US-08-196-989B-11
; Sequence 11, Application US/08196989B
; Patent No. 5585476
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,989B
; FILING DATE: 15-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: MAC-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-196-989B-11

Query Match 61.6%; Score 1465; DB 1; Length 450;
Best Local Similarity 68.6%; Pred. No. 1e-76;
Matches 303; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 1 MGSLOPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLLTVEGNLVIIAVFT 60
DB 1 MGSLOPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLLTVEGNLVIIAVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATVTPESLANEVMGYWYFGKAWCEIYLADVLEFCTSS 120
DB 61 SRALKAPQNLFLVSLASADILVATVTPESLANEVMGYWYFGKAWCEIYLADVLEFCTSS 120
QY 121 IVHLCAISLDRWVSITQAIIEYNLKRTPRIKAIITVWVISAVISFPPPLISIEKKGCGG 180
DB 121 IVHLCAISLDRWVSITQAIIEYNLKRTPRIKAIITVWVISAVISFPPPLISIEKKGCGG 180
QY 181 PQPAEPCEINDQKWYVSSICISGFFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDAAV 240
DB 181 PQPAEPCEINDQKWYVSSICISGFFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDAAV 240
QY 241 APPGGERPKGLGPERSAFGAEAPLPTQLNGAPGEPAPAGPRDTDALDLESSSSD 300
DB 241 XXX 300
QY 301 HAERPPGERRPERGPRGKGKARASQVKPGDSLPRRGATGIGTPAGPGEERVGAKAS 360
DB 301 XXX 360
QY 361 RWRGRONREKRTFVLAVVIGVFWCWPFFFTYTLTAVGCSVPRTLKFFFWFGYCNSS 420
DB 361 RWRGRONREKRTFVLAVVIGVFWCWPFFFTYTLTAVGCSVPRTLKFFFWFGYCNSS 420

Db 361 xxxxxxxxREKRTFLAVVIGVFVVCWPFPEFTYTLTAVGCSVPRTLKFFFWFGYCNS 420

QY 421 LNPVIYTIENHDFRRAFKILC 442

Db 421 LNPVIYTIENHDFRRAFKILC 442

RESULT 9

US-08-760-936-11

; Sequence 11, Application US/08760936

; Patent No. 5856443

; GENERAL INFORMATION:

; APPLICANT: MacLennan, A. John

; TITLE OF INVENTION: Molecular Cloning and Expression of

; TITLE OF INVENTION: G-Protein Coupled Receptors

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: US

; ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/760,936

FILING DATE: December 6, 1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Doran R.

REGISTRATION NUMBER: 38,261

REFERENCE/DOCKET NUMBER: MAC-100C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 352-375-8100

TELEFAX: 352-372-5800

APPLICATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 450 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: protein

US-08-760-936-11

Query Match 61.6%; Score 1465; DB 2; Length 450;

Best Local Similarity 68.6%; Pred. No. 1e-76;

Matches 303; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 1 MGSLOPDAGNASWNGTEAPGGGARATPYSLOVTLTVCLAGLMLLTVFGNVLIIVAVFT 60

Db 1 MGSLOPDAGNASWNGTEAPGGGARATPYSLOVTLTVCLAGLMLLTVFGNVLIIVAVFT 60

QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFGKAWCEIYLALDVLFTSS 120

Db 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFGKAWCEIYLALDVLFTSS 120

QY 121 IVHLCALISLDRYWSITQAIIEYNLKRTPRRIKAIITVWVISAVISFPPILSIEKKGGGG 180

Db 121 IVHLCALISLDRYWSITQAIIEYNLKRTPRRIKAIITVWVISAVISFPPILSIEKKGGGG 180

QY 181 PQPAEPRCEINDQKWYVISSCIGSFAPCLIMLVYVRIYQIAKRRTVPSRGPDAVA 240

Db 181 PQPAEPRCEINDQKWYVISSCIGSFAPCLIMLVYVRIYQIAKRRTVPSRGPDAVA 240

QY 241 APPGGETERRPKGLGPEPSAGPGGAEAEPPLPTQLNGAPGEPAPAGPRDLDLDESSSD 300

Db 241 xx 300

QY 301 HAERPPGPRRPERGPRGKAKARASQVKKPGDSLPRRGGATGIGTPAAGPEERVGAKAS 360

Db 301 xx 360

QY 361 RWGRQNRERKRTFLAVVIGVFVVCWPFPEFTYTLTAVGCSVPRTLKFFFWFGYCNS 420

Db 361 xxxxxxxxREKRTFLAVVIGVFVVCWPFPEFTYTLTAVGCSVPRTLKFFFWFGYCNS 420

QY 421 LNPVIYTIENHDFRRAFKILC 442

Db 421 LNPVIYTIENHDFRRAFKILC 442

RESULT 10

US-08-194-338-4

; Sequence 4, Application US/08194338

; Patent No. 5474898

; GENERAL INFORMATION:

; APPLICANT: Venter, John C.

; APPLICANT: Fraser, Claire M.

; APPLICANT: McCombie, William R.

; TITLE OF INVENTION: OCTOPAMINE RECEPTOR

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson and Bear

; STREET: 620 Newport Center Drive, Sixteenth Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: USA

; ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/194,338

FILING DATE: 08-FEB-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/676,174

FILING DATE: 28-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Israelsen, Ned A.

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: NIH101.001DV1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 461 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

US-08-194-338-4

Query Match 47.9%; Score 1140.5; DB 1; Length 461;

Best Local Similarity 50.7%; Pred. No. 3.1e-58;

Matches 248; Conservative 41; Mismatches 99; Indels 101; Gaps 12;

QY 10 NASWNGTEAPGGGARAT-----PYSLOVTLTVCLAGLMLLTVFGNVLIIVAVFT 60

Db 19 NAAAGAGERSGGVANASGASWGPFRGQYSAGAVAGLAAYVGLIVFTVGVNVLIIVAVLT 78

QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFGKAWCEIYLALDVLFTSS 120

Db 79 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFGQVWCGVYLALDVLFTSS 138

QY 121 IVHLCALISLDRYWSITQAIIEYNLKRTPRRIKAIITVWVISAVISFPPILSIEKKGGGG 180

```
|||||
Db 139 IVHLCAISLDRKWSVTGAVEYNLKRTPRRVKATIVAVWIISAVISFPLVSLYRQPDGA- 197
QY 181 PQAEPCEINDQKWYVISSCIGSFAPCLIMLVYRIYQIAKRTRVPPSRGPDAVA 240
Db 198 ---AYPOGLNDETWYILSSCISQSFAPCLIMGLVARIYRAKRRTRLSEKRAP---Y 251
QY 241 APPGTERRPKGLGPERSAGPGAE---AEPPTQLNGAPGEPAPAGPRDTALDLEESS 297
Db 252 GPDGASPTTENG LG---AAAGEARTGTARPRP-----PTWARTR----- 287
QY 298 SSDHAERP---PGPRRPERGPRGCKARASQVKPGDSLPRRGPGATGIGTPAGPGEER 353
Db 288 ---AAQRRRGAGPGLR--RGGRRRAGAEG-----GAGGADGGAGAGPAAQ 328
QY 354 VGAAKASRWG-----RQNRKRTFVLAVVIG 381
Db 329 SGALTASRSPGPGRLSRASSRSEVFLSRRRARRASSVCRRKVAQAAREKRTFVLAVVWG 388
QY 382 VFVVCWPEPFEFTYTLTAV---GCSVPRTLKFFFWEGYCNSSLNPVITYTFNHDRRAFK 438
Db 389 VFVLCWPEPFEFTYSLYGICREACQVPGLKFFFWIGYCNSSLNPVITYTFNODFRASF 448
QY 439 KILCRGDRK 447
Db 449 HILFRRRRR 457

RESULT 11
US-08-118-270-19
; Sequence 19, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-19
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Query Match 44.0%; Score 1046.5; DB 1; Length 330;
Best Local Similarity 50.7%; Pred. No. 5.2e-53;
Matches 216; Conservative 38; Mismatches 55; Indels 117; Gaps 9;

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QY 36 LVCLAGLMLLTVEGNVLIIVFTSRALKAPQNLFLVSLASADILVATLVIPESLANEV 95
Db 4 LAAVGFLIVFTVGNLVLIIVAVLTSRALRAPQNLFLVSIASADILVATLVMPESLANEI 63
QY 96 MGWYFGKAWCEIYALADVLECTSSIVHLCAISLDRYWSITQAIENLKRTPRRIKAIIT 155
Db 64 M-YWYFGQVWCYVLAIDVLECTSSIVHLCAISLDRYWSVTQAVEYNLKRTPRRVKATIV 122
QY 156 TWVVISAVISFPLISIEKKGGGGQPQAEPRCEINDQKWYVISSCIGSFAPCLIMILV 215
Db 123 AVLISAVISFPLVSLYRQPDGA---AYPOGLNDETWYILSSCISQSFAPCLITYLV 178
QY 216 YVRIYQIAKRTRVPPSRGPDVAAPPGCTERRPKGLGPERSAGPGAEAEPLPTQLNG 275
Db 179 YARIYRAKRRTRLSEKRAP-----VGPDGAS---PTTENG 212
QY 276 APGEPAPAGPRDTALDLEESSSSSDHAERPPGPRRPERGPRGCKARASQVKPGDSLPRR 335
Db 213 L----- 213
QY 336 GPGATGIGTPAGGEEERVGAKE--ASRWGR-----QNRKRTFVLAVVIGVEV 384
Db 214 -----GAAGEARTGTARFLSRRRARRASSVCRRKVAQAAREKRTFVLAL---VEV 260
QY 385 VCWPEPFEFTYTLTAV---GCSVPRTLKFFFWEGYCNSSLNPVITYTFNHDRRAFKIL 441
Db 261 LCWPEPFEFTYSLYGICREACQVPGLKFFFWIGYCNSSLNPVITYTFNODFRPSFKIL 320
QY 442 CRGDRK 447
Db 321 FRRRRR 326
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RESULT 12
PCT-US93-08528-19
; Sequence 19, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
```


APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-20

Query Match 43.2%; Score 1029; DB 5; Length 330;
Best Local Similarity 53.0%; Pred. No. 5.2e-52;
Matches 221; Conservative 41; Mismatches 55; Indels 100; Gaps 14;

QY 33 TLTIVCLAGLMLTVEGNLVIIAFTSRALKAPQNLFLVSLASADILVATLVIPFSLA 92
DB 1 TAAIAAATFFILFTIFGNALVITAVLSRLRAPQNLFLVSLAADIIVATLIIIPFSLA 60
QY 93 NEVMGYWYFGKAWCEIYLALDVLFCTSSIVHLCAISLDYWSITQAIENLKRTPRRIKA 152
DB 61 NELGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDYMAVSRALEYNSKRTPRRIKC 120
QY 153 IITVWVISAVISFPPLISIEKKGGGGPQP-AEPRCEINDOKWYVIVSSCIGSEFAPCLI 211
DB 121 IILTVMIAAVISLPLI---YKDGQGPQPRGRPOCKLNOEAWYILSS-IGSFAPCLI 175
QY 212 MILVYVRIQIAKRTVRPPSRGPDVAAPPGGTERRPKGLGPERSAAGPGGAEPLEPT 271
DB 176 -LLVYLRITYLIAKR-----SNRRGPRA-----KCGPGQGESK----- 206
QY 272 QLNGAPGERAPAGPRDTDALDLESSSSDHAERPPGPRPERGPRGKGKARASQVAPGDS 331
DB 207 -----QPRP-----DH-----GGAIASAKLP--- 222
QY 332 LPRRGATGIGTPAGPGEERYGAAKASRWGRQN--REKRTFVLAVVIGVFVWCP 389
DB 223 -----AIASGRG---VGAIGGQWRRRAHYTREKRTFVLAVVIGVFVLCWEP 267
QY 390 FFEYTLTAV--GCSVPRTLFKFEFFWGYCNSLNPIYTIENHDFRAFKILCR 443
DB 268 FFEYSYLGAIKPKHCKVPHGLQFEFFWIGYCNSLNPIYTIENODF-RMFRILCR 323

RESULT 15
US-07-676-174A-2
Sequence 2, Application US/07676174A
Patent No. 5344776
GENERAL INFORMATION:
APPLICANT: Vantor, J. Craig
TITLE OF INVENTION: Octopamine receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: Eleventh Floor, 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/676,174A
FILING DATE: 19910328
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/79117/KIK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)861-3000
TELEFAX: (202)822-8944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 601 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-676-174A-2

Query Match 27.3%; Score 649; DB 1; Length 601;
Best Local Similarity 32.7%; Pred. No. 3.8e-30;
Matches 164; Conservative 75; Mismatches 161; Indels 102; Gaps 14;

QY 31 QVTLVCLAGLMLTVEGNLVIIAFTSRALKAPQNLFLVSLASADILVATLVIPFS 90
DB 108 EALLTALVLS-VIIVLFIIGNILVLSVFYTKPLRIQVNFIVSLAVADLVALLVLPFN 166
QY 91 LANEVMGYWYFGKAWCEIYLALDVLFCTSSIVHLCAISLDYWSITQAIENLKRTPRRI 150
DB 167 VAYSILGRWEFGIHLCKMLTCDVLCCTSSILNCAIALDRYWAITDPIYNAOKRTVGRV 226
QY 151 KAITVWVISAVISFPPLISIEKKGGGGPOPAE---PCEINDOKWYVIVSSCIGSEF 206
DB 227 LLISGVWLLSLISSPPLI-----GWNQWPEFTSATPCELTSGRGYVIYSSIGSFE 279
QY 207 APCLIMILVYVRIQIAKRTVRPPSRGPDVAAPPGGTERRPKGLGPERSAAGPGAEA 266
DB 280 IPLAIMIVYIEIFATRRLRERARANKLNTIALK--STELPMANSSPVAAASNGSKS 337
QY 267 EPLPTQL-----NGAPGERAPAGP----- 285
DB 338 RLASWLCCGRDRAOFATPMIQNDQESISSETHQPODSSKAGPHGNSDPQOOHVVLVYK 397
QY 286 ---RDTAL-----DLESSSSDHAER-----PPGPRPERGPRGKGKARA- 323
DB 398 SRAKTKDSIKHGTGRGRKSQSSSTCEPHGEQOLLPAGGDGSCQPGGSHSGGKSDAE 457
QY 324 -----SQQKPGDSLPRGR-GATGIGTPAGPGEERYGAAK---ASRW 362
DB 458 ISTESGDPKGCIOQVCTQADEQTSKLTLPQOSTGVAASVYTLQKKTSGVNOFIEEQ 517
QY 363 RGRONREKRTFVLAVVIGVFVWCPFEFTYTLTAVGCSV--PRTLEK-FFWFGYCNS 419
DB 518 KISLSKERRARATLGIIMGVFICWLEFFLMYVILPF-CQTCPCPTNKFNFITWILGIINS 576
QY 420 SLNPVITYTFNHDERRAFKKIL 441
DB 577 GLNPVITYTFNLDYRRAFKRL 598

Search completed: February 14, 2003, 13:48:22
Job time : 17.5 secs

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-
-
•

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OM protein - protein search, using sw model

Run on: February 14, 2003, 12:02:50 ; Search time 12.5 Seconds

(without alignments)
919.760 Million cell updates/sec

Title: US-09-636-259B-4

Perfect score: 2380

Sequence: 1 MGSLPDAGNASWNGTEAPG.....HDFRAFKKILCRGDRKRIY 450

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1126.5	47.3	450	9	US-10-077-870-4	Sequence 4, Appl1
2	1126.5	47.3	450	10	US-09-825-923-4	Sequence 4, Appl1
3	1126	47.3	447	9	US-10-077-870-2	Sequence 2, Appl1
4	1126	47.3	447	10	US-09-825-923-2	Sequence 2, Appl1
5	649	27.3	601	10	US-09-782-980-84	Sequence 84, Appl1
6	649	27.3	601	10	US-09-884-430-8	Sequence 8, Appl1
7	590	24.8	422	9	US-10-166-101-3	Sequence 3, Appl1
8	585.5	24.6	377	12	US-10-005-010-2	Sequence 2, Appl1
9	585	24.6	451	10	US-09-993-844-6	Sequence 6, Appl1
10	580	24.4	376	9	US-10-166-101-5	Sequence 5, Appl1
11	577.5	24.3	390	12	US-10-005-010-4	Sequence 4, Appl1
12	573.5	24.1	517	10	US-09-951-622-10	Sequence 10, Appl1
13	566.5	23.8	520	9	US-10-185-991-4	Sequence 4, Appl1
14	560	23.5	497	12	US-10-052-589-2	Sequence 2, Appl1
15	555	23.3	390	9	US-10-166-101-6	Sequence 6, Appl1
16	553.5	23.3	572	9	US-10-185-991-2	Sequence 2, Appl1
17	547	23.0	466	9	US-10-185-991-6	Sequence 6, Appl1
18	545.5	22.9	466	10	US-09-951-622-11	Sequence 11, Appl1
19	542.5	22.8	501	10	US-09-951-622-9	Sequence 9, Appl1

20	510.5	21.4	370	9	US-10-109-532A-2	Sequence 2, Appl1
21	505	21.2	400	10	US-09-895-211-4	Sequence 4, Appl1
22	505	21.2	400	10	US-09-895-211-6	Sequence 6, Appl1
23	501.5	21.1	445	9	US-09-349-755-5	Sequence 5, Appl1
24	501.5	21.1	445	9	US-09-166-334-5	Sequence 5, Appl1
25	501.5	21.1	445	10	US-09-350-206-5	Sequence 5, Appl1
26	497	20.9	366	9	US-10-166-101-2	Sequence 2, Appl1
27	497	20.9	366	9	US-10-166-101-7	Sequence 7, Appl1
28	489.5	20.6	408	10	US-09-895-211-5	Sequence 5, Appl1
29	489.5	20.6	445	9	US-09-349-755-2	Sequence 2, Appl1
30	489.5	20.6	445	9	US-09-166-334-2	Sequence 2, Appl1
31	489.5	20.6	445	10	US-09-350-206-2	Sequence 2, Appl1
32	486.5	20.4	394	10	US-09-993-844-7	Sequence 7, Appl1
33	482.5	20.3	408	10	US-09-993-844-5	Sequence 5, Appl1
34	478	20.1	382	10	US-09-993-844-5	Sequence 10, Appl1
35	464	19.5	478	9	US-10-029-009-10	Sequence 2, Appl1
36	464	19.5	498	9	US-10-029-009-22	Sequence 22, Appl1
37	463	19.5	460	10	US-09-884-430-6	Sequence 82, Appl1
38	463	19.5	460	10	US-09-884-430-6	Sequence 82, Appl1
39	461.5	19.4	279	10	US-09-864-761-36992	Sequence 36992, A
40	460	19.3	359	10	US-09-951-622-13	Sequence 13, Appl1
41	452.5	19.0	445	10	US-09-989-861-16	Sequence 16, Appl1
42	444	18.7	388	10	US-09-989-861-8	Sequence 8, Appl1
43	441.5	18.6	359	10	US-09-989-861-19	Sequence 19, Appl1
44	440	18.5	460	9	US-10-166-101-4	Sequence 4, Appl1
45	435	18.3	387	10	US-09-989-861-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-10-077-870-4
; Sequence 4, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-870-4

Query Match 47.3%; Score 1126.5; DB 9; Length 450;
Best Local Similarity 53.2%; Pred. No. 2e-63;
Matches 243; Conservative 50; Mismatches 105; Indels 59; Gaps 14;
QY 27 PYSLOYTLIVCLAGLMLLTVEGVNVIYIAVFTSRALKAPQNLFLVSLASADILVATLV 86
DB 6 PYSVQATFAIAAATFLILFTIFGNALVILAVLTSRLRAPQNLFLVSLAADIIVATLI 65
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DB 66 IPFSLANELLGVIYFRRTWCEYIALDVLFCTSSIVHLCAISLDRYWAVSRALRYNSKRT 125
QY 147 PRRIKAIITWVVISAVISFPPLISIEKGGGGPQP-AEPRCEINDOKWYVSSCIGSF 205
DB 126 PRRIKAIITWVLIAAVISLPLI---YKGDQGPQPRGRPOCKLNOEAWYTIASSIGSF 181
QY 206 FAPCLIMILVYVRIOIAKRTRVPPSRGPDAAVAPDGTERRPKGLGPERSAGPGAE 265
DB 182 FAPCLIMILVYLRILYIAKR-----SNRGRPRAKGPGGEGSKQPR---PDHGCALASAK 233
QY 266 AEPLPT-----QLNG---ADGEPAPA-GPRDTDALDEES-----SS 298

Db 234 LPALASVASAREVNGHSKSTGEKEGETPEDTGTTRALPPSWAALPNSGQGQKEGVCASP 293
QY 299 SDHAERPPGRRPERGPRGKGKARASQVKPGD--SLPRRPG-----ATGIGTPAAGPGE 351
Db 294 EDEAEE-----EEEEEEEECEPQAVPSPASACSPPLQOPQGSRYLATLRGOVLLGRG- 348
QY 352 ERVGAAKASRWGRQ--NREKRTFVLAVVIGVFVVCWPFPEFFTYTLTAV--GCSVPRT 406
Db 349 --VGAIGGQWRRRAQLTREKRTFVLAVVIGVFVLCWPFPEFFSYSLGAICPKHCKVPHG 406
QY 407 LEKFFWFGYCNSSLNPVITYTIFNHDFRAFKILCR 443
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RESULT 2
US-09-825-923-4
; Sequence 4, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Nyyss"nen, Kristiina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kaunonen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT APPLICATION NUMBER: US/09/825,923
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422,985
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-923-4

Query Match 47.3%; Score 1126.5; DB 10; Length 450;
Best Local Similarity 53.2%; Pred. No. 2e-63;
Matches 243; Conservative 50; Mismatches 105; Indels 59; Gaps 14;
QY 27 PYSLOVTLTVCLAGLMLLTVEGNVLIITAVFTSRALKAPQNLFLVSLASADILVATLV 86
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QY 266 AEPLPT-----QLNG---APGEPAPA-GPRDTDALDLEES-----SS 298
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QY 299 SDHAERPPGRRPERGPRGKGKARASQVKPGD--SLPRRPG-----ATGIGTPAAGPGE 351
Db 294 EDEAEE-----EEEEEEEECEPQAVPSPASACSPPLQOPQGSRYLATLRGOVLLGRG- 348
QY 352 ERVGAAKASRWGRQ--NREKRTFVLAVVIGVFVVCWPFPEFFTYTLTAV--GCSVPRT 406
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QY 407 LEKFFWFGYCNSSLNPVITYTIFNHDFRAFKILCR 443
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RESULT 3
US-10-077-870-2
; Sequence 2, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-870-2

Query Match 47.3%; Score 1126; DB 9; Length 447;
Best Local Similarity 53.2%; Pred. No. 2.1e-63;
Matches 243; Conservative 50; Mismatches 102; Indels 62; Gaps 14;
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Db 126 PRIKCIITVWLIIAVISLPLI---YKGDQGPQPRGRPOCKLNOEAWIYLASSIGSF 181
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QY 266 AEPLPT-----QLNG---APGEPAPA-GPRDTDALDLEES-----SS 298
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US-09-825-923-2
; Sequence 2, Application US/09825923


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: Patent NO. US20010016338A1
: GENERAL INFORMATION:
: APPLICANT: Snapir, Amir
: APPLICANT: Heinonen, Paula
: APPLICANT: Alhopuro, Pia
: APPLICANT: Karvonen, Matti
: APPLICANT: Koulou, Markku
: APPLICANT: Pesonen, Ullamari
: APPLICANT: Scheinin, Mika
: APPLICANT: Salonen, Jukka T
: APPLICANT: Tuomainen, Tomi-Pekka
: APPLICANT: Lakka, Timo A
: APPLICANT: Nyyssänen, Kristiina
: APPLICANT: Salonen, Riitta
: APPLICANT: Kauppinen, Jussi
: APPLICANT: Valkonen, Veli-Pekka
: TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
: TITLE OF INVENTION: protein, and uses thereof
: FILE REFERENCE: Alpha-2B-AR variant
: CURRENT APPLICATION NUMBER: US/09/825,923
: PRIOR FILING DATE: 2001-04-05
: PRIOR FILING DATE: 2000-05-25
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn ver. 2.1
: SEQ ID NO 2
: LENGTH: 447
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-925-923-2

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; APPLICANT: Khodadoust, Mehran M.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Busfield, Samantha J.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gu, Wei
; APPLICANT: White, David
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND
; TITLE OF INVENTION: STMTS PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-121CP
; CURRENT APPLICATION NUMBER: US/09/782,980
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US00/02125
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/448,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/276,400
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: 60/117,580
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,195
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/014,348
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/086,892
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/296,208
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 09/063,950
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 09/561,381
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,810
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/087,121
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/672,721
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/049,799
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-782-980-84

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Db 362 FIVALVLPFCSSCHMPTLLGATINWLGYNSLNPVIYAYFNKDFQNAFKKITKCLFCR 421

RESULT 8
US-10-005-010-2

; Sequence 2, Application US/10005010
; Patent No. US20020115149A1
; GENERAL INFORMATION:
; APPLICANT: Weinschank et al, Richard L.
; TITLE OF INVENTION: Method of Obtaining A Composition Comprising A 5-HT1D
; FILE REFERENCE: 36536-BA
; CURRENT APPLICATION NUMBER: US/10/005,010
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/371,705
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-010-2

Query Match 24.6%; Score 585.5; DB 12; Length 377;
Best Local Similarity 31.2%; Pred. No. 8.2e-30;
Matches 138; Conservative 68; Mismatches 151; Indels 85; Gaps 9;

QY 4 LQPDAGNASWNGTEAPGGARATPYSLQVTLTLVCLAGLMLLTVEGNVLTIAVETSRA 63
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Db 69 LHPRANYLIGSLATDILVLSILVPIISAIYITHWNFGQILCDIWLSSDITCCTASILH 128
QY 124 LCAISLDYWSITQAIIEYNLKRTPRIKAIITVWVISAVISFPLISIEKKGCGGPQ 183
Db 129 LCVIALDRYWAITDALEYSKRTAGHAATMAIWAISICISIPPLFWQAKA-----QE 183
QY 184 AEBRCEIN-DQKWYVSSCIGSEFAPCLIMILVYVRIYQIAKRTRVPPSRGPDVAAP 242
Db 184 EMSDCLVNTSQISYTYSTCGAFYIPSVLILYGRYRAARNRLNPPSLYGKRTYA- 242
QY 243 PGCTERRPKGLPERSAGPGGAEAEP LPTQNGAPGEPAPAGPDDTDALDESSSSDHA 302
Db 243 -----HLLTGSAG-----SSLCSLNSSLHGHHS 265
QY 303 ERPPGRPERGPRGKGKARASQVKGPSLPRRGATGIGTPAAGPGEERVGAAKASRW 362
Db 266 HSAGSPL-----PFNHVKIKLADSALER-----KRISAA----- 294
QY 363 RGRQNRKRTFVLAVVIGVFWCWPPEFTYTLTAV--GCSVPRTLKFFFWFGYCN 419
Db 295 -----REKATKILGIIIGAFIICWLPDEFVSVLVPICRDSGWHPALFDFFTWLG 349
QY 420 SLNPVITYTFNHDFRRAFKIL 441
Db 350 LNPITYTFNEEFROAFQKIV 371

RESULT 9
US-09-993-844-6

; Sequence 6, Application US/09993844
; Patent No. US20020106739A1
; GENERAL INFORMATION:
; APPLICANT: Oakley, Robert H.
; APPLICANT: Barak, Lawrence S.
; APPLICANT: Laporte, Stephane A.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Modified G-Protein Coupled Receptors
; FILE REFERENCE: 033072-026

; CURRENT APPLICATION NUMBER: US/09/993,844
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,772
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/260,363
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence of 5HT1AR-V2R chimera
; OTHER INFORMATION: expressed from the pEARB-1/5HT1AR vector
US-09-993-844-6

Query Match 24.6%; Score 585; DB 10; Length 451;
Best Local Similarity 34.2%; Pred. No. 1e-29;
Matches 166; Conservative 59; Mismatches 164; Indels 96; Gaps 20;

QY 1 MSLQPDAGNASWNGTEAP-----GG---GARATPYSLQVTLTLVCLAGLMLLTVEGNV 52
Db 1 MDVLSPGGN---NTTSPAPFETGNTTGISDVTVSQVITSL--LLGTLIFCAVLGNA 55
QY 53 LVIIAVFTSRALKAPONFLVSLASADILVATLVIPESLANEVMGYWFGKAWCEIYAL 112
Db 56 CVVAIALERSLQNVANYLIGSLAVTDLWVSVLVPMAALYQVNLKWTIGQVTCDFIAL 115
QY 113 DVLCTSSIVHLCAISLDYWSITQAIIEYNLKRTPRIKAIITVWVISAVISFPLISI 172
Db 116 DVLCTSSIVHLCAIALDRYWAITDPIYVNRTPRAAALISLTWLGFLISIPML-- 173
QY 173 EKKGGGGGPQ-AEP-RCEINDQKWYVSSCIGSEFAPCLIMILVYVRIYQIAK---RRT 227
Db 174 ---GWRTPEDRSDDPDACITISKDHGYTYSTGAFYIPPLMLLVLYGRIFRAFRIRKT 229
QY 228 RVPPSRRGPD---AVAAP-----GCTERRPKGLPERSAGPGGAEAEP LPTQNGA- 276
Db 230 VKKVEKTGADTRHGASPAPOPKSVNGESGRNWRILGVESKA--GGALC-----ANGAV 281
QY 277 -PGEAPAGPRD DALDLEE-----SSSDHAERPPGPRRPERGPRGKGKARASQVKGDS 331
Db 282 RQGD-----DGAALVIEVHRYGNSKEHLPLP-----SEAGP----- 313
QY 332 LPRRGATGIGTPAAGPGEERVGAAKASRWGRQ-NREKRTFVLAVVIGVFWCWP 390
Db 314 -----TPCAPASFERNERNNAEAKRKMALAREFKTVKTLGIMGTIFLCWLP 361
QY 391 FETTYTLTAV--GCSVPRTLKFFFWFGYCNSSLNPVIYTYTFNHDFRRAFKIL---CR 443
Db 362 FIVALVLPFCSSCHMPTLLGATINWLGYNSLNPVIYAYFNKDFQNAFKKITKCNFCA 421
QY 444 GDRKR 448
Db 422 AARGR 426

RESULT 10
US-10-166-101-5

; Sequence 5, Application US/10166101
; Publication No. US2003000823A1
; GENERAL INFORMATION:
; APPLICANT: Weinschank, Richard L.
; APPLICANT: Branchek, Theresa
; APPLICANT: Hartig, Paul
; TITLE OF INVENTION: DNA Encoding A 5-HT1F Receptor And Uses Thereof
; FILE REFERENCE: 39318-C
; CURRENT APPLICATION NUMBER: US/10/166,101
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/246,075
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 08/483,222

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; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/117,006
; PRIOR FILING DATE: 1994-08-22
; PRIOR APPLICATION NUMBER: PCT/US93/00149
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: 07/817,920
; PRIOR FILING DATE: 1992-01-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 5
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-166-101-5
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Query Match      24.4%; Score 580; DB 9; Length 376;
Best Local Similarity 31.2%; Pred. No. 1.8e-29;
Matches 138; Conservative 66; Mismatches 152; Indels 86; Gaps 9;
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OY 4 LOPDAGNASWNGTEAPGGARATPYSLQVTLTLVCLAGLLMLTVEGNVLIIAVFTSRA 63
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 11 LPOEASNRSLNATETSEAWDPRTLQALKISLAVV--LSVITLATVLSNAFVLTILLTRK 68

OY 64 LKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWYFGKAWCEIYALDVLCTSSIVH 123
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 69 LHTPPANYLIGSLATYDLVLSILVMPISMAYTITHTWNGOILCDIWLSSDITCCTASILH 128

OY 124 LCAISLDYWSITQAIENYLNKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGGGP 183
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Db 129 LCVIALDRYWAITDALEYSKRRTAGHAATMIAIWAISICISIPPLFWROAKA-----QE 183

OY 184 AEPREIN-DQKWYVISSCIGSFAPCLIMILVYVRIYQIAKRTRVPPSRGPDVAAP 242
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Db 184 EMSDCLVNTSQISYTIYSTCGAFYIPSVLLIILYGRYRAARNRILNPPSLYGKFTTA- 242

OY 243 PGTERRRPKGLGPERSAGPGGAEPPLPTQLNGAPGPAPAGPRDTDALDESSSSSDHA 302
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Db 243 -----HLITGSG-----SSLSLNSLSLHEGHS 264

OY 303 ERPPGRRRPERGPRGKAKARASQVKGPSLPRRPGATGIGTPAAGPGEERVGAAKASRW 362
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 265 HSAGSPL-----FFNHVYKILADSALER-----KRISA----- 293

OY 363 RGRONREKRTFVLAVVIGVFWCWPPEFTYTLTAV---GCSVPRTLKFFWEGYCNS 419
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Db 294 -----RERKATKILGILGAFICWLPFEVSVSLVPLICRDSQWHPGLFDFETWLGILNS 348

OY 420 SLNPVITYTFNHDFRAFKKIL 441
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Db 349 LINPITYVNEEFROAFQKIV 370
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RESULT 11
US-10-005-010-4
; Sequence 4, Application US/10005010
; Patent No. US20020115149A1
; GENERAL INFORMATION:
; APPLICANT: Weinschank et al, Richard L.
; TITLE OF INVENTION: Method of Obtaining A Composition Comprising A 5-HT1D
; TITLE OF INVENTION: Selective Compound
; FILE REFERENCE: 36536-BA
; CURRENT APPLICATION NUMBER: US/10/005,010
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/371,705
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-010-4
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Query Match      24.3%; Score 577.5; DB 12; Length 390;
Best Local Similarity 30.6%; Pred. No. 2.7e-29;
Matches 140; Conservative 60; Mismatches 152; Indels 105; Gaps 11;
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OY 6 PDAGNASW-----NGTEAPGGARATPY-----SLQVTLTLVCLAGLLMLTVEGNVLVI 55
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Db 12 PPAGSETWVPQANLSSAPQNSCAKDIYQDSISLPMKVLVLMALLATLATLSNAFVI 71

OY 56 IAVFTSRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWYFGKAWCEIYALDVL 115
   | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 72 ATVYTRKRLHTPPANYLIASLAVTDLVLSILVMPISMTYVTGRWTLGQVCDFWLSSDIT 131

OY 116 FCTSSIVHLCAISLDYWSITQAIENYLNKRTPRRIKAIITVWVISAVISFPPLISIEKK 175
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Db 132 CCTASTLHLCVIALDRYWAITDAVEYSAKRTPKRAVMIALVWVFESISISLPPFFWROAK 191

OY 176 GGGGPPQPAEPREIN-DQKWYVISSCIGSFAPCLIMILVYVRIYQIAKR-TRVPPSR 233
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Db 192 A-----EEVSECVNTDHLITYVYSTVGAFYFPTLLIALYGRITYEARSRILKQTPNR 246

OY 234 RG-----PDVAAPPGGTERRRPKGLGPERSAGPGGAEPPLPTQLNG-APGEPAPAGPRD 287
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Db 247 TGRRLTRAQLITDSPGSTS-----VTSINSRVDPVSESG--- 282

OY 288 TDALDESSSSSDHAERPPGRRPERGPRGKAKARASQVKGPSLPRRPGATGIGTPAA 347
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 283 -----SPVYVNOYK----- 291

OY 348 GPGEERVGAAKASRWGRONREKRTFVLAVVIGVFWCWPPEFTYTLTAV---GCSVP 404
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Db 292 ----VRSDALLEKKKLMARERAKFTLGIILGAFIYCWLPFEIISLVMPICKDACWEH 347

OY 405 RTLKFFFWFGYCNSSLNPVITYTFNHDFRAFKKIL 441
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Db 348 LAIFDFFTWLGYLNSLINPITYTMSNEDFKQAFHKLI 384
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RESULT 12
US-09-951-622-10
; Sequence 10, Application US/09951622
; Patent No. US20020106734A1
; GENERAL INFORMATION:
; APPLICANT: Daniel R. Soppet et al.
; TITLE OF INVENTION: ADRENERGIC RECEPTOR
; FILE REFERENCE: PFI28D2C1
; CURRENT APPLICATION NUMBER: US/09/951,622
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/339,244
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: 09/030,582
; PRIOR FILING DATE: 1998-02-25
; PRIOR FILING DATE: 1995-06-06
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US94/09051
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 517
; TYPE: PRT
; ORGANISM: human
US-09-951-622-10
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Query Match      24.1%; Score 573.5; DB 10; Length 517;
Best Local Similarity 29.3%; Pred. No. 6.2e-29;
Matches 131; Conservative 82; Mismatches 131; Indels 103; Gaps 8;
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OY 10 NASWNGTEAPGGARATPYSLQVTLTLVCLAGLLMLTVEGNVLIIAVFTSRALKAPON 69
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Db 22 NANFTGPNOTSSNSTLPQLDITRAISVGLVGAFLFAIVGNILVIISVACNRHLRPTN 81

OY 70 LFLVSLASADILVATLVIPFSLANEVMGYWYFGKAWCEIYALDVLCTSSIVHLCAISL 129
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Db 82 YEIVNLAMADLLSFTVLPFSAALEVLGYWVIGRIFCDIWAADVLCCTASILSICAISI 141
QY 130 DRYWSITQAIENYLNKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGQPA---EP 186
Db 142 DRYIGVRSLOYPPLVTRKRAILALLSVWVLSVISIGPL-----GWKEPAPNDK 193
QY 187 RCEINDOKWYVVISGIGSEFPAPCLIMILVYRIYQIAKRTRVPPSRGPDVAAPPGT 246
Db 194 ECGVTEEPFYALFSSLSGYIPLAVILVMYCRVYIVAKRTTK----- 235
QY 247 ERRPKGLPERSAGPGAEEAPLPTQLNGAPGEPAPAGPRDTDALDLESSSSDHAERPP 306
Db 236 -NLEAGVMKEMS-----NSKELTLRIHSKNFHED--- 263
QY 307 GPRRPERGPRGKGKARASQVKGDSLPRGPGATGIGTPAAGPGEERVGAAKASRWGRQ 366
Db 264 -----TLSSTKAKGHNPRSSIAVKLFK----- 286
QY 367 NREKRTFVLAVVIGVFWCWFPEFFTYTLTAVGCSV--PRTLFKFFFWGYCNSSLNPV 424
Db 287 SREKKAATLGLVGMFILLCWLPFFIALPLGSLFSTLKPDPDAVFKVFWLGYFNSCLNPI 346
QY 425 IYTIENHDFRRAFKIL---CRGDRKR 448
Db 347 IYPCSSKEFKRAFVRILGCQCRGRRR 373

RESULT 13

US-10-185-991-4
; Sequence 4, Application US/10185991
; Publication No. US20030022900A1

GENERAL INFORMATION:

APPLICANT: Charles Gluchowski, et al.
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
TREAT BENIGN PROSTATIC HYPERPLASIA

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/185,991

FILING DATE: 28-Jun-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/444,783

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 520 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-185-991-4

Query Match 23.8%; Score 566.5; DB 9; Length 520;

Best Local Similarity 29.1%; Pred. No. 1.7e-28;
Matches 130; Conservative 82; Mismatches 132; Indels 103; Gaps 8;

QY 10 NASWNGTEAPGGARATPYSLQVTLTVCLAGLMLTVFGNVLIIVAVFTSRALKAPQN 69
Db 22 NANFTGPNQTSNSTLPOLDITRAISVGLVGAFLFAIVGNILVILSVACNRLHPTN 81
QY 70 LFLVSLASADILVATLVIPPSLANEVMGYWFGKAWCEIYLALDVLFTCTSSIVHLCAISL 129
Db 82 YEIVNLAMADLLSFTVLPFSAALEVLGYWVIGRIFCDIWAADVLCCTASILSICAISI 141
QY 130 DRYWSITQAIENYLNKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGQPA---EP 186
Db 142 DRYIGVRSLOYPPLVTRKRAILALLSVWVLSVISIGPL-----GWKEPAPNDK 193
QY 187 RCEINDOKWYVVISGIGSEFPAPCLIMILVYRIYQIAKRTRVPPSRGPDVAAPPGT 246
Db 194 ECGVTEEPFYALFSSLSGYIPLAVILVMYCRVYIVAKRTTK----- 235
QY 247 ERRPKGLPERSAGPGAEEAPLPTQLNGAPGEPAPAGPRDTDALDLESSSSDHAERPP 306
Db 236 -NLEAGVMKEMS-----NSKELTLRIHSKNFHED--- 263
QY 307 GPRRPERGPRGKGKARASQVKGDSLPRGPGATGIGTPAAGPGEERVGAAKASRWGRQ 366
Db 264 -----TLSSTKAKGHNPRSSIAVKLFK----- 286
QY 367 NREKRTFVLAVVIGVFWCWFPEFFTYTLTAVGCSV--PRTLFKFFFWGYCNSSLNPV 424
Db 287 SREKKAATLGLVGMFILLCWLPFFIALPLGSLFSTLKPDPDAVFKVFWLGYFNSCLNPI 346
QY 425 IYTIENHDFRRAFKIL---CRGDRKR 448
Db 347 IYPCSSKEFKRAFVRILGCQCRGRRR 373

RESULT 14

US-10-052-589-2

; Sequence 2, Application US/10052589

; Patent No. US20020133832A1

GENERAL INFORMATION:

APPLICANT: Perez, Dianne

APPLICANT: Zusck, Michael

TITLE OF INVENTION: Model systems for neurodegenerative and cardiovascular disorder

FILE REFERENCE: 26473/04200

CURRENT APPLICATION NUMBER: US/10/052,589

CURRENT FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: US 09/568,255

PRIOR FILING DATE: 2000-05-10

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentln version 3.0

SEQ ID NO 2

LENGTH: 497

TYPE: PRT

ORGANISM: Mesocricetus sp.

US-10-052-589-2

Query Match 23.5%; Score 560; DB 12; Length 497;
Best Local Similarity 29.1%; Pred. No. 4.1e-28;

Matches 136; Conservative 82; Mismatches 132; Indels 118; Gaps 11;

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Db 1 MNPDLDTGHTNSAPAQWGLKADANFTGPNQTSNSTLPOLDVTRAISVGLVGAFLFAI 60
QY 49 FGNVLVITAVFTSRALKAPQNLFLVSLASADILVATLVIPPSLANEVMGYWFGKAWCEI 108
Db 61 VGNILVILSVACNRLHRTPTNYFTVNLAIADLLSFTVLPFSATLVGLGYWVIGRIFCDI 120
QY 109 YLALDVLECTSSIVHLCAISLDRYWSITQAIENYLNKRTPRRIKAIITVWVISAVISFP 168
Db 121 WAAVDVLCCTASILSICAISIDRYIGVRSLOYPPLVTRKRAILALLSVWVLSVISIGP 180


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BASE COUNT      463 a      1027 c      938 g      495 t
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Query Match          81.0%; Score 1093.4; DB 4; Length 2923;
Best Local Similarity 89.8%; Pred. No. 2e-127;
Matches 1221; Conservative 0; Mismatches 126; Indels 12; Gaps 4;
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Db 1509 ATGGGCTCCCTGCAGCCGCGAGCGGGCAACGCGAGCTGGAACGGAGCCGCGGGG 1568
QY 61 GGGGGGCGCCGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGGCTGGCC 120
Db 1569 GGGGGGCGCCGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGGCTGGCT 1628
QY 121 GGCCTGCTCATGCTGCTCAACCGTGTTCGGCAACGCTGCTCATCATCGCCGTGTTACG 180
Db 1629 GGCCTGCTCATGCTGCTCAACAGTGTTCGGTAACGTGCTTGTATCATGCTGTGTTCACA 1688
QY 181 AGCCGCGGCTCAAGGGGCCCCAAAACCTCTTCCTGCTGTCTGCGCTCGCCGCGACATC 240
Db 1689 AGCCGCGGCTCAAGGGGCCCCAGAATCTTCTCTGCTGTCTGCTGCGCGGACATC 1748
QY 241 CTGGTGGCCACGCTGCTCATCCCTTTCGCTGGCCCAACGAGTCAATGCGCTACTGTAC 300
Db 1749 CTGGTGGCCACGCTGCTCATCCCTTTCGCTGGCCCAACGAGTCAATGCGCTACTGTAC 1808
QY 301 TTCGGCAAGGCTGTGTCAGATCTACCTGCGGCTCGACGTGCTCTCTGCAAGCTGCTCC 360
Db 1809 TTCGGCAAGGCTGTGTCAGATCTACCTGCGGCTCGACGTGCTCTCTGCAAGCTGCTCC 1868
QY 361 ATCGTGACCTGTGCGCCATCAGCCTGAGCCGCTACTGTCCATCACACAGGCCATGAG 420
Db 1869 ATAGTGACCTGTGCGCCATCAGCCTGAGTCGTTACTGTCCATCACACAGGCCATGAG 1928
QY 421 TACAACCTGAAGCGCACGCGCGCGCATCAAGGCCATCATCATCACCCTGTGGTCATC 480
Db 1929 TACAACCTGAAGCGCACGCGCGCATCAAGGCCATCATCATCACCCTGTGGTCATC 1988
QY 481 TCGGCGGTCAATCTCTCCCGCGCTCATCTCCATCGAGAAGAAGGGCGCGCGCGGC 540
Db 1989 TCGGCGGTCAATCTCTCCCGCGCTCATCTCCATCGAGAAGAAGGGCGAGGTGCG 2048
QY 541 CCGCAGCGCGCGCGAGCGCGGCTGCGAGATCAACGACGAGAGTGTACGTATCTGTCG 600
Db 2049 CAGCGGTGCGCGCAACCGCGCTGTGAGATCAACGACGAGAGTGTACGTATCTGTCG 2108
QY 601 TGCATCGGCTCTCTTTCGCTCCCTGCTCATCATGATCTGCTCTACGTGCGCATCTAC 660
Db 2109 AGCATCGGCTCTCTTTCGCGCCCTGCTCATCATGATCTGCTCTATGTGCGCATCTAC 2168
QY 661 CAGATCGCCAAGCGTGCACCCGCGTGCACCCAGCGCGCGGGTCCGAGCGCGCTGCGC 720
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QY 721 GC---GCCGCGGGGGGCGACCGAGCGAGCGCCCAAGGGGTGCGCGCGCGAGC---GCAGC 774
Db 2229 GCTGAGCTGCGCAGGAGCGCGCGAGCGCGCCCAACGCGCTTGCGCGCGCGCGCGC 2288
QY 775 GCGGGCGCGGGGGCGCAGAGCGCGCAACCGCTGCCACCCAGCTCAACGGCGCGCTGCG 834
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Db 2289 GTGGGCCCCGTGGGCGCCCGAGAGGTGCTGCTGACAGGTCCAGCTCAATGTGCCCCGGGG 2348
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Db 2349 GAGCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2405
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Db 2466 GCGAAGCGCGCGCGAGCGAGCGAGTGAAGCCGGGCGGACAGCGCTGCGCGCGCGCGCGG 2525
QY 1015 GCGACGGGATCGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1071
Db 2526 GCGACGGGCTGGGGGCGACCGCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 2585
QY 1072 AAGCGTGGCGCTGGCGCGCGCGCGCGCGCGCGCGCGAGAACCGCGAGAACCGCTTACGTT 1131
Db 2586 AAGCGTGGCGCTGGCGCGCGCGCGCGCGCGCGCGCGAGAACCGCGAGAACCGCTTACGTT 2645
QY 1132 GTGTCATCGGAGTGTTCGTGTGTGTGTGTGTTCCTCCCTTCTTCTTACCTACACGCTCACG 1191
Db 2646 GTGTCATCGGAGTGTTCGTGTGTGTGTGTGTTCCTCCCTTCTTCTTACCTACACGCTCACG 2705
QY 1192 GCCGTGGGCTGCTCCGTCGACGACGCGCTTCAAAATCTTCTTCTGTTGCGCTACTGCG 1251
Db 2706 GCCATGGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCTTCAAGTCTTCTTCTGTTGCGCTACTGCG 2765
QY 1252 AACAGCTGCTGAACCGCGGTCAATCTACACCATCTTCAACGATTTCCGCGCGCTTC 1311
Db 2766 AACAGCTGCTGAACCGCGGTCAATCTACACCATCTTCAATCAAGACTTCCGCGCGCTTC 2825
QY 1312 AAGAAGATCTCTGTGCGGGGCGACGGAAGCGATGTCG 1350
Db 2826 AAGAAGATCTCTGTGCGGGGCGACGGAAGCGATGTCG 2864
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Job time : 4479.27 secs

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BASE COUNT	213 a	461 c	446 g	260 t		
ORIGIN						
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Pred. No. 2e-127; Mismatches 160; Indels 0; Gaps 0;						
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ORIGIN						
Query Match	Best Local Similarity	Matches	Conservative	Score	DB	Length
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Pred. No. 2e-127; Mismatches 160; Indels 0; Gaps 0;						
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ORIGIN						
Query Match	Best Local Similarity	Matches	Conservative	Score	DB	Length
81.0%;	88.1%;	1190;	0;	1094;	10;	1380;
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BASE COUNT	213 a	461 c	446 g	260 t		
ORIGIN						
Query Match	Best Local Similarity	Matches	Conservative	Score	DB	Length
81.0%;	88.1%;	1190;	0;	1094;	10;	1380;
Pred. No. 2e-127; Mismatches 160; Indels 0; Gaps 0;						
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BASE COUNT	213 a	461 c	446 g	260 t		
ORIGIN						
Query Match	Best Local Similarity	Matches	Conservative	Score	DB	Length
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Db	781	ACCGCGGGCGCGAGAGCCGAGCCGCTGCCCCACCCAGCTTAACGGCGCCCGGGGAGCCCC	840
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QY	961	GCCCCGAGCGACCCAGGTGAACCCCGGGCGACAGCCTGCCCGCGCGCGGGCGCGGCGCAG	1020
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RESULT 15
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DEFINITION Bos taurus alpha2D adrenergic receptor gene, complete cds.
ACCESSION  U79030
VERSION    U79030.1   GI:3282232
KEYWORDS
SOURCE
ORGANISM   Bos taurus.
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REFERENCE  1 (bases 1 to 2923)
            Venkataraman,V., Duda,T. and Sharma,R.K.
            The bovine alpha 2D-adrenergic receptor gene: structure, expression
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            Mol. Cell. Biochem. 177 (1-2), 113-123 (1997)
JOURNAL   9811113
MEDLINE   9450652
PUBMED
REFERENCE  2 (bases 1 to 2923)
            Venkataraman,V., Duda,T.M. and Sharma,R.K.
            Direct Submission
            Submitted (20-NOV-1996) Cell Biology, UMDNJ-SOM, 2 Medical Ctr Dr,
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JOURNAL
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Db	601	TCCATCGGCTCTTCTTGGGCTTGGCTCATCATGATCTGTCTACGTGCGTATCTAC	660		
OY	661	CAGATCGCCAAAGCGTCGACCCGCGCTGCCACCAAGCGCGGGTCCGGACGCGCTGCGC	720		
Db	661	CAGATCGCCAAAGCGTCGACCCGCGCTGCCCGCCAGTCCGCGGGTCCGGACGCGCTGTTCC	720		

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Db	1261	CTGAACCGTGTATCTACACCATTTTCAACACGACTTCCGCGCGCTTCAAGAAGATC	1320		
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LOCUS					
DEFINITION		Rat alpha-2-adrenergic receptor protein (RG20) gene, complete cds.			
ACCESSION		M62372			
VERSION		M62372.1 GI:206615			
KEYWORDS		alpha-2-adrenergic receptor; transmembrane protein.			
SOURCE		Rattus norvegicus			
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
REFERENCE		1 (bases 1 to 1380)			
AUTHORS		Lanier,S.M., Downing,S., Duzic,E. and Homcy,C.J.			
TITLE		Isolation of rat genomic clones encoding subtypes of the alpha			
JOURNAL		2-adrenergic receptor. Identification of a unique receptor subtype			
MEDLINE		J. Biol. Chem. 266 (16), 10470-10478 (1991)			
PUBMED		91244823			
FEATURES		1645350			
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DEFINITION
ACCESSION      U79031
VERSION      U79031.1 GI:3282234
KEYWORDS
SOURCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 1552)
Chalberg,S.C., Duda,T., Rhine,J.A. and Sharma,R.K.
Molecular cloning, sequencing and expression of an alpha
2-adrenergic receptor complementary DNA from rat brain
Mol. Cell. Biochem. 97 (2), 161-172 (1990)
JOURNAL
MEDLINE      91125329
PUBMED      2177834
2 (bases 1 to 1552)
Wypijewski,K., Duda,T. and Sharma,R.K.
Structural, genetic and pharmacological identity of the rat alpha
2-adrenergic receptor subtype ca2-47 and its molecular
characterization in rat adrenal, adrenocortical carcinoma and
bovine retina
Mol. Cell. Biochem. 144 (2), 181-190 (1995)
JOURNAL
MEDLINE      95349560
PUBMED      7623790
3 (bases 1 to 1552)
Venkataraman,V., Duda,T.M. and Sharma,R.K.
Direct Submission
Submitted (20-NOV-1996) Cell Biology, UMDNJ-SOM, 2 Medical Ctr.
Dr., Stratford, NJ 08084, USA
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BASE COUNT 268 a 590 c 562 g 308 t

ORIGIN

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DB 610 TCGGCGCTCATCTCTTCCCGCGCTCATCTCCATCGAGAAGAAGGGCGCGCGCGG 669
QY 541 CCGGAGCGCGCGCGAGCGCGCGCTGCGAGATCAACGACGAGAAGTGTTACGTCATCTCG 600
DB 670 CAGGAGCGCGCGCGAGCGCGCGCTGCGAGATCAACGACGAGAAGTGTTACGTCATCTCT 729
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DB 730 TGCATCGGCTCTTCTGCTCCCTGCTCATCATGATCTGCTTATGTCGATCTAT 789
QY 661 CAGATCGCAAGCGTGCACCGCGCGGTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCG 720
DB 790 CAGATGAGCAAGCGCGCGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 849
QY 721 GCG 780
DB 850 GCGCTGCG 909
QY 781 CCGGCGCGCGCGCGAGAGCGCGCAACCGCTGCCACCGAGCTCAACGCGCGCGCGCGCG 840

DB 910 CGCGTGGCGCGCGGAGCGCGGAGCGCGCTACCCGCTCAGCTCAACGGTGGCCCCGGGAGGCC 969
QY 841 GCGCGCGCGCGCGCGCGCGCGCGAGACCGGAGCGCGCTGAGCTGAGAGAGAGCTGCTCCGAC 900
DB 970 GCGCGCGCTGGCGCGCGCGCGCGCTGACGGGCTGAGACTCGAGAGAGAGCTGCTGAG 1029
QY 901 CAGCGCGAGCGCGCTCCAGCGCGCGCGCGAGACCGGAGCGCGGTCGCCGGGCAAGCAAG 960
DB 1030 CAGCGCGAGCGCGCGCGCGCGCGCGCGAGCTCGAGCGCGCGCGCTCGGGCGCAAGCAAG 1089
QY 961 GCGCGAGCGAGCGAGGTGAAGCGCGCGGAGACAGCGCTGCGCGCGCGCGCGCGCGCGAG 1020
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DB 1150 GGGCGCGGGGCGCGCGCGCGCGAGCTGGGGCGGGGAGAGCGCGCGCGCGCGCGCG 1209
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DB 1270 GCGGTGTTCGTGCTGCTGCTGCTTCCCTTCTTCACTTCACTTCACTACAGCGCGCTAGGC 1329
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DB 1330 TGCTCGGTGCCCGCGCGCGCTCTTCAAGTTCCTTCTGCTGCTGCTGCAACAGCTCG 1389
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DB 1390 CTGAATCCGTTATCTACACCATCTTCAATCAAGACTTCCGCGCGCGCTTCAAGAGATC 1449
QY 1321 CTCTGTGCGGGGAGACGGAAGCGGATCGTG 1350
DB 1450 CTCTGCCGTGGGAGACGGAAGCGGATCGTG 1479

RESULT 12
CPU25722 2291 bp DNA linear ROD 05-SEP-2001
LOCUS Cavia porcellus alpha-2A adrenoceptor gene, complete cds.
DEFINITION
ACCESSION U25722
VERSION U25722.1 GI:818874
KEYWORDS

SOURCE
ORGANISM Cavia porcellus.
Cavia porcellus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
1 (bases 1 to 2291)
Svensson,S.P., Bailey,T.J., Porter,A.C., Richman,J.G. and
Regan,J.W.

TITLE
Heterologous expression of the cloned guinea pig alpha 2A, alpha
2B, and alpha 2C adrenoceptor subtypes. Radioligand binding and
functional coupling to a CAMP-responsive reporter gene

JOURNAL
MEDLINE Biochem. Pharmacol. 51 (3), 291-300 (1996)
96152573

PUBMED
REFERENCE 8573196
2 (bases 1 to 2291)
Richman,J.G.

AUTHORS
TITLE Direct Submission

JOURNAL
SUBMITTED (26-APR-1995) Jeremy G. Richman, University of Arizona,
Pharmacology and Toxicology, College of Pharmacy, Room 235, Tucson,
AZ 85721, USA

FEATURES
source location/Qualifiers
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/strain="Sasco Hartley albino"
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/clone="(GP) alpha-2A"
49..1401

CDS

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BASE COUNT 223 a 546 c 499 g 253 t

ORIGIN Chromosome 10q23-q25.

Query Match 97.6%; Score 1317.4; DB 9; Length 1521;
Best Local Similarity 99.4%; Pred. No. 2.9e-155;
Matches 1343; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

QY 1 ATGGGCTCCCTGACGCCGAGCGGGGCAACGCGAGCTGGAACGGGACGAGCGCGCGGG 60
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DB 119 GGGCGCGCGCGCGCGCGCGCGCTTACCTCCCTGCAGGTGACGCTGACGCTGTGCTGGCC 178
QY 121 GGCTGCTCATGCTGCTCACCCTGTTCGGCAACGTGCTGCTCATCATCGCCGTGTTACAG 180
DB 179 GGCTGCTCATGCTGCTCACCCTGTTCGGCAACGTGCTGCTCATCATCGCCGTGTTACAG 238
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DB 359 TTGCGCAAGGCTTGTGTCGAGATCTACCTGCGCTGCGAGTGTCTTCTGACGCTGCTCC 418
QY 361 ATCGTGACCTGTGCGCCATCAGCCCTGACCGCTACTGTTCCATCACAAGGCCATCGAG 420
DB 419 ATCGTGACCTGTGCGCCATCAGCCCTGACCGCTACTGTTCCATCACAAGGCCATCGAG 478
QY 421 TACAACCTGAAGCGCAGCGCGCGCGCGCGCATCAAGGCCATCATCAACCGTGTGGTCAATC 480
DB 479 TACAACCTGAAGCGCAGCGCGCGCGCGCGCATCAAGGCCATCATCAACCGTGTGGTCAATC 538
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DB 659 TGCATCGGCTCTTCTTCTGCTCCCTGCGCTCATCATGATCTCTGTTACGTCGCGCATCTAC 718
QY 661 CAGATCGCCAAGGCTGCGACCGCGCTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
DB 719 CAGATCGCCAAGGCTGCGACCGCGCTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 778
QY 721 GCG 780
DB 779 GCG 838

QY 781 CCGGGGGCGCAGAGCGCCGAACCGCTGCCACCCAGCTCAACGGCGCGCGCGCGCGCGCGCC 840
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QY 841 GCG 900
DB 899 GCG 958
QY 901 CACGCCGAGCGGCTCCAGGGCG 960
DB 959 CACGCCGAGCGGCTCCAGGGCG 1018
QY 961 GCGCGAGCGCAGGTGAAGCG 1020
DB 1019 GCGCGAGCGCAGGTGAAGCG 1077
QY 1021 GGGATCGGGACCGCGCGCTGCAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
DB 1078 GGGATCGGGACCGCGCGCTGCAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1137
QY 1081 CGCTGCG 1139
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QY 1140 CCGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1199
DB 1198 CCGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1257
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DB 1258 GTGCTCCGTGCGCAGCAGCGCTCTTCAAAATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1317
QY 1260 GTTGAACCCGGTCACTCAACCATCTTCAACGACGATTTCCGCCGCGCGCTTCAAGAAGAT 1319
DB 1318 GTTGAACCCGGTCACTCAACCATCTTCAACGACGATTTCCGCCGCGCGCTTCAAGAAGAT 1377
QY 1320 CCTCTGTCGGGGGACAGGAAGCGGATCGTG 1350
DB 1378 CCTCTGTCGGGGGACAGGAAGCGGATCGTG 1408

RESULT 11
PIGA2AR 1728 bp DNA linear MAM 27-APR-1993
LOCUS
DEFINITION Porcine alpha2A-adrenergic receptor (PORA2AR) gene, complete cds.
ACCESSION J05652
VERSION J05652.1 GI:164303
KEYWORDS alpha-2A-adrenergic receptor.
Porcine liver DNA.
SOURCE
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 1728)
Guyer,C.A., Horstman,D.A., Wilson,A.L., Clark,J.D., Kragoe,E.J.Jr.
and Limbird,L.E.
JOURNAL Unpublished (1990)
REFERENCE 2 (bases 70 to 1582)
Guyer,C.A., Horstman,D.A., Wilson,A.L., Clark,J.D., Cragoe,E.J. Jr.
and Limbird,L.E.
TITLE Cloning, sequencing, and expression of the gene encoding the
porcine alpha 2-adrenergic receptor. Allosteric modulation by Na+,
H+, and amiloride analogs
JOURNAL J. Biol. Chem. 265 (28), 17307-17317 (1990)
MEDLINE 91009167
PUBMED 2170371
COMMENT Draft entry and computer-readable sequence for [J. Biol. Chem.
(1990) in press] kindly submitted
by C.A.Guyer, 02-AUG-1990.
FEATURES
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/db_xref="taxon:9823"
130..1482


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Query Match 98.2%; Score 1325.4; DB 9; Length 3604;
Best Local Similarity 99.8%; Pred. No. 2.5e-156;
Matches 1348; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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QY 61 GGGGGCGCCCGGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGCTGCTGGCC 120
Db 2138 GGGGGCGCCCGGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGCTGCTGGCC 2197
QY 121 GGCCTGCTCATGCTGCTACCGCTGTTCGGCAACGCTGCTCATCATCGCCGTTTCACG 180
Db 2198 GGCCTGCTCATGCTGCTACCGCTGTTCGGCAACGCTGCTCATCATCGCCGTTTCACG 2257
QY 181 AGCCGCGCGCTCAAGGCGGCCAAAACCTCTTCTGCTGTGTCTCTGGCCTCGCGGACATC 240
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QY 301 TTCGGCAAGGCTTGTGGAGATCTACCTGGCGCTGACGCTCTTCTGACGCTGCTCC 360
Db 2378 TTCGGCAAGGCTTGTGGAGATCTACCTGGCGCTGACGCTCTTCTGACGCTGCTCC 2437
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QY 421 TACAACCTGAAGCGCAGCGCGCGCCGATCAAGGCCATCATCATCACCGTGTGGTCAATC 480
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QY 481 TCGGCCGTCATCTCTCCCGCGCTCATCTCCATCGAGAAGAGGCGCGCGCGCGG 540
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QY 601 TGCATCGGCTCTCTCTGCTCCGCTCATCATGATCCTGCTACGTCGCGATCTAC 660
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QY 661 CAGATCGCCAAGCGTGCACCCGCGTGCACCCAGCGCGGGGTCCGGACGCCGCTCGCC 720
Db 2738 CAGATCGCCAAGCGTGCACCCGCGTGCACCCAGCGCGGGGTCCGGACGCCGCTCGCC 2797
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QY 721 GCGCCCGCGGGGCGACCGAGCGCGAGCCCAAGGGTCTGCGCCCGGAGCGCGCGGGC 780
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QY 1021 GGGATCGGAGCGCGCGCTGCAGGGCGCGGGGAGAGAGCGCGCTCGGCGCTCCAGAGCGCTCG 1080
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QY 1081 CGCTGGCGCGGGGCGCGCAGAACCCCGAGAACCGCTTACAGTTCTGCTGCGCGCTGCTCAT 1139
Db 3157 CGCTGGCGCGGGGCGCGCAGAACCCCGAGAACCGCTTACAGTTCTGCTGCGCGCTGCTCAT 3216
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Db 3397 CCTCTGTGCGGGGGGACAGAGAGCGGATCGTG 3427

RESULT 10
HUMADRA
LOCUS
DEFINITION Human platelet alpha-2-adrenergic receptor gene, complete cds.
ACCESSION M18415
VERSION M18415.1 GI:178191
KEYWORDS alpha-2-adrenergic receptor; alpha-adrenergic receptor.
SOURCE Human (lambda-EMBL 3 library) DNA.
ORGANISM Homo sapiens
REFERENCE
  1. (bases 1 to 1521)
AUTHORS Kobilka, R.K., Matsui, H., Kobilka, T.S., Yang-Feng, T.L., Francke, U.,
  Caron, M.G., Lefkowitz, R.J. and Regan, J.W.
TITLE cloning, sequencing, and expression of the gene coding for the
  human platelet alpha 2-adrenergic receptor
JOURNAL Science 238 (4827), 650-656 (1987)
MEDLINE 88042789
PUBMED 2823383
FEATURES
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of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: PBACE3.6

This sequence is the entire insert of clone RP11-348N5 The true left end of clone RP11-479A21 is at 179266 in this sequence. The true right end of clone RP11-313D6 is at 44800 in this sequence.

FEATURES	Location/Qualifiers
source	1. .204908

BASE COUNT	62115	a	36724	c	39536	g	66533	t
ORIGIN								

Query Match	99.98%	Score 1348.4;	DB 9;	Length 204908;
Best Local Similarity	99.98%	Pred. No. 1.5e-159;		
Matches 1349; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

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QY	61	GGCGGCGCGGGGCAACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGCTGGCC	120
Db	195630	GGCGGCGCGGGGCAACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGCTGGCC	195689
QY	121	GGCGTCTCATGTGCTGCTACCGGTTCGGCAACGTGCTGTCATCATCGCCGTTCACG	180
Db	195690	GGCGTCTCATGTGCTGCTACCGGTTCGGCAACGTGCTGTCATCATCGCCGTTCACG	195749
QY	181	AGCGCGCGCTCAAGGCGGCCCAAAACCTTCTCTGCTGCTGCTGCGCTGGCCGACATC	240
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QY	241	CTGTTGGCCACGCTCGTCACTCCCTTCTCGCTGGCCAAAGAGTCATGGGCTACTGTAC	300
Db	195810	CTGTTGGCCACGCTCGTCACTCCCTTCTCGCTGGCCAAAGAGTCATGGGCTACTGTAC	195869
QY	301	TTCGGCAAGGCTTGGTGCAGATCTACCTGGCGCTCGACGTGCTCTTCGACGTCGTCC	360
Db	195870	TTCGGCAAGGCTTGGTGCAGATCTACCTGGCGCTCGACGTGCTCTTCGACGTCGTCC	195929
QY	361	ATCGTGACCTGTGGCCATCAGCCTGGAACCGCTACTGTCCATCACACAGGCCATCGAG	420
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QY	481	TGCGCCGTCTCTCTTCCCGCGCTCATCTTCATCGAGAAGAAGGGCGGCGGCGGC	540
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QY	661	CAGATCGCAAGCGTCGACCCCGCTGCACACCAGCGCGCGGGGTCCGGAGCGCGTCC	720
Db	196230	CAGATCGCAAGCGTCGACCCCGCTGCACACCAGCGCGCGGGGTCCGGAGCGCGTCC	196289
QY	721	GGCGCGCGGGGCAACCGAGCGGACCGCAAGGTCGTGGCCCCCGAGCGCAGCGCGGC	780
Db	196290	GGCGCGCGGGGCAACCGAGCGGACCGCAAGGTCGTGGCCCCCGAGCGCAGCGCGGC	196349
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Db	196350	CCGGGGGGCGCAGAGGCGCCGAACCGCTGCCCCACCCAGCTCAACGGCGCCCTGGCGAGGCC	196409
QY	841	GGCGCGGGCGGCGCGCGGACACCGACGCGCTGGACCTGGAGAGAGCTCGTCTTCCGAC	900
Db	196410	GGCGCGGCGGCGCGCGGACACCGACGCGCTGGACCTGGAGAGAGCTCGTCTTCCGAC	196469
QY	901	CACGCGGAGCGGCGCTCCAGGGGCCCCGCGAGACCCGAGCGCGGTCCCCGGGGCAAGGCAAG	960
Db	196470	CACGCGGAGCGGCGCTCCAGGGGCCCCGCGAGACCCGAGCGCGGTCCCCGGGGCAAGGCAAG	196529
QY	961	GCCCCGAGCGAGCCAGTGAAGCCGGGGCGACAGCTCGCGCGCGCGGGCGCGGGGCGACG	1020
Db	196530	GCCCCGAGCGAGCCAGTGAAGCCGGGGCGACAGCTCGCGCGCGCGGGCGCGGGGCGACG	196589
QY	1021	GGGATCGGGAGCGCGCGCTGCAGGGGCCCCGGGAGAGAGCGCGCTCGGGGCTGCCAAGCGCTCG	1080
Db	196590	GGGATCGGGAGCGCGCGCTGCAGGGGCCCCGGGAGAGAGCGCGCTCGGGGCTGCCAAGCGCTCG	196649
QY	1081	CGCTGGCGCGGGCGCGCAGAACCGCGAGAAAGCGCTTCACGTTTCGTGCGCGTGGTCAATC	1140
Db	196650	CGCTGGCGCGGGCGCGCAGAACCGCGAGAAAGCGCTTCACGTTTCGTGCGCGTGGTCAATC	196709
QY	1141	GGAGTGTTCGTGTGTGTGTTCCCTTCTTCTTCACTACACGCTCACGGCCGTGGG	1200
Db	196710	GGAGTGTTCGTGTGTGTGTTCCCTTCTTCTTCACTACACGCTCACGGCCGTGGG	196769
QY	1201	TGCTCCGTGCACGACAGCGCTTCAAAATTCTTCTGTGTTGGGCTACTGCAACAGCTCG	1260
Db	196770	TGCTCCGTGCACGACAGCGCTTCAAAATTCTTCTGTGTTGGGCTACTGCAACAGCTCG	196829
QY	1261	TTGAACCCCGGTATCTACACCAATCTTCAACACAGATTTTCGGCGCGCTTCAAGAAAGATC	1320
Db	196830	TTGAACCCCGGTATCTACACCAATCTTCAACACAGATTTTCGGCGCGCTTCAAGAAAGATC	196889
QY	1321	CTCTGTCTGGGGGACAGGAAGCGGATCGTG 1350	
Db	196890	CTCTGTCTGGGGGACAGGAAGCGGATCGTG 196919	

RESULT	9
HUMADRA2R	
LOCUS	HUMADRA2R 3604 bp DNA linear PRI 30-OCT-1994
DEFINITION	Human alpha 2 adrenergic receptor gene, complete cds.
ACCESSION	M23533
VERSION	M23533.1 GI:178195
KEYWORDS	adrenergic receptor; alpha-2 adrenergic receptor.
SOURCE	Human DNA.
ORGANISM	Homo sapiens

REFERENCE AUTHORS TITLE	1 (bases 1 to 3604)
<u>Fraser, C.M.</u> , Arakawa, S., McCombie, W.R. and Venter, J.C. Cloning, sequence analysis, and permanent expression of a human	11

alpha 2-adrenergic receptor in Chinese hamster ovary cells. Evidence for independent pathways of receptor coupling to adenylyl cyclase attenuation and activation
J. Biol. Chem. 264 (20), 11754-11761 (1989)

JOURNAL
MEDLINE
PUBMED
COMMENT

~~J. Biol. Chem. 264 (20), 11754-11761 (1989)
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Draft entry and computer-readable sequence for [1] kindly submitted
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1 (bases 1 to 204908)
Johnson, C.
Direct Submission
Submitted (13-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Dec 5, 2001 this sequence version replaced gi:16944857.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr10
RP11-348N5 is from the library RPCI-11.2 constructed by the group

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Mao, Z.-M., Tang, K., Li, B.-M. and Jing, N.-H.
Cloning and expression of human alpha-2a adrenergic receptor in
Sisy cells
Unpublished
2 (bases 1 to 3653)
Mao, Z.-M., Tang, K., Li, B.-M. and Jing, N.-H.
Direct Submission
Submitted (01-JUL-2000) Shanghai Institute of Physiology, Chinese
Academy of Sciences, 320 Yue Yang Road, Shanghai 200031, P.R. China
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Liu,L. and Yuan,L.
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 Liu,L. and Yuan,L.
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 Submitted (17-APR-2001) Key Laboratory of Molecular Biology,
 General Hospital of Airforce, Fucheng Road No. 30, Beijing 100036,
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VERSION AF262016.2 GI:9864781
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ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,
Beschi,M. and Agabiti Rosel,E.
TITLE A search for genetic variability in the human alpha-2 adrenergic
receptor on chromosome 10

JOURNAL
REFERENCE Unpublished
2 (bases 1 to 1941)
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,
Beschi,M. and Agabiti Rosel,E.

TITLE Direct Submission
JOURNAL Submitted (29-APR-2000) Medical and Surgical Sciences, University
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
REFERENCE 3 (bases 1 to 1941)
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,
Beschi,M. and Agabiti Rosel,E.

TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Medical and Surgical Sciences, University
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
REMARK Sequence update by submitter
COMMENT On Aug 22, 2000 this sequence version replaced gi:9837145.
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DEFINITION Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.
ACCESSION AF281308
VERSION AF281308.1 GI:9652209
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SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted G1 coupling
J. Biol. Chem. 275 (49), 38518-38523 (2000)

JOURNAL MEDLINE 20356293

PUBMED 10948191

REFERENCE 2 (bases 1 to 1353)
AUTHORS Small,K.M., Forbes,S.L., Bridges,K.M. and Liggett,S.B.
TITLE Direct Submission
Submitted (22-JUN-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA

JOURNAL

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DEFINITION Sequence 24 from Patent WO0179561.
ACCESSION AX350512
VERSION AX350512.1 GI:18616107
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 24 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten M. (US)

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VERSION AF316894.1 GI:12698667
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liiggett,S.B.
TITLE An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling
JOURNAL J. Biol. Chem. 275 (49), 38518-38523 (2000)

JOURNAL MEDLINE 20556293
PUBMED 10948191
REFERENCE 2 (bases 1 to 1353)
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liiggett,S.B.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 12:29:07 ; Search time 4002.27 Seconds
(without alignments)
9816.632 Million cell updates/sec

Title: US-09-636-259B-2
Perfect score: 1350
Sequence: 1 atgggtccctgcagccgga.....gggacaggaagcgatcgtg 1350

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
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19: em_mu:*
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22: em_ov:*
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24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1350	100.0	1350	6	AX350513	AX350513 Sequence
2	1350	100.0	1353	9	AF316894	AF316894 Homo sapi
3	1348.4	99.9	1350	6	AX350512	AX350512 Sequence
4	1348.4	99.9	1353	9	AF281308	AF281308 Homo sapi
5	1348.4	99.9	1941	9	AF262016	AF262016 Homo sapi
6	1348.4	99.9	3612	9	AY032736	AY032736 Homo sapi
7	1348.4	99.9	3653	9	AF284095	AF284095 Homo sapi
8	1348.4	99.9	204908	9	AF158163	AF158163 Human DNA
9	1325.4	98.2	3604	9	HUMADRA2R	M23533 Human alpha
10	1317.4	97.6	1521	9	HUMADRA	M18415 Human plate
11	1150	85.2	1728	4	PIGA2AR	J05652 Porcine alp
12	1133.8	84.0	2291	10	CPU25722	U25722 Cavia porce
13	1105.2	81.9	1552	10	RRU79031	U79031 Rattus norv
14	1094	81.0	1380	10	RATRG20	M62372 Rat alpha-2
15	1093.4	81.0	2923	4	BTU79030	U79030 Bos taurus
16	1082.8	80.2	1454	10	MUSALP2ADB	M99377 Mouse alpha
17	1082.8	80.2	204317	2	AC113491	AC113491 Mus muscu
18	915.4	67.8	7353	6	AX344975	AX344975 Sequence
19	915.4	67.8	7353	6	AX348496	AX348496 Sequence
20	836.4	62.0	7353	6	AX344974	AX344974 Sequence
21	836.4	62.0	7353	6	AX348495	AX348495 Sequence
22	528	39.1	1386	6	AX350528	AX350528 Sequence
23	527.4	39.1	1491	9	HUMADRA2C	J03853 Human kidne
24	527.4	39.1	4850	9	HSU72648	U72648 Homo sapien
25	524.8	38.9	1389	9	AF280399	AF280399 Homo sapi
26	517.8	38.4	1995	10	CPU25724	U25724 Cavia porce
27	517.2	38.3	1374	6	AX350530	AX350530 Sequence
28	514	38.1	1377	9	AF280400	AF280400 Homo sapi
29	512.4	38.0	1382	6	E07358	E07358 gDNA encodi
30	512.4	38.0	1382	9	HUMA2C1TA	D13538 Human alpha
31	505.2	37.4	3461	5	TRU345040	AJ345040 Takifugu
32	464.4	34.4	1503	10	MUSALP2ADA	M99376 Mouse alpha
33	464.4	34.4	1745	10	RATA2AR	D00819 Rattus norv
34	463.6	34.3	1380	10	RATRG10	M62371 Rat alpha-2
35	462	34.2	2991	10	RNA2C4	X57659 R. norvegic
36	462	34.2	5221	10	MUSADRA	M97516 Mus musculu
37	460.4	34.1	1704	10	RATA2BADR	M58316 Rat alpha-2
38	447.6	33.2	22842	9	AC0922603	AC0922603 Homo sapi
39	446	33.0	1344	6	AX350490	AX350490 Sequence
40	446	33.0	1344	9	AF316895	AF316895 Homo sapi
41	443	32.8	1353	6	AX350489	AX350489 Sequence
42	443	32.8	9842	9	AF005900	AF005900 Homo sapi
43	439.8	32.6	2072	9	HUMADRA2RA	M34041 Human alpha
44	426.6	31.6	1149	4	CVI315935	AJ315935 Chaetophr
45	413	30.6	1492	4	DVU04310	U04310 Didelphis v

ALIGNMENTS

RESULT 1
AX350513 1350 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 25 from Patent WO0179561.
DEFINITION AX350513
ACCESSION AX350513
VERSION AX350513.1 GI:18616108
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Liggett,S.B. and Small,K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 25 25-OCT-2001;

Pred. No. is the number of results predicted by chance to have a

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Best Local Similarity 87.8%; Pred. No. 1;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY      1 GGGGGCACCAGCGCAGGCCCAAGGCTCTGGCCCCGAGCG 41
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Db 130828 GGGGGCGCCGATCGACAGCCCAAGGGCTGGCCCCGAGCG 130788
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RESULT 15
CPU25722      CPU25722      2291 bp      DNA      linear      ROD 05-SEP-2001
LOCUS          Cavia porcellus alpha-2A adrenoceptor gene, complete cds.
DEFINITION
ACCESSION      U25722
VERSION        U25722.1 GI:818874
KEYWORDS
SOURCE          Cavia porcellus.
ORGANISM        Cavia porcellus.
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
                1 (bases 1 to 2291)
                Svensson,S.P., Bailey,T.J., Porter,A.C., Richman,J.G. and
                Regan,J.W.
TITLE          Heterologous expression of the cloned guinea pig alpha 2A, alpha
                2B, and alpha 2C adrenoceptor subtypes. Radioligand binding and
                functional coupling to a CAMP-responsive reporter gene
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JOURNAL      Biochem. Pharmacol. 51 (3), 291-300 (1996)
MEDLINE      96152573
PUBMED      8573196
REFERENCE    2 (bases 1 to 2291)
AUTHORS      Richman,J.G.
TITLE        Direct Submission
JOURNAL      Submitted (26-APR-1995) Jeremy G. Richman, University of Arizona,
                Pharmacology and Toxicology, College of Pharmacy, Room 235, Tucson,
                AZ 85721, USA

FEATURES
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/strain="Sasco Hartley albino"
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/clone="(GP) alpha-2A"
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/product="alpha-2A adrenoceptor"
/protein_id="AAA67074.1"
/db_xref="GI:818875"
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Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db      778 GGGGGCGCCGAGCGCGGCCCAATGGCTGGCCCTGAGCG 818
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Search completed: February 15, 2003, 16:55:31
Job time : 253.55 secs

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SAVISFPPLISIEKKAGGGGQQAEPRECIINDQKWYISSIGSEFAPCLIMILVYVR
IYQIAKRRTRVPPSRGPDAAALPGAEERRNGLGERGVAGAEAPLPVOLNGA
PGEPAAGPRDADGLDLESSSSSEHAERPPGPRRSEGRPAKSKARASQVKPGDSLPR
RGPAGPGAGATGAGEERGAKASRWGRQNRKRETFVLAVVIGVFVVCWPEPFEF
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BASE COUNT 268 a 590 c 562 g 308 t
ORIGIN

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Best Local Similarity 90.2%; Pred. No. 0.84;
Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGGGGCACCAGCGCAGGCCCAAGGCTGTGGCCCCGAGCG 41
Db 859 GGGGGCGCCGAGCGCAGGCCCAATGGCCTAGCCCCGAGCG 899

RESULT 12
LOCUS MUSALP2ADB 1454 bp DNA linear ROD 27-APR-1993
DEFINITION Mouse alpha-2 adrenergic receptor, complete cds.
ACCESSION M99377
VERSION M99377.1 GI:191882
KEYWORDS alpha-2 adrenergic receptor.
SOURCE Mus musculus (strain 129/Sv) DNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1454)
AUTHORS Link, R., Daunt, D., Barsh, G., Chruscinski, A. and Kobilka, B.
TITLE Cloning of two mouse genes encoding alpha 2-adrenergic receptor
subtypes and identification of a single amino acid in the mouse
alpha 2-C10 homolog responsible for an interspecies variation in
antagonist binding
JOURNAL Mol. Pharmacol. 42 (1), 16-27 (1992)
MEDLINE 92342131
PUBMED 1353249

FEATURES
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/strain="129/Sv"
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51..1403
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BASE COUNT 229 a 481 c 467 g 277 t
ORIGIN

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Best Local Similarity 87.8%; Pred. No. 2.6;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 GGGGGCACCAGCGCAGGCCCAAGGCTGTGGCCCCGAGCG 41
Db 780 GGGGGCGCCGATCGCAGGCCCAAGGGCTGGCCCCGAGCG 820

RESULT 13

RRU79031

LOCUS RRU79031 1552 bp mRNA linear ROD 14-JUN-2000
DEFINITION Rattus norvegicus alpha2D adrenergic receptor mRNA, complete cds.
ACCESSION U79031
VERSION U79031.1 GI:3282234
KEYWORDS Rattus norvegicus.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1552)
AUTHORS Chalberg, S.C., Duda, T., Rhine, J.A. and Sharma, R.K.
TITLE Molecular cloning, sequencing and expression of an alpha
2-adrenergic receptor complementary DNA from rat brain
Mol. Cell. Biochem. 97 (2), 161-172 (1990)

JOURNAL 2177834
MEDLINE 91125329
PUBMED 2177834
REFERENCE 2 (bases 1 to 1552)
AUTHORS Wypijewski, K., Duda, T. and Sharma, R.K.
TITLE Structural, genetic and pharmacological identity of the rat alpha
2-adrenergic receptor subtype CA2-47 and its molecular
characterization in rat adrenal, adrenocortical carcinoma and
bovine retina
Mol. Cell. Biochem. 144 (2), 181-190 (1995)

JOURNAL 7623790
MEDLINE 95349560
PUBMED 7623790
REFERENCE 3 (bases 1 to 1552)
AUTHORS Venkataraman, V., Duda, T.M. and Sharma, R.K.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-1996) Cell Biology, UMDNJ-SOM, 2 Medical Ctr.
Dr., Stratford, NJ 08084, USA

FEATURES
source Location/Qualifiers
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CDS

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Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 GGGGGCACCAGCGCAGGCCCAAGGCTGTGGCCCCGAGCG 41
Db 730 GGGGGCGCCGATCGCAGGCCCAAGGGCTGGCCCCGAGCG 770

RESULT 14
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DEFINITION Mus musculus clone RP23-358H2, WORKING DRAFT SEQUENCE, 24 ordered
pieces.
AC113491
AC113491.3 GI:21327601
AC113491
AC113491.3
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 3653)
AUTHORS Mao,Z.-M., Tang,K., Li,B.-M. and Jing,N.-H.
TITLE Cloning and expression of human alpha-2A adrenergic receptor in
SY5Y cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3653)
AUTHORS Mao,Z.-M., Tang,K., Li,B.-M. and Jing,N.-H.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-2000) Shanghai Institute of Physiology, Chinese
Academy of Sciences, 320 Yue Yang Road, Shanghai 200031, P.R. China
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IYQIAKRTRVPPSRGRPDAAVAPGTERPNGLGPERSAGGGAEAEPILPTQLNGA
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BASE COUNT 681 a 1168 c 1028 g 776 t
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Best Local Similarity 97.6%; Pred. No. 0.027;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGGCACCAGCGCAGCCCAAGGGTCTGGGCCCCGAGCG 41
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Db 1609 GGGGGCACCAGCGCAGCCCAACGGTCTGGGCCCCGAGCG 1649
RESULT 10
AL158163 204908 bp DNA linear PRI 13-DEC-2001
LOCUS Human DNA sequence from clone Rp11-348N5 on chromosome 10, complete
DEFINITION
sequence.
ACCESSION AL158163
VERSION AL158163.11 GI:17384427
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 204908)
AUTHORS Johnson,C.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Dec 5, 2001 this sequence version replaced gi:16944857.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr10
Rp11-348N5 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
This sequence is the entire insert of clone Rp11-348N5 The true
left end of clone Rp11-479A21 is at 179266 in this sequence. The
true right end of clone Rp11-313D6 is at 44800 in this sequence.

FEATURES
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Best Local Similarity 97.6%; Pred. No. 0.013;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGGCACCAGCGCAGCCCAAGGGTCTGGGCCCCGAGCG 41
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Db 196299 GGGGGCACCAGCGCAGCCCAACGGTCTGGGCCCCGAGCG 196339
RESULT 11
PIGA2AR 1728 bp DNA linear MAM 27-APR-1993
LOCUS Porcine alpha2A-adrenergic receptor (PORA2AR) gene, complete cds.
DEFINITION
ACCESSION J05652
VERSION J05652.1 GI:164303
KEYWORDS alpha-2A-adrenergic receptor.
SOURCE Porcine liver DNA.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 1728)
AUTHORS Guyer,C.A., Horstman,D.A., Wilson,A.L., Clark,J.D., Kragoe,E.J.Jr.
and Limbird,L.E.
JOURNAL Unpublished (1990)
REFERENCE 2 (bases 70 to 1582)
AUTHORS Guyer,C.A., Horstman,D.A., Wilson,A.L., Clark,J.D., Cragoe,E.J. Jr.
and Limbird,L.E.
TITLE Cloning, sequencing, and expression of the gene encoding the
porcine alpha 2-adrenergic receptor. Allosteric modulation by Na+,
H+, and amiloride analogs
JOURNAL J. Biol. Chem. 265 (28), 17307-17317 (1990)
MEDLINE 91009167
PUBMED 2170371
COMMENT Draft entry and computer-readable sequence for [J. Biol. Chem.
(1990) In press] kindly submitted
by C.A.Guyer, 02-AUG-1990.
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130..1482
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ORIGIN

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Best Local Similarity 97.6%; Pred. No. 0.03;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGGGCACCAGCGCAGGCCCAAGGCTCTGGCCCCGAGCG 41
|||||
Db 1248 GGGGGCACCAGCGCAGGCCCAACGCTCTGGCCCCGAGCG 1288

RESULT 7

HUMADRA2R 3604 bp DNA linear PRI 30-OCT-1994
LOCUS Human alpha 2 adrenergic receptor gene, complete cds.
DEFINITION M23533
ACCESSION M23533.1 GI:178195
VERSION M23533.1
KEYWORDS adrenergic receptor; alpha-2 andadrenergic receptor.
SOURCE Human DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 3604)
AUTHORS Fraser,C.M., Arakawa,S., McCombie,W.R. and Venter,J.C.
TITLE Cloning, sequence analysis, and permanent expression of a human
alpha 2-adrenergic receptor in Chinese hamster ovary cells.
Evidence for independent pathways of receptor coupling to adenylylate
cyclase attenuation and activation

JOURNAL J. Biol. Chem. 264 (20), 11754-11761 (1989)
MEDLINE 89308571
PUBMED 2568356

COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by W.R.McCombie, 30-MAR-1989.

FEATURES Location/Qualifiers
source 1..3604

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BASE COUNT 555 a 1272 c 1134 g 643 t
ORIGIN

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Best Local Similarity 97.6%; Pred. No. 0.027;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGGGCACCAGCGCAGGCCCAAGGCTCTGGCCCCGAGCG 41
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Db 2807 GGGGGCACCAGCGCAGGCCCAACGCTCTGGCCCCGAGCG 2847

RESULT 8

AY032736 3612 bp DNA linear PRI 12-MAY-2001
LOCUS Homo sapiens alpha-2A adrenergic receptor (ADR2AR) gene, complete
DEFINITION cds.
cvs.

AY032736
AY032736.1 GI:14029162

REFERENCE

1 (bases 1 to 3612)
AUTHORS Liu,L. and Yuan,L.
TITLE Human alpha-2A adrenergic receptor gene and the genotype of -1296
nucleotide and motionsickness

JOURNAL

2 (bases 1 to 3612)
AUTHORS Liu,L. and Yuan,L.
TITLE Direct Submission
JOURNAL Submitted (17-APR-2001) Key Laboratory of Molecular Biology,
General Hospital of Airforce, Fucheng Road No. 30, Beijing 100036,
China

FEATURES Location/Qualifiers
source 1..3612

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BASE COUNT 555 a 1278 c 1136 g 643 t
ORIGIN

Query Match 96.1%; Score 39.4; DB 9; Length 3612;
Best Local Similarity 97.6%; Pred. No. 0.027;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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|||||
Db 2814 GGGGGCACCAGCGCAGGCCCAACGCTCTGGCCCCGAGCG 2854

RESULT 9

AF284095 3653 bp mRNA linear PRI 27-MAR-2001
LOCUS Homo sapiens alpha-2A adrenergic receptor mRNA, complete cds.
DEFINITION AF284095
ACCESSION AF284095.1 GI:13447750
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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PGEAPAGPRDTPDALDLEESSSDHAERPPRRPERGPRGKGAKASQVKPGDSLPR
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BASE COUNT 200 a 490 c 442 g 221 t

ORIGIN

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Best Local Similarity 97.6%; Pred. No. 0.032;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGCACCGACGCGCAGGCCAAGGGTCTGGCCCCGAGCG 41
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Db 730 GGGGCACCGACGCGCAGGCCAAGGGTCTGGCCCCGAGCG 770

RESULT 5

HUMADRA 1521 bp DNA linear PRI 30-OCT-1994
LOCUS Human platelet alpha-2-adrenergic receptor gene, complete cds.
DEFINITION M18415
ACCESSION M18415.1 GI:178191
VERSION alpha-2-adrenergic receptor; alpha-adrenergic receptor.
KEYWORDS Human (lambda-EMBL 3 library) DNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1521)
AUTHORS Kobilka,B.K., Matsui,H., Kobilka,T.S., Yang-Feng,T.L., Francke,U.,
Caron,M.G., Lefkowitz,R.J. and Regan,J.W.
TITLE Cloning, sequencing, and expression of the gene coding for the
human platelet alpha 2-adrenergic receptor
JOURNAL Science 238 (4827), 650-656 (1987)
MEDLINE 88042789
PUBMED 2823383

FEATURES

source Location/Qualifiers
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ORIGIN Chromosome 10q23-q25.

Query Match 96.1%; Score 39.4; DB 9; Length 1521;
Best Local Similarity 97.6%; Pred. No. 0.032;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 788 GGGGCACCGACGCGCAGGCCAAGGGTCTGGCCCCGAGCG 828

RESULT 6

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LOCUS Homo sapiens adrenergic receptor alpha-2A gene, complete cds.
DEFINITION AF262016
ACCESSION AF262016
VERSION AF262016.2 GI:9864781
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1941)
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,
Beschi,M. and Agabiti Rosel,E.
TITLE A search for genetic variability in the human alpha-2 adrenergic
receptor on chromosome 10
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1941)
TITLE Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,
Beschi,M. and Agabiti Rosel,E.
JOURNAL Direct Submission
AUTHORS Submitted (29-APR-2000) Medical and Surgical Sciences, University
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
REFERENCE 3 (bases 1 to 1941)
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,
Beschi,M. and Agabiti Rosel,E.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Medical and Surgical Sciences, University
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
REMARK Sequence update by submitter
COMMENT On Aug 22, 2000 this sequence version replaced gi:9837145.
FEATURES

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Geography 10:151-160, 1996"
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BASE COUNT 305 a 676 c 624 g 336 t


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FEATURES                                Liggett, Stephen B. (US) ; Small, Kersten M. (US)
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AF316894      1353 bp      DNA      linear      PRI 07-FEB-2001
LOCUS      AF316894
DEFINITION      Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete
ACCESSION      AF316894
VERSION      AF316894.1 GI:12698667
KEYWORDS
SOURCE      .
ORGANISM      Homo sapiens.
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              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 1353)
REFERENCE      Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
AUTHORS      An asn to lys polymorphism in the third intracellular loop of the
              human alpha 2A-adrenergic receptor imparts enhanced
              agonist-promoted G1 coupling
              J. Biol. Chem. 275 (49), 38518-38523 (2000)
              20556293
JOURNAL      MEDLINE
PUBMED      10948191
REFERENCE      2 (bases 1 to 1353)
AUTHORS      Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE      Direct Submission
JOURNAL      Submitted (26-OCT-2000) Internal Medicine, University of
              Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA
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FEATURES
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DEFINITION	Sequence 24	from Patent WO0179561.			
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VERSION	AX350512.1	GI:18616107			
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1	Liggett,S.B. and Small,K.M.			
JOURNAL	Alpha-2 adrenergic receptor polymorphisms				
FEATURES	Patent: WO 0179561-A 24 25-OCT-2001;				
source	Liggett, Stephen B. (US) ; Small, Kersten M. (US)				
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Db	730	GGGGCACCAGCGCGCCCAAGGGTCTGGCCCCGAGCG	770		
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DEFINITION	Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.				
ACCESSION	AF281308				
VERSION	AF281308.1	GI:9652209			
KEYWORDS	human.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 1353)				
JOURNAL	Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.				
MEDLINE	An asn to lys polymorphism in the third intracellular loop of the				
PUBMED	agonist-promoted Gi coupling				
REFERENCE	J. Biol. Chem. 275 (49), 38518-38523 (2000)				
AUTHORS	2 (bases 1 to 1353)				
TITLE	Small,K.M., Forbes,S.L., Bridges,K.M. and Liggett,S.B.				
JOURNAL	Submitted (22-JUN-2000) Internal Medicine, University of				
FEATURES	Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA				
source	1..1353				

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OM nucleic - nucleic search, using sw model

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Searched: 2054640 seqs, 14551402878 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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35: em_htg_rod:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	41	100.0	1353	9 AF316894	AF316894 Homo sapi
3	39.4	96.1	1350	6 AX350512	AX350512 Sequence
4	39.4	96.1	1353	9 AF281308	AF281308 Homo sapi
5	39.4	96.1	1521	9 HUMADRA	M18415 Human plate
6	39.4	96.1	1941	9 AF262016	AF262016 Homo sapi
7	39.4	96.1	3604	9 HUMADRA2R	M23533 Human alpha
8	39.4	96.1	3612	9 AY032736	AY032736 Homo sapi
9	39.4	96.1	3653	9 AF284095	AF284095 Homo sapi
10	39.4	96.1	204908	9 AL158163	AL158163 Human DNA
11	34.6	84.4	1728	4 PIGA2AR	J05652 Porcine alp
12	33	80.5	1454	10 MUSALP2ADB	M99377 Mouse alpha
13	33	80.5	1552	10 RRU79031	U79031 Rattus norv
14	33	80.5	204317	2 AC113491	AC113491 Mus muscu
15	31.4	76.6	2291	10 CPU25722	U79030 Bos taurus
16	31.4	76.6	2923	4 BTU79030	U25722 Cavia porce
17	29.8	72.7	1380	10 RATR620	U79030 Bos taurus
18	25.8	62.9	163156	2 AP004085	M62372 Rat alpha-2
19	25	61.0	1263	9 HSACAA1	AP004085 Oryza sat
20	25	61.0	26621	2 AC020878	X65140 H.sapiens A
21	25	61.0	39407	2 AC010648	AC020878 Mus muscu
22	25	61.0	51146	2 AC090342	AC010648 Homo sapi
23	25	61.0	64711	2 AC114552	AC090342 Homo sapi
24	25	61.0	65069	9 AC112706	AC114552 Mus muscu
25	25	61.0	100000	9 AP000498	AC112706 Homo sapi
26	25	61.0	144494	9 AC099534	AP000498 Homo sapi
27	25	61.0	176291	2 AC023583	AC099534 Homo sapi
28	25	61.0	182224	9 AC093116	AC023583 Homo sapi
29	25	61.0	203230	2 AC026346	AC093116 Homo sapi
30	25	61.0	270000	9 AB026898	AC026346 Homo sapi
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33	24	58.5	8113	14 HSBICP4A	AL603644 Rhizobium
34	24	58.5	135301	14 BHV1CGEN	L14320 Bovine herp
35	24	58.5	135301	14 BHV1CGEN	AJ004801 Bovine he
36	24	58.5	147425	2 AC094576	AJ004801 Bovine he
37	23.6	57.6	3036	6 AX056468	AC094576 Rattus no
38	23.6	57.6	3514	9 AF100318	AX056468 Sequence
39	23.6	57.6	81740	9 AL663123	AF100318 Homo sapi
40	23.4	57.1	4734	10 MMGLUR	AL663123 Human DNA
41	23.4	57.1	5579	1 AHY276030	X66367 M.musculus
42	23.4	57.1	7353	6 AX344974	AJ276030 Aeromonas
43	23.4	57.1	7353	6 AX348495	AX344974 Sequence
44	23.4	57.1	82195	2 AC121221	AX348495 Sequence
45	23.4	57.1	178418	2 AC013243	AC121221 Rattus no

ALIGNMENTS

RESULT 1
AX350513
LOCUS AX350513 1350 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 25 from Patent WO0179561.
ACCESSION AX350513
VERSION AX350513.1 GI:18616108
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Liggett,S.B. and Small,K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 25 25-Oct-2001;

; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3018
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-802-127-6

Query Match 53.2%; Score 21.8; DB 10; Length 3018;
Best Local Similarity 78.8%; Pred. No. 62;
Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CGGCTCCAGGGCCCGCAGACCCGAGCGCGT 33
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Db 1339 CGGCTCCAGGGCCCGCAGAGCGCGCATAGT 1307

RESULT 14
US-09-802-127-4/c
; Sequence 4, Application US/09802127
; Patent No. US20020045212A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: No. US20020045212A1e1 Human GTPase Activator Proteins
; FILE REFERENCE: 035800/158994
; CURRENT APPLICATION NUMBER: US/09/802,127
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,611
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)...(3095)
US-09-802-127-4

Query Match 53.2%; Score 21.8; DB 10; Length 3391;
Best Local Similarity 78.8%; Pred. No. 61;
Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CGGCTCCAGGGCCCGCAGACCCGAGCGCGT 33
||| ||||| ||||| ||| ||
Db 1416 CGGCTCCAGGGCCCGCAGAGCGCGCATAGT 1384

RESULT 15
US-09-764-868-1501/c
; Sequence 1501, Application US/09764868
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1501
; LENGTH: 5968
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1501

Query Match 53.2%; Score 21.8; DB 9; Length 5968;
Best Local Similarity 78.8%; Pred. No. 58;
Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CGGCTCCAGGGCCCGCAGACCCGAGCGCGT 33
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Db 225 CGGCTCCAGGGCCCGCAGAGCGCGCATAGT 193

Search completed: February 13, 2003, 07:50:17
Job time : 9.82052 secs

; LENGTH: 1675
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-808-387-21

Query Match 53.2%; Score 21.8; DB 10; Length 1675;
Best Local Similarity 70.7%; Pred. No. 66;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 CGGCCTCAGAGCCCGCAGACCCGAGCGCGGTCCCGGGG 41
||||| ||||| ||||| || || ||||| ||
Db 1427 CGGCCCCCAGCTCCCGCTGAGCCCCCGGTGTCCCGCTG 1467

RESULT 11
US-09-793-306-162/c
; Sequence 162, Application US/09793306
; Patent No. US20020098200A1
; GENERAL INFORMATION:
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Skelky, Yasir
; APPLICANT: Owendale, Pamela
; APPLICANT: Jen, Shylan
; APPLICANT: Lodes, Michael
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
; TITLE OF INVENTION: of Tuberculosis
; FILE REFERENCE: 014058-008740US
; CURRENT APPLICATION NUMBER: US/09/793,306
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/185,037
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 60/223,828
; PRIOR FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 162
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: MO-2 (aspartokinase)
; NAME/KEY: CDS
; LOCATION: (1)..(1266)
; OTHER INFORMATION: MO-2
US-09-793-306-162

Query Match 53.2%; Score 21.8; DB 10; Length 1863;
Best Local Similarity 70.7%; Pred. No. 65;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 CGGCCTCAGAGCCCGCAGACCCGAGCGCGGTCCCGGGG 41
||||| ||||| ||||| || || ||||| ||
Db 1111 CCGCCGCGCAGCGCTCAGAGACGTGCGGTGACCCCGGGG 1071

RESULT 12

US-09-796-753-31
; Sequence 31, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246

; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 31
; LENGTH: 2576
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-753-31

Query Match 53.2%; Score 21.8; DB 9; Length 2576;
Best Local Similarity 70.7%; Pred. No. 63;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 CGGCCTCAGAGCCCGCAGACCCGAGCGCGGTCCCGGGG 41
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Db 154 CGGCCTGTGTGTCGCGCGGCGGCGCGCGGTCTCCCGG 194

RESULT 13

US-09-802-127-6/c
; Sequence 6, Application US/09802127
; Patent No. US20020045212A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: NO. US20020045212A1 Human GTPase Activator Proteins
; FILE REFERENCE: 035800/158994
; CURRENT APPLICATION NUMBER: US/09/802,127
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,611

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; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 304
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(441)
; OTHER INFORMATION: n = A,T,C or G
; US-09-854-133-304
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Query Match          53.2%; Score 21.8; DB 9; Length 441;
Best Local Similarity 70.7%; Pred. No. 76;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
OY 1 CGGCCTCCAGGGCCCGCAGACCCGAGCGCGTCCCGGGG 41
    11111 11111111111111111111111111111111
Db 93 CCGCCTCTCAGACCCAGACGATCCAGGCGGCTCCCTGGGG 133
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RESULT 7

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US-09-738-973-304
; Sequence 304, Application US/09738973
; Patent No. US20020110563A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Fling, Steven P.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Algate, Paul A.
; APPLICANT: Secrist, Heather
; APPLICANT: Indirias, Carol Yoseph
; APPLICANT: Benson, Darin R.
; APPLICANT: Elliot, Mark
; APPLICANT: Mannion, Jane
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C9
; CURRENT APPLICATION NUMBER: US/09/738,973
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 304
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(441)
; OTHER INFORMATION: n = A,T,C or G
; US-09-738-973-304
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Query Match          53.2%; Score 21.8; DB 10; Length 441;
Best Local Similarity 70.7%; Pred. No. 76;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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```
OY 1 CGGCCTCCAGGGCCCGCAGACCCGAGCGCGTCCCGGGG 41
    11111 11111111111111111111111111111111
Db 93 CCGCCTCTCAGACCCAGACGATCCAGGCGGCTCCCTGGGG 133
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RESULT 8

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US-09-808-387-25
; Sequence 25, Application US/09808387
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; Patent No. US20020132293A1
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; APPLICANT: Tonis Timmusk
; APPLICANT: Cemines Research
; TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
; TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
; FILE REFERENCE: CEMRES.001A
; CURRENT APPLICATION NUMBER: US/09/808,387
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-808-387-25
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```
Query Match          53.2%; Score 21.8; DB 10; Length 955;
Best Local Similarity 70.7%; Pred. No. 70;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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```
OY 1 CGGCCTCCAGGGCCCGCAGACCCGAGCGCGTCCCGGGG 41
    11111 11111111111111111111111111111111
Db 707 CGGCCCCAGCTCCCGCTGAGCCCCCGGTGTCCCGGTG 747
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RESULT 9

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US-09-808-387-23
; Sequence 23, Application US/09808387
; Patent No. US20020132293A1
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; APPLICANT: Tonis Timmusk
; APPLICANT: Cemines Research
; TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
; TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
; FILE REFERENCE: CEMRES.001A
; CURRENT APPLICATION NUMBER: US/09/808,387
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1129
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-808-387-23
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Query Match          53.2%; Score 21.8; DB 10; Length 1129;
Best Local Similarity 70.7%; Pred. No. 69;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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OY 1 CGGCCTCCAGGGCCCGCAGACCCGAGCGCGTCCCGGGG 41
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Db 881 CGGCCCCAGCTCCCGCTGAGCCCCCGGTGTCCCGGTG 921
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RESULT 10

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US-09-808-387-21
; Sequence 21, Application US/09808387
; Patent No. US20020132293A1
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; APPLICANT: Tonis Timmusk
; APPLICANT: Cemines Research
; TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
; TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
; FILE REFERENCE: CEMRES.001A
; CURRENT APPLICATION NUMBER: US/09/808,387
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
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; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
; FILE REFERENCE: B8116 US CIP
; CURRENT APPLICATION NUMBER: US/09/931,457A
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/424,976
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/065,385
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/049,406
; PRIOR FILING DATE: 1997-06-12
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 44
; LENGTH: 1402
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-931-457A-44
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Query Match          53.7%; Score 22; DB 9; Length 1402;
Best Local Similarity 73.7%; Pred. No. 58;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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OY 4 CCTCCAGGGCCCCGACAGCCGAGCGCGTCCCGGGG 41
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Db 303 CGTCCAGAGACCTCGCCCGCGGGCGGTTCGACGGGG 340
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RESULT 3
US-09-815-242-7695/c
; Sequence 7695, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7695
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1998)
US-09-815-242-7695
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Query Match          53.7%; Score 22; DB 10; Length 1998;
Best Local Similarity 73.7%; Pred. No. 56;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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OY 3 GCCTCCAGGGCCCCGACAGCCGAGCGCGTCCCGGG 40
      11|||||1111111111111111111111111111
Db 1513 GCTTCAGAGCACCGCCGACTCGACCGCGTCGCCGGG 1476
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RESULT 4
US-10-044-090-592
; Sequence 592, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 592
; LENGTH: 3006
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1683849CB1
US-10-044-090-592
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Query Match          53.7%; Score 22; DB 12; Length 3006;
Best Local Similarity 73.7%; Pred. No. 54;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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Db 1418 CCTCCAGAGACCCCGCAGTGCAGCGCGACAGCGCCCGGAG 1455
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RESULT 5
US-09-764-877-3220/c
; Sequence 3220, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3220
; LENGTH: 19616
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3220
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Query Match          53.7%; Score 22; DB 10; Length 19616;
Best Local Similarity 73.7%; Pred. No. 44;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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OY 1 CGGCCTCAGGGCCCCGACAGCCGAGCGCGTCCCGG 38
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Db 13958 CCGCCTTCAGGGCCCCACAGTCATTTGGCGCGCTCTCCG 13921
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RESULT 6
US-09-854-133-304
; Sequence 304, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
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OM nucleic - nucleic search, using sw model

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(without alignments)
7403.688 Million cell updates/sec

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Perfect score: 41
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	22	53.7	1402	9 US-09-931-457A-44	Sequence 44, Appli
c 3	22	53.7	1998	10 US-09-815-242-7695	Sequence 7695, Ap
c 4	22	53.7	3006	12 US-10-044-090-592	Sequence 592, App
c 5	22	53.7	19616	10 US-09-764-877-3220	Sequence 3220, Ap
c 6	21.8	53.2	441	9 US-09-854-133-304	Sequence 304, App
c 7	21.8	53.2	441	10 US-09-738-973-304	Sequence 304, App
c 8	21.8	53.2	955	10 US-09-808-387-25	Sequence 25, Appli
c 9	21.8	53.2	1129	10 US-09-808-387-23	Sequence 23, Appli
c 10	21.8	53.2	1675	10 US-09-808-387-21	Sequence 21, Appli
c 11	21.8	53.2	1863	10 US-09-793-306-162	Sequence 162, App
c 12	21.8	53.2	2576	9 US-09-796-753-31	Sequence 31, Appli
c 13	21.8	53.2	3018	10 US-09-802-127-6	Sequence 6, Appli
c 14	21.8	53.2	3391	10 US-09-802-127-4	Sequence 4, Appli
c 15	21.8	53.2	5968	9 US-09-764-868-1501	Sequence 1501, Ap
c 16	21.6	52.7	5222	10 US-09-416-384A-1	Sequence 1, Appli
c 17	21.6	52.7	5566	10 US-09-416-384A-4	Sequence 4, Appli
c 18	21.4	52.2	64	9 US-10-057-940-10	Sequence 10, Appli
c 19	21.4	52.2	865	10 US-09-804-615-1	Sequence 1, Appli

c 20	21.4	52.2	1274	10 US-09-919-172-93	Sequence 93, Appl
c 21	21.2	51.7	1667	9 US-10-078-770-81	Sequence 81, Appl
c 22	21.2	51.7	2048	9 US-10-174-590-533	Sequence 533, App
c 23	21.2	51.7	2048	9 US-10-176-758-533	Sequence 533, App
c 24	21.2	51.7	2048	9 US-10-175-737-533	Sequence 533, App
c 25	21.2	51.7	2048	9 US-10-173-706-533	Sequence 533, App
c 26	21.2	51.7	2048	9 US-10-175-738-533	Sequence 533, App
c 27	21.2	51.7	2048	9 US-10-175-752-533	Sequence 533, App
c 28	21.2	51.7	2048	9 US-10-176-482-533	Sequence 533, App
c 29	21.2	51.7	2048	9 US-10-176-757-533	Sequence 533, App
c 30	21.2	51.7	2048	9 US-10-174-572-533	Sequence 533, App
c 31	21.2	51.7	2048	9 US-10-180-552-533	Sequence 533, App
c 32	21.2	51.7	2048	9 US-10-180-557-533	Sequence 533, App
c 33	21.2	51.7	2048	9 US-10-173-700-533	Sequence 533, App
c 34	21.2	51.7	2048	9 US-10-174-579-533	Sequence 533, App
c 35	21.2	51.7	2048	9 US-10-174-579-533	Sequence 533, App
c 36	21.2	51.7	2048	9 US-10-174-582-533	Sequence 533, App
c 37	21.2	51.7	2048	9 US-10-174-588-533	Sequence 533, App
c 38	21.2	51.7	2048	9 US-10-175-739-533	Sequence 533, App
c 39	21.2	51.7	2048	9 US-10-175-740-533	Sequence 533, App
c 40	21.2	51.7	2048	9 US-10-175-743-533	Sequence 533, App
c 41	21.2	51.7	2048	9 US-10-176-488-533	Sequence 533, App
c 42	21.2	51.7	2048	9 US-10-176-492-533	Sequence 533, App
c 43	21.2	51.7	2048	9 US-10-176-747-533	Sequence 533, App
c 44	21.2	51.7	2048	9 US-10-176-750-533	Sequence 533, App
c 45	21.2	51.7	2048	9 US-10-176-985-533	Sequence 533, App

ALIGNMENTS

RESULT 1
US-10-033-026-9/c
Sequence 9, Application US/10033026
Patent No. US20020147309A1
GENERAL INFORMATION:
APPLICANT: Lipscombe, Diane
TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
FILE REFERENCE: B1055/7000
CURRENT APPLICATION NUMBER: US/10/033, 026
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/268, 163
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: US 60/077, 901
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 7011
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: CDS
LOCATION: 1..7008
US-10-033-026-9

Query Match 61.5%; Score 25.2; DB 12; Length 7011;
Best Local Similarity 78.9%; Pred. No. 5.1;
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CGGCTCCAGGCGCCCGAGACCCGAGCGGTCGCCG 38
||||| | ||||||| | ||||||| | |||||||
Db 88 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCCG 51

RESULT 2
US-09-931-457A-44
Sequence 44, Application US/09931457A
Patent No. US20020157132A1
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Allen, Stephen M.


```

1 CITY: RAHWAY
2 STATE: NJ
3 COUNTRY: USA
4 ZIP: 07065
5
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Floppy disk
8 COMPUTER: IBM PC compatible
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10 SOFTWARE: PatentIn Release #1.0, Version #1.25
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: PCT/US95/07784
13 FILING DATE:
14 CLASSIFICATION:
15 ATTORNEY/AGENT INFORMATION:
16 NAME: THIES, J. ERIC
17 REGISTRATION NUMBER: 35,382
18 REFERENCE/DOCKET NUMBER: 19132
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: (908)594-3904
21 TELEFAX: (908) 594-4720
22 INFORMATION FOR SEQ ID NO: 10:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 1150 base pairs
25 TYPE: nucleic acid
26 STRANDEDNESS: single
27 TOPOLOGY: unknown
28 MOLECULE TYPE: DNA (genomic)
29 HYPOTHETICAL: NO
30 ANTI-SENSE: NO
31 PCT-US95-07784-10

```

Query Match	53.7%;	Score 22;	DB 5;	Length 1150;
Best Local Similarity	73.7%;	Pred. No. 74;		
Matches	28;	Conservative	0;	Mismatches 10;
			Indels	0;
			Gaps	0;

Qy 1 CGGCTTCAGAGGGCCCCGAGACCCGAGCGGTCGCCG 38
 ||||| | ||||| | ||||| ||||| |||||
 Db 340 CGGCATCTCGGCGCGGTGGACCACTGCGCGGTCTCCG 377

RESULT 14
US-09-382-106-1/c

```

: Sequence 1, Application US/09382106
: Patent No. 6221631
: GENERAL INFORMATION:
:   APPLICANT: Huang, Jiansheng
:   APPLICANT: Jiang, Xinhé
:   APPLICANT: McDevitt, Damien
:   APPLICANT: Van Horn, Stephanie
:   TITLE OF INVENTION: tkta
:   FILE REFERENCE: GM10236
:   CURRENT APPLICATION NUMBER: US/09/382,106
:   CURRENT FILING DATE: 1999-08-24
:   NUMBER OF SEQ ID NOS: 2
:   SOFTWARE: FastSeq for Windows Version 3.0
:   SEQ ID NO 1
:   LENGTH: 1998
:   TYPE: DNA
:   ORGANISM: Pseudomonas aeruginosa
US-09-382-106-1

```

Query Match	53.7%;	Score 22;	DB 4;	Length 1998;
Best Local Similarity	73.7%;	Pred. No. 70;		
Matches 28;	Conservative	0;	Mismatches 10;	Indels 0;
			Gaps	0;

Oy 3 GCGCTTCAGGGCCCCGCGACGCCGAGCGCGGTCCCGGG 40
||| ||| ||| ||| ||| ||| ||| |||
Db 1513 GCCTTCAGGGCCCACCGCGCGACTTCGACC GGCGTGC GCCGG 1476

RESULT 15
US-08-592-126-102
; Sequence 102, Application US/08592126

```

: Patent No. 5821091
: GENERAL INFORMATION:
: APPLICANT: Gregory Dolganov
: TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
: TITLE OF INVENTION: Polypeptides
: NUMBER OF SEQUENCES: 151
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: 350 Cambridge Avenue, Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/592,126
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sholtz, Charles K.
: REGISTRATION NUMBER: 38,615
: REFERENCE/DOCKET NUMBER: 4600-0111
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 324-0880
: TELEFAX: (415) 324-0960
: INFORMATION FOR SEQ ID NO: 102:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2200 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: G89con.seq
: US-08-592-126-102

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Query Match	53.28;	Score 21.8;	DB 1;	Length 2200;
Best Local Similarity	70.7%;	Pred. No. 79;		
Matches 29;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;
QY	1	CGGCTTCAGGGCCCCCGAGACCCGAGCGCGTCCCGGGG	41	
Db	144	CAGCCTCCGGCGGGCCCGAGCGCCGCGACGACGAGTCGGCGGG	184	

Search completed: February 13, 2003, 07:47:18
Job time : 22.1902 secs

```
; NAME: THIES, J. ERIC
; REGISTRATION NUMBER: 35,382
; REFERENCE/DOCKET NUMBER: 19132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3904
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-264-861A-11

Query Match      53.7%; Score 22; DB 1; Length 783;
Best Local Similarity 73.7%; Pred. No. 78;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1 CGGCCTCCAGGGCCCCGACAGACCCGAGCGGTCCTCCCG 38
        |||||  ||  |||||  |  ||||  |||||  |||
Db      279 CGGCATCTCGGGCGGGGTGGACCACTGCGCGGTCTCCG 316

RESULT 11
PCT-US95-07784-11
; Sequence 11, Application PC/TUS9507784
; GENERAL INFORMATION:
; APPLICANT: MOTAMEDI, HAIDEH
; APPLICANT: SHAFIEE, ALI
; TITLE OF INVENTION: EXPRESSION CASSETTES USEFUL IN
; TITLE OF INVENTION: CONSTRUCTION OF INTEGRATIVE AND REPLICATIVE EXPRESSION
; TITLE OF INVENTION: VECTORS FOR STREPTOMYCES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: J. ERIC THIES
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07784
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: THIES, J. ERIC
; REGISTRATION NUMBER: 35,382
; REFERENCE/DOCKET NUMBER: 19132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3904
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PCT-US95-07784-11

Query Match      53.7%; Score 22; DB 5; Length 783;
Best Local Similarity 73.7%; Pred. No. 78;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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QY      1 CGGCCTCCAGGGCCCCGACAGACCCGAGCGGTCCTCCCG 38
        |||||  ||  |||||  |  ||||  |||||  |||
Db      279 CGGCATCTCGGGCGGGGTGGACCACTGCGCGGTCTCCG 316

RESULT 12
US-08-264-861A-10
; Sequence 10, Application US/08264861A
; Patent No. 5622866
; GENERAL INFORMATION:
; APPLICANT: MOTAMEDI, HAIDEH
; APPLICANT: SHAFIEE, ALI
; TITLE OF INVENTION: EXPRESSION CASSETTES USEFUL IN
; TITLE OF INVENTION: CONSTRUCTION OF INTEGRATIVE AND REPLICATIVE EXPRESSION
; TITLE OF INVENTION: VECTORS FOR STREPTOMYCES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: J. ERIC THIES
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,861A
; FILING DATE: 23-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: THIES, J. ERIC
; REGISTRATION NUMBER: 35,382
; REFERENCE/DOCKET NUMBER: 19132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3904
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-264-861A-10

Query Match      53.7%; Score 22; DB 1; Length 1150;
Best Local Similarity 73.7%; Pred. No. 74;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1 CGGCCTCCAGGGCCCCGACAGACCCGAGCGGTCCTCCCG 38
        |||||  ||  |||||  |  ||||  |||||  |||
Db      340 CGGCATCTCGGGCGGGGTGGACCACTGCGCGGTCTCCG 377

RESULT 13
PCT-US95-07784-10
; Sequence 10, Application PC/TUS9507784
; GENERAL INFORMATION:
; APPLICANT: MOTAMEDI, HAIDEH
; APPLICANT: SHAFIEE, ALI
; TITLE OF INVENTION: EXPRESSION CASSETTES USEFUL IN
; TITLE OF INVENTION: CONSTRUCTION OF INTEGRATIVE AND REPLICATIVE EXPRESSION
; TITLE OF INVENTION: VECTORS FOR STREPTOMYCES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: J. ERIC THIES
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
```



```
; Patent No. 5859201
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,629
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-972-629-1

Query Match          56.1%; Score 23; DB 2; Length 4692;
Best Local Similarity 74.4%; Pred. No. 32;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      3 GCCTCCAGGGCCCGCAGACCCGAGCGCGTCCCGGGG 41
      1 | | | | | | | | | | | | | | | | | | | |
Db      2146 GGCACCGGGGCGCTGCAGAGCTGGCGCGCCCTGGG 2184

RESULT 6
US-08-972-630-1
; Sequence 1, Application US/08972630
; Patent No. 5869271
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,630
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-972-630-1

Query Match          56.1%; Score 23; DB 2; Length 4692;
Best Local Similarity 74.4%; Pred. No. 32;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      3 GCCTCCAGGGCCCGCAGACCCGAGCGCGTCCCGGGG 41
      1 | | | | | | | | | | | | | | | | | | | |
Db      2146 GGCACCGGGGCGCTGCAGAGCTGGCGCGCCCTGGG 2184
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RESULT 7
US-08-672-211-1
; Sequence 1, Application US/08672211
; Patent No. 5874273
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,211
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-672-211-1
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/153,599A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V.
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: FER2159P0041US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2299 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-153-599A-1

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Query Match          61.0%; Score 25; DB 4; Length 2299;
Best Local Similarity 75.6%; Pred. No. 9.1;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 1 CGGCTCCAGGGCCCCCGACGCCGAGCGCGTCCCGGGG 41
Db 1601 CGGCTCCAGTTCGAGAGACCTGTCGCGGTCGTCGGG 1641

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RESULT 3
US-08-916-917-1
; Sequence 1, Application US/08916917
; Patent No. 5856132
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip Thomas
; APPLICANT: Braselmann, Sylvia
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,917
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 8549-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-916-917-1

```

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Query Match          56.1%; Score 23; DB 2; Length 4692;
Best Local Similarity 74.4%; Pred. No. 32;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 3 GCCTCAGGGCCCCCGACGCCGAGCGCGTCCCGGGG 41
Db 2146 GGCACCCGGGCGCTGCAGAGCTGGGCGCCCGCCCTGGG 2184

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RESULT 4
US-08-972-631-1
; Sequence 1, Application US/08972631
; Patent No. 5856133
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,631
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-972-631-1

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Query Match          56.1%; Score 23; DB 2; Length 4692;
Best Local Similarity 74.4%; Pred. No. 32;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 3 GCCTCAGGGCCCCCGACGCCGAGCGCGTCCCGGGG 41
Db 2146 GGCACCCGGGCGCTGCAGAGCTGGGCGCCCGCCCTGGG 2184

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RESULT 5
US-08-972-629-1
; Sequence 1, Application US/08972629

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 06:16:02 ; Search time 2.19024 Seconds
(without alignments)
5740.812 Million cell updates/sec

Title: US-09-636-259B-1_COPY_730_770

Perfect score: 41
Sequence: 1 cggcctccaggccccgcag.....cccgagcgcggtcccgagg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	25.2	61.5	7011	4	US-09-268-163-9	Sequence 9, Appli
2	25	61.0	2299	4	US-09-153-599A-1	Sequence 1, Appli
3	23	56.1	4692	2	US-08-916-917-1	Sequence 1, Appli
4	23	56.1	4692	2	US-08-972-631-1	Sequence 1, Appli
5	23	56.1	4692	2	US-08-972-629-1	Sequence 1, Appli
6	23	56.1	4692	2	US-08-972-630-1	Sequence 1, Appli
7	23	56.1	4692	2	US-08-972-211-1	Sequence 1, Appli
8	23	56.1	4692	3	US-09-225-170-1	Sequence 1, Appli
C 9	22.4	54.6	949	4	US-09-247-155-148	Sequence 148, App
10	22	53.7	783	1	US-08-264-861A-11	Sequence 11, Appli
11	22	53.7	783	5	PCT-US95-07784-11	Sequence 11, Appli
12	22	53.7	1150	1	US-08-264-861A-10	Sequence 10, Appli
13	22	53.7	1150	5	PCT-US95-07784-10	Sequence 10, Appli
C 14	22	53.7	1998	4	US-09-382-106-1	Sequence 1, Appli
15	21.8	53.2	2200	1	US-08-592-126-102	Sequence 102, App
C 16	21.8	53.2	4403765	4	US-09-103-840A-2	Sequence 2, Appli
17	21.4	52.2	1866	4	US-09-224-048A-1	Sequence 1, Appli
C 18	21.4	52.2	3411	4	US-08-890-865A-3	Sequence 3, Appli
19	21.4	52.2	4403765	4	US-09-103-840A-2	Sequence 2, Appli
C 20	21.2	51.7	4771	3	US-08-840-062-3	Sequence 3, Appli
21	20.8	50.7	436	4	US-09-397-787-257	Sequence 257, App
22	20.8	50.7	835	6	5223425-7	Patent No. 5223425
C 23	20.8	50.7	1120	3	US-08-586-165-1	Sequence 1, Appli
24	20.8	50.7	1290	4	US-09-149-476-81	Sequence 81, Appli
C 25	20.8	50.7	2537	6	5168051-1	Patent No. 5168051
C 26	20.8	50.7	2745	4	US-09-661-753-28	Sequence 28, Appli
C 27	20.8	50.7	2745	5	PCT-US94-03705-3	Sequence 3, Appli

C 28	20.8	50.7	2838	4	US-08-246-489-1	Sequence 1, Appli
29	20.8	50.7	3937	3	US-08-586-165-8	Sequence 8, Appli
30	20.8	50.7	4040	2	US-08-685-118-1	Sequence 1, Appli
31	20.8	50.7	4040	2	US-08-915-495-1	Sequence 1, Appli
32	20.8	50.7	4040	2	US-08-914-520-1	Sequence 1, Appli
33	20.8	50.7	4411529	4	US-09-103-840A-1	Sequence 1, Appli
34	20.6	50.2	336	2	US-08-577-492-36	Sequence 36, Appli
35	20.6	50.2	336	4	US-09-079-630-36	Sequence 36, Appli
C 36	20.6	50.2	4233	4	US-09-056-105-27	Sequence 27, Appli
C 37	20.4	49.8	2470	1	US-07-745-206A-14	Sequence 14, Appli
C 38	20.4	49.8	2470	2	US-08-311-363-14	Sequence 14, Appli
C 39	20.4	49.8	5467	1	US-07-745-206A-12	Sequence 12, Appli
C 40	20.4	49.8	5467	2	US-08-311-363-12	Sequence 12, Appli
C 41	20.4	49.8	6854	4	US-09-194-905-7	Sequence 7, Appli
C 42	20.4	49.8	7175	1	US-08-455-543A-8	Sequence 8, Appli
C 43	20.4	49.8	7175	2	US-08-193-078B-8	Sequence 8, Appli
C 44	20.4	49.8	7175	2	US-08-223-305C-8	Sequence 8, Appli
C 45	20.4	49.8	7175	2	US-08-149-097D-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-268-163-9/c
; Sequence 9, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/09/268,163B
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 60/077,901
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 7011
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..7008
; US-09-268-163-9

Query Match 61.5%; Score 25.2; DB 4; Length 7011;
Best Local Similarity 78.9%; Pred. No. 7;
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CGGCTCCAGGCGCCCGAGACCCGAGCCGCTCCCG 38
DB 88 CGGCCCCCGCGCCCGCGCCCGAGCCGCTCCCG 51

RESULT 2
US-09-153-599A-1
; Sequence 1, Application US/09153599A
; Patent No. 6420177
; GENERAL INFORMATION:
; APPLICANT: Weber, J. Mark
; APPLICANT: Luu, B. Minh
; TITLE OF INVENTION: Method for Strain Improvement of
; TITLE OF INVENTION: Erythromycin Producing Bacterium
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson Avenue, 2 Prudential Plaza
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601

ORIGIN

Query Match 63.9%; Score 26.2; DB 12; Length 765;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGCTTCAGGGCCCGCAGACCCGAGCGCG 32
|||||
Db 74 GGCTTCAGGGCCCGCAGACCCGAGCGCG 44

RESULT 14

BF343380/c 779 bp mRNA linear EST 22-NOV-2000
LOCUS 602014679F1 NCI_CGAP_Brn64 Homo sapiens CDNA clone IMAGE:4150483
DEFINITION 5', mRNA sequence.

ACCESSION BF343380
VERSION BF343380.1 GI:11290651
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
TITLE 1 (bases 1 to 779)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://limage.llnl.gov
Plate: LLAM9413 row: n column: 20
High quality sequence stop: 643.

FEATURES

SOURCE

1. .779
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4150483"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP library."

BASE COUNT 166 a 180 c 258 g 174 t 1 others
ORIGIN

Query Match 63.9%; Score 26.2; DB 12; Length 779;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGCTTCAGGGCCCGCAGACCCGAGCGCG 32
|||||
Db 63 GGCTTCAGGGCCCGCAGACCCGAGCGCG 33

RESULT 15

BM083862/c 780 bp mRNA linear EST 16-NOV-2001
LOCUS BM083862
DEFINITION limagec_6-2000/sjo343bdf42.x2 NIH_MGC_20 Homo sapiens CDNA clone
IMAGE:3543837 5', mRNA sequence.

ACCESSION BM083862
VERSION BM083862.1 GI:16972621
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
1 (bases 1 to 780)

AUTHORS Kale,P.I., Harsch,T.J., Folta,P.A., Nelson,D.O., Sanders,C.G. and
Prange,C.K.
TITLE The I.M.A.G.E. Consortium quality control effort: clone
resequencing for verification

JOURNAL

COMMENT

Unpublished (2001)
Contact: Prange CK
The I.M.A.G.E. Consortium
Lawrence Livermore National Laboratory
Livermore, CA, USA
Email: help@image.llnl.gov
This read has been produced as part of the I.M.A.G.E. Consortium
quality control effort. High quality sequence is defined as having
100 or more base pairs with a phred quality value of 20 or greater,
where a sliding window of 4 base pairs with a phred quality value
of 15 or greater marks the beginning and end of the sequence. For
information on obtaining this clone, please contact
info@image.llnl.gov.
Plate: LICM238 row: a column: 22
Seq primer: -21ml3
High quality sequence stop: 780.
Location/Qualifiers

FEATURES

SOURCE

1. .780
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3543837"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 173 a 167 c 264 g 172 t 4 others
ORIGIN

Query Match 63.9%; Score 26.2; DB 13; Length 780;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGCTTCAGGGCCCGCAGACCCGAGCGCG 32
|||||
Db 93 GGCTTCAGGGCCCGCAGACCCGAGCGCG 63

Search completed: February 15, 2003, 18:02:50
Job time : 85.5273 secs

SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 687)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM8452 row: f column: 11
High quality sequence start: 2
High quality sequence stop: 614.
Location/Qualifiers
1. 687
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3459466"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH108"
/note="Organ: cervix; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."
BASE COUNT 144 a 167 c 222 g 154 t
ORIGIN
Query Match 63.9%; Score 26.2; DB 10; Length 687;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GGCTCCAGGGCCCGCAGACCCGAGCCGG 32
|||||
Db 50 GGCTCCAGGGCCCGCAGACCCGAGCCGG 20
RESULT 12
BG766353 757 bp mRNA linear EST 15-MAY-2001
LOCUS 60273906F1 NIH_MGC_49 Homo sapiens CDNA clone IMAGE:4868991 5',
DEFINITION mRNA sequence.
ACCESSION BG766353
VERSION BG766353.1 GI:14077006
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 757)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1739 row: p column: 16
High quality sequence stop: 615.
Location/Qualifiers
1. 757
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4868991"
/clone_lib="NIH_MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library." 1
BASE COUNT 181 a 162 c 255 g 159 t
ORIGIN
Query Match 63.9%; Score 26.2; DB 12; Length 757;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GGCTCCAGGGCCCGCAGACCCGAGCCGG 32
|||||
Db 58 GGCTCCAGGGCCCGCAGACCCGAGCCGG 28
RESULT 13
BG716838 765 bp mRNA linear EST 08-MAY-2001
LOCUS 602677955F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:4801333 5',
DEFINITION mRNA sequence.
ACCESSION BG716838
VERSION BG716838.1 GI:13996025
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 765)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki Toshlyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10693 row: m column: 14
High quality sequence stop: 755.
Location/Qualifiers
1. 765
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4801333"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTGTGTTTAA-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."
BASE COUNT 168 a 169 c 261 g 167 t

Plate: LCM198 row: f column: 16
High quality sequence stop: 607.
Location/Qualifiers
1. .634
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3528591"
/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 151 a 130 c 219 g 133 t 1 others

ORIGIN

Query Match 63.9%; Score 26.2; DB 10; Length 634;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GGCTCCAGGGGGCCGACACCCGAGCGCGG 32
|||||
Db 34 GGCTCCAGGGGGCGGCGACACCCGAGCGCGG 4

RESULT 9 660 bp mRNA linear EST 21-JUL-2000
BE389699/c 601281941F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603731 5',
LOCUS mRNA sequence.
DEFINITION BE389699
ACCESSION BE389699.1 GI:9335064
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 660)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM249 row: a column: 12
High quality sequence stop: 610.
Location/Qualifiers
1. .660
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3603731"
/clone_lib="NIH_MGC_44"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 153 a 140 c 223 g 144 t

ORIGIN

Query Match 63.9%; Score 26.2; DB 10; Length 660;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GGCTCCAGGGGGCCGACACCCGAGCGCGG 32
|||||
Db 49 GGCTCCAGGGGGCGGCGACACCCGAGCGCGG 19

RESULT 10 670 bp mRNA linear EST 21-JUL-2000
BE391389/c 601284042F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605723 5',
LOCUS mRNA sequence.
DEFINITION BE391389
ACCESSION BE391389.1 GI:9336754
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 670)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM254 row: d column: 12
High quality sequence stop: 615.
Location/Qualifiers
1. .670
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3605723"
/clone_lib="NIH_MGC_44"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 156 a 140 c 226 g 148 t

ORIGIN

Query Match 63.9%; Score 26.2; DB 10; Length 670;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GGCTCCAGGGGGCCGACACCCGAGCGCGG 32
|||||
Db 49 GGCTCCAGGGGGCGGCGACACCCGAGCGCGG 19

RESULT 11 687 bp mRNA linear EST 09-AUG-2000
BE547791/c 601073643F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3459466 5',
LOCUS mRNA sequence.
DEFINITION BE547791
ACCESSION BE547791.1 GI:9776436
VERSION EST.
KEYWORDS

```

/tissue_type="brain"
/dev_stage="fetal"
/lab_host="xl-2blue"
/note="Vector: PAMPl; site_1: NotI; site_2: SalI"
BASE COUNT      101 a      101 c      162 g      86 t
ORIGIN

Query Match      63.9%; Score 26.2; DB 9; Length 450;
Best Local Similarity 90.3%; Pred. No. 5.1e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GGCCTCCAGGGCCCCGCGACGCCGAGCCGCGG 32
    ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 112 GGCCTCCAGGGCGCGCGCAGACCCGAGCCCGG 82

RESULT 6
BE408607/c      610 bp      mRNA      linear      EST 21-JUL-2000
LOCUS
DEFINITION
601304118F1 NIH_MGC_21 Homo sapiens CDNA clone IMAGE:3638356 5',
mRNA sequence.
ACCESSION
BE408607
VERSION
BE408607.1 GI:9345057
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 610)
NIH-MGC http://mgc.nci.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM339 row: d column: 05
High quality sequence stop: 610.
Location/Qualifiers
1. 610
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3638356"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```
BASE COUNT      145 a      127 c      208 g      130 t
ORIGIN
```

```
Query Match      63.9%; Score 26.2; DB 10; Length 610;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GGCCTCCAGGGCCCCGCGACGCCGAGCCGCGG 32
    ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 46 GGCCTCCAGGGCGCGCGCAGACCCGAGCCCGG 16
```

```
RESULT 7
BG287661/c
LOCUS      BG287661      627 bp      mRNA      linear      EST 21-FEB-2001
```

```
DEFINITION
602384488F1 NIH_MGC_93 Homo sapiens CDNA clone IMAGE:4513772 5',
mRNA sequence.
ACCESSION
BG287661
VERSION
BG287661.1 GI:13041716
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 627)
NIH-MGC http://mgc.nci.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10400 row: o column: 21
High quality sequence stop: 627.
Location/Qualifiers
1. 627
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4513772"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bladder; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH-MGC library."
```

```
FEATURES
source
location/Qualifiers
1. 627

BASE COUNT      149 a      130 c      217 g      131 t
ORIGIN
```

```
Query Match      63.9%; Score 26.2; DB 12; Length 627;
Best Local Similarity 90.3%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GGCCTCCAGGGCCCCGCGACGCCGAGCCGCGG 32
    ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 GGCCTCCAGGGCGCGCGCAGACCCGAGCCCGG 36
```

```
RESULT 8
BE294050/c      634 bp      mRNA      linear      EST 20-JUL-2000
LOCUS
DEFINITION
601173259F1 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:3528591 5',
mRNA sequence.
ACCESSION
BE294050
VERSION
BE294050.1 GI:9177580
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
```

```
REFERENCE
1 (bases 1 to 634)
NIH-MGC http://mgc.nci.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
```

Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 445.
Location/Qualifiers

FEATURES
source

1. 561
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6136374"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 63 a 215 c 210 g 73 t
ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 561;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTCCAGGGCCCGCAGACCGGCGGTCCCGGG 41
|||||
Db 261 CGGCTCCAGGGCCCGCAGACCGGCGGTCCCGGG 221

RESULT 4
AA341747/c 219 bp mRNA linear EST 21-APR-1997
LOCUS AA341747 Fetal kidney II Homo sapiens cDNA 5' end, mRNA sequence.
DEFINITION
AA341747
ACCESSION
AA341747.1 GI:1993984
VERSION
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 219)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,
Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon

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Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13-21.

FEATURES
source

1. 219
/organism="Homo sapiens"
/db_xref="ATCC (inhost):143413"
/db_xref="taxon:9606"
/clone_lib="Fetal kidney II"
/dev_stage="fetus"
/note="Organ: kidney; Vector: pBluescript KS-; Site_1:
XhoI; Site_2: EcoRI"
Location/Qualifiers
BASE COUNT 41 a 47 c 82 g 49 t
ORIGIN

Query Match 63.9%; Score 26.2; DB 9; Length 219;
Best Local Similarity 90.3%; Pred. No. 5.3e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCTCCAGGGCCCGCAGACCGGCGGG 32
|||||
Db 48 GGCTCCAGGGCCCGCAGACCGGCGGG 18

RESULT 5
AL036562/c 450 bp mRNA linear EST 29-FEB-2000
LOCUS AL036562 DKFZP564K1262_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
DEFINITION DKFZP564K1262 5', mRNA sequence.
ACCESSION AL036562
VERSION AL036562.1 GI:5406104
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 450)
Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Blum H
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by LMU (Ludwig Maximilians University,
Munich/Germany) within the cDNA sequencing consortium of the German
Genome Project.
s1 sequence also available.
This clone (DKFZP564K1262) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source

1. 450
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZP564K1262"
/clone_lib="564 (synonym: hfbr2)"

Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center This clone is
available royalty-free through LNL; please contact the IMAGE
consortium (info@image.lnl.gov) for further information
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco.

FEATURES
source
location/Qualifiers
1.453
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6136736"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
Superscript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT
ORIGIN
41 a 189 c 164 g 59 t

Query Match
Best Local Similarity 100.0%; Score 41; DB 14; Length 453;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCTCCAGGGCCCCGACAGCCGCGCTCCCGGGG 41
|||||
Db 261 CGGCCTCCAGGGCCCCGACAGCCGCGCTCCCGGGG 221

RESULT 2
BM967243/c 492 bp mRNA linear EST 29-APR-2002
LOCUS 1j32c09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
DEFINITION CDNA clone IMAGE:6136336 5' similar to SW:A2AA_HUMAN P08913
ACCESSION BM967243
VERSION ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.
KEYWORDS BM967243.1 GI:19561038
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 492)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
, M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
, Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTS: 1j32c09.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812

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Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 455.

FEATURES
source
location/Qualifiers
1.492
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6136336"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
Superscript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT
ORIGIN
44 a 202 c 182 g 64 t

Query Match
Best Local Similarity 100.0%; Score 41; DB 14; Length 492;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCTCCAGGGCCCCGACAGCCGCGGTCCTCCCGGGG 41
|||||
Db 261 CGGCCTCCAGGGCCCCGACAGCCGCGGTCCTCCCGGGG 221

RESULT 3
BM967248/c 561 bp mRNA linear EST 29-APR-2002
LOCUS 1j32d04.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
DEFINITION CDNA clone IMAGE:6136374 5' similar to SW:A2AA_HUMAN P08913
ACCESSION BM967248
VERSION ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.
KEYWORDS BM967248.1 GI:19561047
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 561)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
, M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
, Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTS: 1j32d04.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 12:34:42 ; Search time 81.5273 Seconds
(without alignments)
8144.696 Million cell updates/sec

Title: US-09-636-259B-1_COPY_730_770

Perfect score: 41
Sequence: 1 cggcctccagggcccccgcag.....ccccgagcgcgltcccccgggg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_hnv:*
20: em_gss_pln:*
21: em_gss_vtl:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	453	14	BQ129312 ij34d05.y
2	41	100.0	492	14	BM967243 ij32c09.y
3	41	100.0	561	14	BM967248 ij32d04.y
4	26.2	63.9	219	9	AA341747
5	26.2	63.9	450	9	AL036562
6	26.2	63.9	610	10	BE408607

C	7	26.2	63.9	627	12	BG287661	BG287661	602384488
C	8	26.2	63.9	634	10	BE294050	BE294050	601173259
C	9	26.2	63.9	660	10	BE389699	BE389699	601281941
C	10	26.2	63.9	670	10	BE391389	BE391389	601284042
C	11	26.2	63.9	687	10	BE547791	BE547791	601073643
C	12	26.2	63.9	757	12	BG766353	BG766353	602739064
C	13	26.2	63.9	765	12	BG716838	BG716838	602677955
C	14	26.2	63.9	779	12	BF343380	BF343380	602014679
C	15	26.2	63.9	780	13	BM083862	BM083862	1magegc_6
C	16	26.2	63.9	803	12	BG393766	BG393766	602416612
C	17	26.2	63.9	820	13	BI598372	BI598372	603250073
C	18	26.2	63.9	825	13	BI752848	BI752848	603022059
C	19	26.2	63.9	851	13	BI758754	BI758754	603023734
C	20	26.2	63.9	857	12	BG421007	BG421007	602451068
C	21	26.2	63.9	861	13	BI762445	BI762445	603048837
C	22	26.2	63.9	879	13	BI756691	BI756691	603024518
C	23	26.2	63.9	903	12	BF529249	BF529249	602040153
C	24	26.2	63.9	928	12	BF026419	BF026419	601671438
C	25	26.2	63.9	938	9	AL554987	AL554987	AL554987
C	26	26.2	63.9	946	9	AL523383	AL523383	AL523383
C	27	26.2	63.9	973	12	BE744766	BE744766	601573186
C	28	26.2	63.9	993	12	BG260594	BG260594	602372150
C	29	26.2	63.9	993	14	BQ055651	BQ055651	AGENCOURT
C	30	26.2	63.9	1050	13	BM450744	BM450744	AGENCOURT
C	31	26.2	63.9	1052	12	BG285154	BG285154	602409443
C	32	26.2	63.9	1072	14	BQ054234	BQ054234	AGENCOURT
C	33	26.2	63.9	1101	13	BM547005	BM547005	AGENCOURT
C	34	26.2	63.9	1125	13	BM557455	BM557455	AGENCOURT
C	35	26.2	63.9	1127	14	BM807737	BM807737	AGENCOURT
C	36	26.2	63.9	1159	13	BM466243	BM466243	AGENCOURT
C	37	25.6	62.4	330	14	BM738222	BM738222	K-EST0002
C	38	25.2	61.5	444	9	AA216676	AA216676	zq95b08.r
C	39	24.8	60.5	383	9	AI078720	AI078720	oy12d12.s
C	40	24.8	60.5	404	9	AA845046	AA845046	ak58b05.s
C	41	24.8	60.5	520	9	AA526962	AA526962	n106b07.s
C	42	24.6	60.0	491	10	BE408876	BE408876	601303748
C	43	24.6	60.0	530	10	BE410573	BE410573	601303408
C	44	24.6	60.0	587	13	BI438438	BI438438	1c23d08.y
C	45	24.6	60.0	611	13	BI195653	BI195653	602754384

ALIGNMENTS

RESULT 1
BQ129312/c 453 bp mRNA linear EST 29-APR-2002
LOCUS ij34d05.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
DEFINITION CDNA clone IMAGE:6136736 5' similar to SW: A2A_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.

ACCESSION BQ129312
VERSION BQ129312.1 GI:20203223

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 453)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T., Jackson,Y. and Bowers,Y.

AUTHORS

TITLE
JOURNAL
COMMENT
Other_ESTs: ij34d05.x1
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812

Db 220 CCCCCAGGGCCCCGCGGACCCCGAGCCGCGCAGCCCC 188

RESULT 15

AAF21895/C
ID AAF21895 standard; DNA; 1093 BP.

AC AAF21895;

DT 27-MAR-2001 (first entry)

DE Human breast and ovarian cancer associated antigen gene SEQ ID 282.

KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antinflammatory; antiulcer; vulnerary; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease; ds.

OS Homo sapiens.

PN WO200055173-A1.

PD 21-SEP-2000.

PF 08-MAR-2000; 2000WO-US05881.

PR 12-MAR-1999; 99US-0124270.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

DR WPI; 2000-611515/58.

DR P-PSDB; AAB58992.

PT New human breast and ovarian cancer associated gene sequences and the
PT polypeptides encoded by these genes, useful in the prevention,
PT treatment and diagnosis of cancer, immune disorders, cardiovascular
PT disorders and neurological diseases -

PS Claim 1; Page 698; 1299pp; English.

CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic; immunosuppressive;
CC nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
CC antidiabetic; antinflammatory; antiulcer; vulnerary; anticonvulsant;
CC antibacterial; antifungal; antiparasitic and cardiant activity. The
CC polynucleotide and protein sequences are used in the diagnosis of
CC particularly breast and ovarian cancer. The nucleic acid sequences,
CC proteins, agonists and agonists may also be used in the diagnosis,
CC prevention and treatment of immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; cardiovascular disorders such as
CC myocardial ischaemias; wound healing; neurological diseases such as
CC cerebral anoxia and epilepsy; and infectious diseases.

XX Sequence 1093 BP; 208 A; 362 C; 308 G; 209 T; 6 other;

Query Match 56.1%; Score 23; DB 21; length 1093;
Best Local Similarity 74.4%; Pred. No. 2.3e+02;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 2 GGCCTCCAGGGCCCCCGAGACCCGAGCGCGTCCCCGGG 40
Db 130 GGGACCCAGTGCCTCCGAAGACCCGAGCACCTTCCATGGG 92

Search completed: February 15, 2003, 14:29:34
Job time : 68.0206 secs

PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
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PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
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PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
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PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.

PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
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PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
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PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 38594; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosstatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 61710 BP; 11560 A; 18542 C; 18148 G; 13460 T; 0 other;

Query Match 57.1%; Score 23.4; DB 22; Length 61710;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 5 CTCACGGGCCCGCAGACCCGAGCGGCTCCCC 37

PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
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PR 17-NOV-2000; 2000US-0249217.
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PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 38593; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For

CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 37664 BP; 6667 A; 11245 C; 10958 G; 8794 T; 0 other;

Query Match 57.1%; Score 23.4; DB 22; Length 37664;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 CTCGAGGCCCCGACACCCGAGCGGTCGCC 37
| | | | | | | | | | | | | | | | | | | | | |
Db 220 CCCGAGGCCCCGCGGACCCCGAGCGCCAGCCCC 188

RESULT 14
AAK83782/c
ID AAK83782 standard; DNA; 61710 BP.
XX
AC AAK83782;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38594.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.

XX 07-JUL-2000; 2000EP-0114089.
PF
XX
PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
DR P-PSDB; AAM93659.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
PS Claim 8; SEQ ID NO 3531; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a full length
CC human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 2239 BP; 362 A; 734 C; 712 G; 431 T; 0 other;

Query Match 57.1%; Score 23.4; DB 22; Length 2239;
Best Local Similarity 73.2%; Pred.No.1.6e+02;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 CGGCGTCGAGGGCCCGCAGACCCGCGCGTCCCGGGG 41
DB 1386 CTGCATGCAGTGCCCGCAGCAGCTGACGAGGTTCCCGGGG 1346

RESULT 13
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ID AAK83781 standard; DNA; 37664 BP.
XX
AC AAK83781;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:38593.
XX
KW Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
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PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
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PR 30-AUG-2000; 2000US-0227009.
PR 01-SEP-2000; 2000US-0229287.
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PR 01-SEP-2000; 2000US-0229344.
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PR 05-SEP-2000; 2000US-0229509.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
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PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.

Db 72903 CGGCATCCGGCGCCAGCGGACCACTGCCGGTCTCCG 72940

RESULT 10

AAH21860/C

ID AAH21860 standard; cDNA; 7185 BP.

AC AAH21860;

DT 16-AUG-2001 (first entry)

DE Mouse N-calcium channel alpha 1B subunit encoding cDNA SEQ ID NO:1.

XX Mouse; N-calcium channel alpha 1B subunit; blood pressure control;

KW N-calcium channel knockout animal; blood glucose level control;

KM pain transfer; hypotensive; analgesic; ss.

OS Mus musculus.

EH Key Location/Qualifiers

FT CDS 121..6987

FT /*tag= a /product= "N-calcium channel alpha 1B subunit"

PN WO200130137-A1.

PD 03-MAY-2001.

PE 26-OCT-2000; 2000WO-JP07503.

XX 26-OCT-1999; 99JP-0303809.

PR 16-FEB-2000; 2000JP-0037839.

PR 31-AUG-2000; 2000JP-0261979.

XX (EISA) EISAI CO LTD.

XX Ino M, Miyamoto N, Takahashi E, Oki T, Yoshinaga T, Hatakeyama S;

PI Nidome T, Sawada K, Nishizawa Y, Tanaka I;

XX WPI: 2001-300406/31.

DR P-PSDB; AAB98073.

PT N-type calcium channel deficient non-human animals useful for screening

PS Claim 5; Page 39-49; 64pp; Japanese.

XX The present invention describes an N-type calcium channel deficient

CC non-human animal whose gene for the calcium channel has been disrupted.

CC The gene that is disrupted encodes the N-type calcium channel alpha 1B

CC subunit. Also described are: (1) a method for assaying usefulness of

CC substances using the animal; (2) a method for screening for substances

CC with potential pharmacological use; (3) useful substances found by the

CC method; and (4) a method for producing pharmaceuticals using this method

CC (specifically methods for producing a hypotensive drug, a pain killer

CC and a drug for lowering blood sugar and the substances themselves). The

CC N-type calcium channel deficient non-human animal can be used for

CC screening substances for pharmaceutical use. Active substances include

CC a hypotensive drug, a pain killer and a drug for lowering blood sugar.

CC The present sequence encodes the mouse N-calcium channel alpha 1B

CC subunit from the present invention.

XX Sequence 7185 BP; 1588 A; 2045 C; 1967 G; 1585 T; 0 other;

Query Match 57.6%; Score 23.6; DB 22; Length 7185;

Best Local Similarity 76.3%; Pred. No. 1.2e+02;

Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGGCTTCAGGGCCCGCAGACCCGAGCGGTCCTCCG 38

Db 208 CCGCCCCGCGCGCCCGCGCCCGCAGCCGCTCCCG 171

RESULT 11

AAT13279

ID AAT13279 standard; cDNA; 9444 BP.

AC AAT13279;

DT 20-SEP-1996 (first entry)

DE cDNA to genomic hepatitis C virus RNA.

XX hepatitis C virus; antibody; detection; diagnosis; vaccine;

KW classify; subtype; ss.

OS Hepatitis C virus.

EH Key Location/Qualifiers

FT CDS complement (34..9105)

FT /*tag= a

PN JP08056672-A.

PD 05-MAR-1996.

PE 26-AUG-1994; 94JP-0223933.

PR 26-AUG-1994; 94JP-0223933.

XX (SAYA/) SAYAMA K.

XX WPI: 1996-182301/19.

DR P-PSDB; AAR94462.

PT Hepatitis C virus genomic RNA, DNA and related proteins - useful for

PT detection, diagnosis and identification of hepatitis C virus

PT sub-type

XX Claim 2; Page 9-12; 25pp; Japanese.

XX The present sequence represents cDNA to a hepatitis C virus (HCV)

CC genomic RNA. The sequence encodes a polypeptide contg. a 3023 amino

CC acid sequence (see AAR94462) which can be easily detected by antibodies

CC in an assay for the detection of HCV. The DNA and the protein are

CC useful for classifying the subtype of HCV. At least a part of the

CC protein may be used as a vaccine against HCV.

XX Sequence 9444 BP; 2079 A; 2608 C; 2682 G; 2075 T; 0 other;

Query Match 57.6%; Score 23.6; DB 17; Length 9444;

Best Local Similarity 76.3%; Pred. No. 1.2e+02;

Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 GGCTTCAGGGCCCGCAGACCCGAGCGGTCCTCCCG 39

Db 3487 GGCCACTGAGGGCGCGGAGAGACCCAGCCCATACCCCG 3524

RESULT 12

AAK94594/C

ID AAK94594 standard; cDNA; 2239 BP.

AC AAK94594;

DT 06-NOV-2001 (first entry)

DE Human full-length cDNA, SEQ ID NO: 3531.

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

KW Homo sapiens.

OS Homo sapiens.

PN EP1130094-A2.

PD 05-SEP-2001.


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FT      /*tag= n
FT      /note= "ACP6"
FT      complement (13761..14394)
FT      /*tag= o
FT      /note= "KR6"
FT      complement (14517..15294)
FT      /*tag= p
FT      /note= "ER6"
FT      complement (15438..16587)
FT      /*tag= q
FT      /note= "dehydratase domain (DH) 6"
FT      complement (16587..17820)
FT      /*tag= i
FT      /note= "acylttransferase domain (AT) 6"
FT      complement (17820..19053)
FT      /*tag= s
FT      /note= "KS6"
FT      complement (19116..19326)
FT      /*tag= t
FT      /note= "ACP5"
FT      complement (19464..20097)
FT      /*tag= u
FT      /note= "KR5"
FT      complement (20241..21420)
FT      /*tag= v
FT      /note= "DH5"
FT      complement (21420..22653)
FT      /*tag= w
FT      /note= "AT5"
FT      complement (22653..23892)
FT      /*tag= x
FT      /note= "KS5"
FT      complement (23992..46573)
FT      /*tag= y
FT      /note= "fkxb gene"
FT      complement (24163..24373)
FT      /*tag= z
FT      /note= "ACP4"
FT      complement (24997..26146)
FT      /*tag= aa
FT      /note= "DH4 (inactive)"
FT      complement (26146..27430)
FT      /*tag= ab
FT      /note= "AT4"
FT      complement (27430..28684)
FT      /*tag= ac
FT      /note= "KS4"
FT      complement (28750..28960)
FT      /*tag= ad
FT      /note= "ACP3"
FT      complement (29092..29740)
FT      /*tag= ae
FT      /note= "KR3"
FT      complement (29869..31018)
FT      /*tag= af
FT      /note= "DH3 (inactive)"
FT      complement (31018..32185)
FT      /*tag= ag
FT      /note= "AT3"
FT      complement (32185..33439)
FT      /*tag= ah
FT      /note= "KS3"
FT      complement (33505..33715)
FT      /*tag= ai
FT      /note= "ACP2"
FT      complement (33823..34480)
FT      /*tag= aj
FT      /note= "KR2"
FT      complement (34606..35749)
FT      /*tag= ak
FT      complement (28750..28960)
FT      /*tag= al
FT      /note= "DH2 (inactive)"
```

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FT      /*tag= am
FT      /note= "AT2"
FT      misc_feature      complement (37145..38296)
FT      /*tag= an
FT      /note= "KS2"
FT      misc_feature      complement (38371..38581)
FT      /*tag= ao
FT      /note= "ACP1"
FT      misc_feature      complement (38677..39307)
FT      /*tag= ap
FT      /note= "KR1"
FT      misc_feature      complement (39442..40609)
FT      /*tag= aq
FT      /note= "DH1"
FT      misc_feature      complement (40609..41842)
FT      /*tag= ar
FT      /note= "AT1"
FT      misc_feature      complement (41842..43093)
FT      /*tag= as
FT      /note= "KS of extender module 1 (KS1)"
FT      complement (43144..43660)
FT      /*tag= at
FT      /note= "ACP of loading domain"
FT      misc_feature      complement (43777..44629)
FT      /*tag= au
FT      /note= "ER of loading domain"
FT      misc_feature      complement (44974..46573)
FT      /*tag= av
FT      /note= "COA ligase of laodng domain"
FT      CDS               46754..47788
FT      /*tag= aw
FT      /note= "fkbo gene"
FT      CDS               47785..52272
FT      /*tag= ax
FT      /note= "fkbp gene"
FT      CDS               52275..71465
FT      /*tag= ay
FT      /note= "fkba gene"
FT      misc_feature      52362..53576
FT      /*tag= az
FT      /note= "KS7"
FT      misc_feature      53577..54716
FT      /*tag= ba
FT      /note= "AT7"
FT      misc_feature      54717..55871
FT      /*tag= bb
FT      /note= "DH7"
FT      misc_feature      56019..56819
FT      /*tag= bc
FT      /note= "ER7"
FT      misc_feature      56943..57575
FT      /*tag= bd
FT      /note= "KR7"
FT      misc_feature      57710..57920
FT      /*tag= be
FT      /note= "ACP7"
FT      misc_feature      57990..59243
FT      /*tag= bf
FT      /note= "KS8"
FT      misc_feature      59244..60398
FT      /*tag= bg
FT      /note= "AT8"
FT      misc_feature      60399..61412
FT      /*tag= bh
FT      /note= "DH8 (inactive)"
```

```
Query Match      61.5%; Score 25.2; DB 21; Length 77536;
Best local Similarity 78.9%; Pred. No. 33;
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY      1 CGGCTTCAGGGCCCGCAGACCGAGCGGTCGCCG 38
      |||| ||| |||| | |||| ||||| |||
```

CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.

XX
SQ Sequence 206 BP; 35 A; 45 C; 85 G; 40 T; 1 other;

Query Match 63.9%; Score 26.2; DB 21; Length 206;
Best Local Similarity 90.3%; Pred. No. 32;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCTCCAGGGCCCGCAGACCCGAGCGCG 32
|||||
DB 80 GGCTCCAGGGCCCGCAGACCCGAGCGCG 50

RESULT 8

AAH52225/c
ID AAH52225 standard; cDNA; 576 BP.

XX AAH52225;
AC
XX 10-SEP-2001 (first entry)
DT
XX

DE Human AFP protein encoding cDNA sequence SEQ ID NO:265.

XX Human; secreted protein; secretion; bacterial cell; fungal cell;
KW eukaryotic cell; fusion protein; maltose binding protein;
KW immunoglobulin constant region; polyhistidine tag; ss.
XX
OS Homo sapiens.
XX
PN WO200129221-A2.
XX

PD 26-APR-2001.
XX
XX 20-OCT-2000; 2000WO-US29052.
PF
XX
XX 20-OCT-1999; 99US-0160712.
PR

XX (ZYMO) ZYMOGENETICS INC.

XX Conklin DC, Yee DP;
XX
XX WPI: 2001-300340/31.
DR P-PSDB; AAG81374.
DR

XX Isolated polypeptide for directing secretion of proteins of interest
PT from a host cell including, e.g. bacteria, includes contiguous amino
PT acid residues of polypeptide with specified amino acids -
XX
XX Claim 9; Page 459-460; 617pp; English.
PS

XX AAH52093 to AAH52303 encode the human secreted proteins given in AAG81242
CC to AAG81453. The secreted proteins can be used for directing the
CC secretion of proteins of interest from a host cell including bacteria,
CC fungal cells, and cultured higher eukaryotic cells. The present invention
CC also describes fusion proteins, where a secreted protein of the invention
CC is operably linked via a peptide bond or peptide linker to a second
CC protein selected from the group consisting of maltose binding protein,
CC an immunoglobulin constant region, a polyhistidine tag and a peptide
CC given in AAG81453.

XX Sequence 576 BP; 140 A; 124 C; 199 G; 113 T; 0 other;
SQ

Query Match 63.9%; Score 26.2; DB 22; Length 576;
Best Local Similarity 90.3%; Pred. No. 28;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCTCCAGGGCCCGCAGACCCGAGCGCG 32
|||||
DB 66 GGCTCCAGGGCCCGCAGACCCGAGCGCG 36

RESULT 9

AAAI4651
ID AAAI4651 standard; DNA; 77536 BP.

XX AAAI4651;
AC
XX 08-AUG-2000 (first entry)
DT
XX

DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.

XX FK-520; polyketide synthase; PKS; gene cluster; immunosuppressant;
KW Streptomyces hygroscopicus var. ascomyceticus; immunophilin;
KW FK-506 binding protein; polyketide compound; transplant rejection;
KW graft-versus-host disease; uveitis; alopecia universalis;
KW autoimmune chronic active hepatitis; inflammatory bowel disease;
KW multiple sclerosis; primary biliary cirrhosis; scleroderma;
KW neurite outgrowth; nerve regrowth; Parkinson's disease;
KW Alzheimer's disease; stroke; traumatic spinal cord; brain injury;
KW peripheral neuropathy; ss.

XX Streptomyces hygroscopicus.

XX Key Location/Qualifiers
FH complement (412..1836)
FT CDS

FT /tag= a
FT /note= "fkBW gene"
FT complement (2020..3579)

FT /tag= b
FT /note= "fkbv gene"
FT complement (3969..4496)

FT /tag= c
FT /note= "fkBR2 gene"
FT complement (4595..5488)

FT /tag= d
FT /note= "fkBR1 gene"
FT complement (5601..6818)

FT /tag= e
FT /note= "fkBE gene"
FT complement (6808..8052)

FT /tag= f
FT /note= "fkBF gene"
FT complement (8156..8824)

FT /tag= g
FT /note= "fkBG gene"
FT complement (9122..9883)

FT /tag= h
FT /note= "fkBH gene"
FT complement (9894..10994)

FT /tag= i
FT /note= "fkBI gene"
FT complement (10987..11247)

FT /tag= j
FT /note= "fkBJ gene"
FT complement (11244..12092)

FT /tag= k
FT /note= "fkBK gene"
FT complement (12113..13150)

FT /tag= l
FT /note= "fkBL gene"
FT complement (13212..23988)

FT /tag= m
FT /note= "fkBC gene"
FT complement (13452..13662)

FT misc_feature

KM gene; ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
PS Claim 1; SEQ ID NO 46; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;

Query Match 65.4%; Score 26.8; DB 24; Length 7353;
Best Local Similarity 81.6%; Pred. No. 14;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CGGCTTCAGAGGCCCGCAGACCCGAGCGGTCCTCCCG 38
DB 1444 CGACCTCCAAAACCCCGCAAAACCGAAGCGATCCCCG 1407

RESULT 6
AAD28363/c
ID AAD28363 standard; DNA; 7353 BP.
XX
AC AAD28363;
XX
DT 22-APR-2002 (first entry)
XX
DE Human chemically treated genomic DNA #4.
XX
KW Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;
KW adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
KW behavioural disorder; neurological; psychiatric; cancer; schizophrenia;
KW Tourette's syndrome; smoking; human immunodeficiency virus dementia;
KW drug abuse; migraine; ds.
XX
OS Homo sapiens.
XX
PN WO200202809-A2.
XX
PD 10-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07540.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.

XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-154759/20.
XX
PT Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT gene -
XX
PS Claim 1; Page 36-40; 190pp; English.
XX
CC The invention relates to nucleic acids comprising a segment of chemically
CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC useful for detecting cytosine methylations. The pretreated DNA is useful
CC for the diagnosis or therapy of behavioural disorders, neurological
CC disorders and cancer, in particular major depressive disorder, Tourette's
CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC drug abuse, alcoholism, personality traits, compulsive gambling, human
CC immunodeficiency virus dementia, migraine, behaviours in schizophrenic
CC and schizoaffective patients, and suicidal behaviour in patients with
CC schizophrenia. The nucleic acid is useful for detecting the methylation
CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC (SNPs). The present sequence is human chemically treated genomic DNA.
XX
SQ Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;

Query Match 65.4%; Score 26.8; DB 24; Length 7353;
Best Local Similarity 81.6%; Pred. No. 14;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CGGCTTCAGAGGCCCGCAGACCCGAGCGGTCCTCCCG 38
DB 1444 CGACCTCCAAAACCCCGCAAAACCGAAGCGATCCCCG 1407

RESULT 7
AAC10059/c
ID AAC10059 standard; cDNA; 206 BP.
XX
AC AAC10059;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 14134.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 14134; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from

XX drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
XX WO200218632-A2.
XX
XX 07-MAR-2002.
XX
XX 01-SEP-2001; 2001WO-EP10074.
XX
XX 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
XX Sequence 1733 BP; 271 A; 211 C; 625 G; 626 T; 0 other;
SQ

Query Match 65.4%; Score 26.8; DB 24; Length 1733;
Best Local Similarity 81.6%; Pred. No. 17;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CGGCTTCAGGGCCCGCAGACCCGAGCGGTCCTCCG 38
|| ||||| ||||| ||||| ||||| |||||
Db 564 CGACCTCCAAAAACCCCGCAAAACCGAAGCGATCCCG 527

RESULT 4
ABL32073/c
ID ABL32073 standard; DNA; 1733 BP.
XX
XX ABL32073;
XX
XX 12-JUL-2002 (first entry)
XX
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 34092.
DE
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.

XX
XX Homo sapiens.
OS
XX
XX WO200218632-A2.
PN
XX
XX 07-MAR-2002.
PD
XX
XX 01-SEP-2001; 2001WO-EP10074.
PF
XX
XX 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
XX Sequence 1733 BP; 626 A; 625 C; 211 G; 271 T; 0 other;
SQ

Query Match 65.4%; Score 26.8; DB 24; Length 1733;
Best Local Similarity 81.6%; Pred. No. 17;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CGGCTTCAGGGCCCGCAGACCCGAGCGGTCCTCCG 38
|| ||||| ||||| ||||| ||||| |||||
Db 1170 CGACCTCCAAAAACCCCGCAAAACCGAAGCGATCCCG 1207

RESULT 5
ABL32073/c
ID ABL32073 standard; DNA; 7353 BP.
XX
XX ABL32073;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human immune system associated gene SEQ ID NO: 46.
DE
XX Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytosatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;


```
XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
PA
XX
PI Liggett SB, Small KM;
XX
DR WPI: 2001-611728/70.
DR P-PSDB; AAM52122.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
PS Example 7, Page 151; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcggtgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR gene
CC (GenBank Accession AF281308).
XX
SQ Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;

Query Match          100.0%; Score 41; DB 23; Length 1350;
Best Local Similarity 100.0%; Pred. NO. 0.0011;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCTCCAGGGCCCCGACAGCCGAGCGGTCGCCGGGG 41
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Db 910 CGGCTCCAGGGCCCCGACAGCCGAGCGGTCGCCGGGG 950

RESULT 2
AAI99918 standard; DNA; 1350 BP.
XX
AC AAI99918;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2AAR variant encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1353
FT /*tag= a
FT /product= "alpha-2AAR"
FT allele replace(753,C)
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FT /*tag= b
XX
PN WO200179561-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US12575.
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI: 2001-611728/70.
DR P-PSDB; AAM52123.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
PS Disclosure; Page 152; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcggtgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR variant
CC gene.
XX
SQ Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;

Query Match          100.0%; Score 41; DB 23; Length 1350;
Best Local Similarity 100.0%; Pred. NO. 0.0011;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCTCCAGGGCCCCGACAGCCGAGCGGTCGCCGGGG 41
    |||||||
Db 910 CGGCTCCAGGGCCCCGACAGCCGAGCGGTCGCCGGGG 950

RESULT 3
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ID ABQ47500 standard; DNA; 1733 BP.
XX
AC ABQ47500;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34091.
XX
KW Human; cytosine methylation; 5'-Cpg-3'; uracil; cytosine; diagnosis;
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 11:01:28 ; Search time 11.7706 Seconds
(without alignments)
7844.310 Million cell updates/sec

Title: US-09-636-259B-1_COPY_730_770

Perfect score: 41
Sequence: 1 cgcgctccagggccccgcag.....ccccgagcgcggtcccgggg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	41	100.0	1350	23	AAI99917	Human alpha-2AAR e
2	41	100.0	1350	23	AAI99918	Human alpha-2AAR v
3	26.8	65.4	1733	24	ABQ47500	Oligonucleotide fo
4	26.8	65.4	1733	24	ABQ47501	Oligonucleotide fo
5	26.8	65.4	7353	24	ABL32073	Human immune syste
6	26.8	65.4	7353	24	AAD28363	Human chemically t
7	26.2	63.9	206	21	AAC10059	Human secreted pro
8	26.2	63.9	576	22	AAH52225	Human AFP protein
9	25.2	61.5	77536	21	AAA14651	Nucleotide sequenc

C	10	23.6	57.6	7185	22	AAH21860	Mouse N-calcium ch
	11	23.6	57.6	9444	17	AAT13279	CDNA to genomic he
C	12	23.4	57.1	2239	22	AAK94594	Human full-length
C	13	23.4	57.1	3764	22	AAK83781	Human immune/haema
C	14	23.4	57.1	61710	22	AAK83782	Human immune/haema
C	15	23	56.1	1093	21	AAF21895	Human breast and o
C	16	23	56.1	1396	24	ABK84443	Human CDNA differe
C	17	23	56.1	1596	22	ABA09009	Human PROVI homolo
C	18	23	56.1	1596	22	AAH99678	Human protein enco
	19	23	56.1	4692	19	AAV04633	Porcine phosphino
	20	23	56.1	4692	20	AAV74099	Porcine G-protein
	21	23	56.1	4692	21	AAZ86812	Pig p101 regulator
C	22	22.4	54.6	348	20	AAAX41077	Human secreted pro
C	23	22.4	54.6	949	20	AAZ40845	Secreted protein E
C	24	22.4	54.6	1322	22	AAF27733	Human transport pr
C	25	22.4	54.6	2033	23	ABV24123	Human prostate exp
C	26	22.4	54.6	2033	23	ABV30001	Human prostate exp
C	27	22.4	54.6	2537	19	AAV52933	Human pre-transfor
C	28	22.4	54.6	7110	22	AAF81361	Quorum sensing con
	29	22.4	54.6	12638	22	AAK70641	Human immune/haema
C	30	22	53.7	295	21	AAA42360	Human secreted exp
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	32	22	53.7	1150	17	AAT03650	31-O-desmethyl-FK5
C	33	22	53.7	1998	22	AAS00429	Pseudomonas aerugi
C	34	22	53.7	1998	22	AAS00430	Pseudomonas aerugi
C	35	22	53.7	1998	22	AAS54058	Pseudomonas aerugi
	36	22	53.7	3113	21	AAF21036	Human low adenosin
	37	22	53.7	3113	21	AAA34914	Human adenosine re
	38	22	53.7	3113	23	AAS80768	DNA encoding novel
	39	22	53.7	3113	24	ABK84158	Human CDNA differe
DE	40	22	53.7	13548	21	AAF21037	Human low adenosin
	41	22	53.7	13548	21	AAA34915	Human adenosine re
C	42	22	53.7	19616	22	ABAI6094	Human nervous syst
C	43	22	53.7	19616	22	ABAI6856	Human nervous syst
C	44	22	53.7	19616	22	AAI36855	Human musculoskele
	45	22	53.7	65140	22	AAD17184	Streptomyces nous

ALIGNMENTS

RESULT 1	
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ID	AAI99917 standard; DNA; 1350 BP.
AC	AAI99917;
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DT	18-FEB-2002 (first entry)
XX	
DE	Human alpha-2AAR encoding DNA.
XX	
KW	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW	polymorphic site; allelic variant; cardiovascular disease;
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW	phosphorylation; inositol phosphate; alpha-2AAR;
KW	GenBank Accession AF281308; chromosome 10; ds.
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OS	Homo sapiens.
XX	
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PN	WO200179561-A2.
XX	
PD	25-OCT-2001.
XX	
PF	17-APR-2001; 2001WO-US12575.
XX	
PR	17-APR-2000; 2000US-0551744.
PR	10-AUG-2000; 2000US-0636259.
PR	19-OCT-2000; 2000US-0692077.

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Db 130648 CGGCCCCCGGGGGCCCCCGCAGACCCGAGCGGCCCCCGAG 130609

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RESULT	15
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LOCUS	PIGA2AR 1728 bp DNA linear MAM 27-APR-1993
DEFINITION	Porcine alpha2A-adrenergic receptor (PORA2AR) gene,
ACCESSION	J05652 complete cds.
VERSION	J05652.1 GI:164303
KEYWORDS	alpha-2A-adrenergic receptor.
SOURCE	Porcine liver DNA.
ORGANISM	Sus scrofa
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
JOURNAL	Guyer,C.A., Horstman,D.A., Wilson,A.L., Clark,J.D., Kragoe,E.J.Jr.
REFERENCE	and Limbird,L.E. Unpublished (1990) 2 (bases 70 to 1582)

AUTHORS	Guyer,C.A., Horstman,D.A., Wilson,A.L., Clark,J.D., Cragoe,E.J. Jr. and Limbird,L.E.
TITLE	Cloning, sequencing, and expression of the gene encoding the porcine alpha 2-adrenergic receptor. Allosteric modulation by Na ⁺ , H ⁺ , and amiloride analogs
JOURNAL	J. Biol. Chem. 265 (28), 17307-17317 (1990)
MEDLINE	91009167
PUBMED	2170371
COMMENT	Draft entry and computer-readable sequence for [J. Biol. Chem. (1990) in press] kindly submitted by C.A.Guyer, 02-AUG-1990.
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ORIGIN				

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Search completed: February 15, 2003, 16:45:22
Job time : 246.55 secs

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 204317)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP23-358H2
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 204317)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczký,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 204317)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczký,J., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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JOURNAL Submitted (06-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Jun 6, 2002 this sequence version replaced gi:21313866.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L23807
Center clone name: 358_H_2
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Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 197709 bases at least Q40
Consensus quality: 200412 bases at least Q30
Consensus quality: 201149 bases at least Q20
Insert size: 210000; agarose-fp
Insert size: 202017; sum-of-contigs
Quality coverage: 6.3 in Q20 bases; agarose-fp
Quality coverage: 6.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 7387: contig of 7387 bp in length
7388 7487: gap of 100 bp
7488 7956: contig of 469 bp in length
7957 8056: gap of 100 bp
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9201 9300: gap of 100 bp
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BASE COUNT 229 a 481 c 467 g 277 t
ORIGIN

Query Match 78.0%; Score 32; DB 10; Length 1454;
Best Local Similarity 87.5%; Pred. No. 25;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 CGGCTCCAGGGCCCGCAGACCCGAGCGGTCCTCCGGG 40
Db 960 CGGCCCCCGGGCGCCGACACCCGAGCCCGGGCCCGAG 999

RESULT 12
RRU79031 1552 bp mRNA linear ROD 14-JUN-2000
LOCUS RRU79031
DEFINITION Rattus norvegicus alpha2b adrenergic receptor mRNA, complete cds.
ACCESSION U79031
VERSION U79031.1 GI:3282234
KEYWORDS
SOURCE
ORGANISM Rattus norvegicus.
Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1552)
AUTHORS Chalberg,S.C., Duda,T., Rhine,J.A. and Sharma,R.K.
TITLE Molecular cloning, sequencing and expression of an alpha
2-adrenergic receptor complementary DNA from rat brain
JOURNAL Mol. Cell. Biochem. 97 (2), 161-172 (1990)
MEDLINE 91125329
PUBMED 2177834
REFERENCE 2 (bases 1 to 1552)
AUTHORS Wypijewski,K., Duda,T. and Sharma,R.K.
TITLE Structural, genetic and pharmacological identity of the rat alpha
2-adrenergic receptor subtype ca2-47 and its molecular
characterization in rat adrenal, adrenocortical carcinoma and
bovine retina
JOURNAL Mol. Cell. Biochem. 144 (2), 181-190 (1995)
MEDLINE 95349560
PUBMED 7623790

REFERENCE 3 (bases 1 to 1552)
AUTHORS Venkataraman,V., Duda,T.M. and Sharma,R.K.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-1996) Cell Biology, UMDNJ-SOM, 2 Medical Ctr.
Dr., Stratford, NJ 08084, USA
FEATURES
source Location/Qualifiers
1.1552
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
1.1353
/codon_start=1
/product="alpha2b adrenergic receptor"
/protein_id="AAC24959.1"
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/translation="MGSLQPDAGNSWNGTEAPGGGTRATPYSLQVTVTLVCLAGLLM
LTFVGNVLVITIAVFTSRALAPQNLFLVSLASADILVATLVIPEFLANEMGYWFG
KWMCEIYALDLVLEFCTSSIVHLCALISDRYMSITQAIENLKRTPRRIKAIIVTVWVI
SAVISFPPLISIEKAGGGQPAEPKCEINDQKMYVISSIGSFAPCLIMILVYVR
IYQIAKRRTRVPPSRRGPDACSAAPPGADRPNGLPERGAGTAGAEAPLPTQVNGA
PGEPAAPRPRDGDALDLEESSSEHAERPOGPKPERGPRAGKTKASQYKPGDSLPR
RGPAAGPGASGSGGGEERAGAKASRWGRQRNREKRTFVLAVVIGVFVVCWPEPFF
TYTLIAVGCVPVYQLNFNFFWFGYCNSSLNPVITYTIFNHDFRAAFKILCRGDRKRIV

BASE COUNT 244 a 504 c 498 g 306 t
ORIGIN

Query Match 78.0%; Score 32; DB 10; Length 1552;
Best Local Similarity 87.5%; Pred. No. 25;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CGGCTCCAGGGCCCGCAGACCCGAGCGGTCCTCCGGG 40
Db 910 CGGCCCCAGGGCGCCGCAACCCGAGCGGTCCTCCGGG 949

RESULT 13
CPU25722 2291 bp DNA linear ROD 05-SEP-2001
LOCUS CPU25722
DEFINITION Cavia porcellus alpha-2A adrenoceptor gene, complete cds.
ACCESSION U25722
VERSION U25722.1 GI:818874
KEYWORDS
SOURCE Cavia porcellus.
Cavia porcellus.
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.

REFERENCE 1 (bases 1 to 2291)
AUTHORS Svensson,S.P., Bailey,T.J., Porter,A.C., Richman,J.G. and
Regan,J.W.
TITLE Heterologous expression of the cloned guinea pig alpha 2A, alpha
2B, and alpha 2C adrenoceptor subtypes. Radioligand binding and
functional coupling to a CAMP-responsive reporter gene
JOURNAL Biochem. Pharmacol. 51 (3), 291-300 (1996)
MEDLINE 96152573
PUBMED 8573196

REFERENCE 2 (bases 1 to 2291)
AUTHORS Richman,J.G.
TITLE Direct Submission
JOURNAL Submitted (26-APR-1995) Jeremy G. Richman, University of Arizona,
Pharmacology and Toxicology, College of Pharmacy, Room 235, Tucson,
AZ 85721, USA
FEATURES
source Location/Qualifiers
1.2291
/organism="Cavia porcellus"
/strain="Sasco Hartley albino"
/db_xref="taxon:10141"
/clone="GP" alpha-2A"
49.1401
/codon_start=1
/product="alpha-2A adrenoceptor"
/protein_id="AAA67074.1"
/db_xref="GI:818875"
/translation="MGSLQPDGNSASWNGTEGPGGTRATPYSLQVTVTLVCLVGLLI
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KAMCEIYALDLVLEFCTSSIVHLCALISDRYMSITQAIENLKRTPRRIKAIIVTVWVI
SAVISFPPLISFEKAGGGQPAEPKCEINDQKMYVISSIGSFAPCLIMILVYVR
IYQIAKRRTRVPPSRRGPDAAHAAPPGAEKRPNGLGLERGVGPGAEAPLPTQVNGA
PGEPAAPRPRDADLEESSSEHAERPPGARPERGLRAKSKARASOVKPGDSLPR
RAPGAAGSGTSGSGPGEERGCGAGAKASRWGRQRNREKRTFVLAVVIGVFVVCWPEPFF
TYTLIAVGCSPVPTLTKFFFWFGYCNSSLNPVITYTIFNHDFRAAFKILCRGDRKRIV

BASE COUNT 456 a 593 c 716 g 526 t
ORIGIN

Query Match 78.0%; Score 32; DB 10; Length 2291;
Best Local Similarity 87.5%; Pred. No. 22;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 CGGCTCCAGGGCCCGCAGACCCGAGCGGTCCTCCGGG 40
Db 958 CGGCCCCCGGGGGCGCCGACACCCGAGCGGTCCTCCGGG 997

RESULT 14
AC113491/c 204317 bp DNA linear HTG 06-JUN-2002
LOCUS AC113491
DEFINITION Mus musculus clone RP23-358H2, WORKING DRAFT SEQUENCE, 24 ordered
pieces.
ACCESSION AC113491
VERSION AC113491.3 GI:21327601
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.

REFERENCE 1 (bases 1 to 3653)
AUTHORS Mao,Z.-M., Tang,K., Li,B.-M. and Jing,N.-H.
TITLE Cloning and expression of human alpha-2A adrenergic receptor in
SY5Y cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3653)
AUTHORS Mao,Z.-M., Tang,K., Li,B.-M. and Jing,N.-H.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-2000) Shanghai Institute of Physiology, Chinese
Academy of Sciences, 320 Yue Yang Road, Shanghai 200031, P.R. China
FEATURES
source
1. .3653
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/map="10q23-q25"
/cell_line="SY5Y"
880. .2232
/codon_start=1
/product="alpha-2A adrenergic receptor"
/protein_id="AAK26743.1"
/db_xref="GI:13447751"
/translation="MGSLQPDAGNASWNGTEAPGGARATPYSLOYTLTLVCLAGLLM
LLTFVGNVLVIIVFTSRALKAPQNLFLVSLASADILVATLVIPEFLANEVMGYWFG
KAMCEIYIALDVLFCTSSIVHCAISLDKRWSTQAIENLKRTPRIKAIITVWVI
SAVISFPPLISIEKKGGGGQPPAEPCEINDQKWYVISSCIGSFAPCLIMILVYVR
IYQIAKRTRVPPSRGPDAAVAPPGGTERPGLGPERSGAGGAEPPLPTQNGA
PGEPAAGPRDIDALDLESSSSDHAERPPGPRRPERGPRGKGKARASQVKKPGDSLPR
PGEATGIGTPAGGGERVGAAKASRWGRQNRKRTFVLAVVIGFEVVCWPFEEF
TYTLTAVGCSVPRTLFKEFFWFYGCNSSLNPVIYITIFNHDFRAFKILCRGDRKRIV
"
BASE COUNT 681 a 1168 c 1028 g 776 t
ORIGIN
Query Match 100.0%; Score 41; DB 9; Length 3653;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCCTCCAGGGCCCCGACAGCCGCGCGTCCCCGGGG 41
Db 1789 CGGCCTCCAGGGCCCCGACAGCCGCGCGTCCCCGGGG 1829
RESULT 10
AL158163 204908 bp DNA linear PRI 13-DEC-2001
LOCUS Human DNA sequence from clone RP11-348N5 on chromosome 10, complete
DEFINITION sequence.
ACCESSION AL158163
VERSION AL158163.11 GI:17384427
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 204908)
AUTHORS Johnson,C.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 5, 2001 this sequence version replaced gi:16944857.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
Chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/BCP/Chr10
RP11-348N5 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: PBACE3.6
This sequence is the entire insert of clone RP11-348N5 The true
left end of clone RP11-479A21 is at 179266 in this sequence. The
true right end of clone RP11-313D6 is at 44800 in this sequence.

FEATURES
source
1. .204908
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-348N5"
/clone_lib="RPCI-11.2"
62115 a 36724 c 39536 g 66533 t
BASE COUNT 62115 a 36724 c 39536 g 66533 t
ORIGIN
Query Match 100.0%; Score 41; DB 9; Length 204908;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCCTCCAGGGCCCCGACAGCCGCGCGTCCCCGGGG 41
Db 196479 CGGCCTCCAGGGCCCCGACAGCCGCGCGTCCCCGGGG 196519
RESULT 11
MUSALP2ADB 1454 bp DNA linear ROD 27-APR-1993
LOCUS Mouse alpha-2 adrenergic receptor, complete cds.
DEFINITION M99377
ACCESSION M99377.1 GI:191882
KEYWORDS alpha-2 adrenergic receptor.
SOURCE Mus musculus (strain 129/Sv) DNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1454)
AUTHORS Link,R., Daunt,D., Barsh,G., Chrusciński,A. and Kobilka,B.
TITLE Cloning of two mouse genes encoding alpha 2-adrenergic receptor
subtypes and identification of a single amino acid in the mouse
alpha 2-C10 homolog responsible for an interspecies variation in
antagonist binding
JOURNAL Moll. Pharmacol. 42 (1), 16-27 (1992)
MEDLINE 92342131
PUBMED 1353249
FEATURES
source
1. .1454
/organism="Mus musculus"
/strain="129/Sv"
/db_xref="taxon:10090"
51. .1403
/codon_start=1
/product="alpha-2 adrenergic receptor"
/protein_id="AAA37213.1"
/db_xref="GI:191883"
/translation="MGSLQPDAGNSWNGTEAPGGGTRATPYSLOYTLTLVCLAGLLM
LFTVGNVLVIIVFTSRALKAPQNLFLVSLASADILVATLVIPEFLANEVMGYWFG
KAMCEIYIALDVLFCTSSIVHCAISLDKRWSTQAIENLKRTPRIKAIITVWVI
SAVISFPPLISIEKKGAGGQPPAEPCEINDQKWYVISSCIGSFAPCLIMILVYVR
IYQIAKRTRVPPSRGPDACASAPPGADRPNGLGPERGAGPTGAEPPLPTQNGA
PGEPAAGPRDIDALDLESSSSDHAERPPGPRRPERGPRGKGKARASQVKKPGDSLPR

ORIGIN

Query Match 100.0%; Score 41; DB 9; Length 1941;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCTCCAGGGCCCCGAGACCCGAGCGCGGTCCCGGGG 41
Db 1428 CGGCCTCCAGGGCCCCGAGACCCGAGCGCGGTCCCGGGG 1468

RESULT 7

HUMADRA2R 3604 bp DNA linear PRI 30-OCT-1994
LOCUS Human alpha 2 adrenergic receptor gene, complete cds.
DEFINITION M23533
ACCESSION M23533.1 GI:178195
VERSION M23533.1 GI:178195
KEYWORDS adrenergic receptor; alpha-2 andrenergic receptor.
SOURCE Human DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 3604)
AUTHORS Fraser,C.M., Arakawa,S., McCombie,W.R. and Venter,J.C.
TITLE Cloning, sequence analysis, and permanent expression of a human alpha 2-adrenergic receptor in Chinese hamster ovary cells.
Evidence for independent pathways of receptor coupling to adenylate cyclase attenuation and activation
J. Biol. Chem. 264 (20), 11754-11761 (1989)

JOURNAL MEDLINE 89308571
PUBMED 2568356
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted by W.R.McCombie, 30-MAR-1989.

FEATURES

source location/Qualifiers
1..3604
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="10q23-q25"
1578..1583
/bound_molety="Sp1"
1707..1712
/note="glucocorticoid response element"
1723..1728
/note="GRE related sequence"
2078..3430
/gene="ZNF32"
2078..3430
/gene="ZNF32"
/note="alpha-2 adrenergic receptor old gene name 'ADRA2R'"
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/protein_id="AA51665.1"
/db_xref="GI:178196"
/db_xref="GDB:G00-125-339"
/translation="MGSLOPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLLM
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KAMCEIYLALDVLEFCTSSIVHLCAISLDRYWSITQAIIEYNLKRTPRIKAIITVWVI
SAVISFPPLISIEKKGGGGGQPAEPRCEINDQKWYISSCIGSFAPCLIMILVYVR
IYQIAKRRTRVPPSRKRPDAVAAPPGGTERPNGLGPERISAGSGAEAEPLTQNGA
PGEPAAGPRDITDALDLESSSSDHAERPPRPERGPRGKAKARASQVKPGDSLNG
AGRGKSGRRLQGRGSASGLPRRAGAGGQNRKRTFTFLAVVIGVFVVCWEPFEF
TYTLTAVGCSVPRTLKFFFWFGYCNSSLNPVIYITFNHDFRAFKKILCRGDRKRIV

BASE COUNT 555 a 1272 c 1134 g 643 t
ORIGIN

Query Match 100.0%; Score 41; DB 9; Length 3604;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCTCCAGGGCCCCGAGACCCGAGCGCGGTCCCGGGG 41
Db 2987 CGGCCTCCAGGGCCCCGAGACCCGAGCGCGGTCCCGGGG 3027

RESULT 8

AY032736 3612 bp DNA linear PRI 12-MAY-2001
LOCUS Homo sapiens alpha-2A adrenergic receptor (ADR2AR) gene, complete
DEFINITION cds.

AY032736
AY032736.1 GI:14029162

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens.
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 3612)
AUTHORS Liu,L. and Yuan,L.
TITLE Human alpha-2A adrenergic receptor gene and the genotype of -1296 nucleotide and motionsickness
Unpublished
2 (bases 1 to 3612)
Liu,L. and Yuan,L.
REFERENCE Direct Submission
AUTHORS Submitted (17-APR-2001) Key Laboratory of Molecular Biology,
TITLE General Hospital of Airforce, Fucheng Road No. 30, Beijing 100036,
JOURNAL China

FEATURES

source location/Qualifiers
1..3612
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/map="10q23-q25"
<2085..>3437
/gene="ADR2AR"
<2085..>3437
/gene="ADR2AR"
/product="alpha-2A adrenergic receptor"
2085..3437
/gene="ADR2AR"
/codon_start=1
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/protein_id="AAK51162.1"
/db_xref="GI:14029163"
/translation="MGSLOPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLLM
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KAMCEIYLALDVLEFCTSSIVHLCAISLDRYWSITQAIIEYNLKRTPRIKAIITVWVI
SAVISFPPLISIEKKGGGGGQPAEPRCEINDQKWYISSCIGSFAPCLIMILVYVR
IYQIAKRRTRVPPSRKRPDAVAAPPGGTERPNGLGPERISAGSGAEAEPLTQNGA
PGEPAAGPRDITDALDLESSSSDHAERPPRPERGPRGKAKARASQVKPGDSLPR
RGEGATGIGTPAAGPGEERYGAAKASRWGRQNRKRTFTFLAVVIGVFVVCWEPFEF
TYTLTAVGCSVPRTLKFFFWFGYCNSSLNPVIYITFNHDFRAFKKILCRGDRKRIV

BASE COUNT 555 a 1278 c 1136 g 643 t
ORIGIN

Query Match 100.0%; Score 41; DB 9; Length 3612;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCTCCAGGGCCCCGAGACCCGAGCGCGGTCCCGGGG 41
Db 2994 CGGCCTCCAGGGCCCCGAGACCCGAGCGCGGTCCCGGGG 3034

RESULT 9

AF284095 3653 bp mRNA linear PRI 27-MAR-2001
LOCUS Homo sapiens alpha-2A adrenergic receptor mRNA, complete cds.
DEFINITION AF284095
ACCESSION AF284095.1 GI:13447750
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens.
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

CDS

/product="alpha 2A adrenergic receptor"
1. .1353
/gene="ADRA2A"
/note="G-protein coupled receptor"
/codon_start=1
/product="alpha 2A adrenergic receptor"
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/db_xref="GI:12698668"
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LITVFGNVLVIITAVFTSRALKAPQNLFLVSLASADILVATLVIPESLANEVMGYWYEG
KAWCEIYLADVLCTSSIVHLCAISLDRYWSITQAIENLKRTPRIKAIITVWVI
SAVISFPPLISIEKKGGGGGQPAEPCEINDQKWYISSCIGSEFAPCLIMILVYVR
IYQIAKRRTRVPPSRPGDAVAAPGCTERPKGLGERSAGPGAEPPLPTQLNGA
PGEPAAGPRDITDALDLESSSSDHAERPPGRRPERGPRGKARASQVKPGDSLPR
RGPGATGIGTPAAGPGEERVGAAKASRWGRONREKRTFTFYLAIVIGFVVCWCFPEFF
TYTLTAVGCSVPRTLKFFFWFGYCNSSLNPVIYITIFNHDFRAFKKILCRGDRKRIY
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variation

753
/gene="ADRA2A"
/note="compared to wild type sequence presented in GenBank
Accession Number AF281308; polymorphic sequence encodes
Lys at amino acid 251"
/frequency="Caucasians 0.004; African-Americans 0.05"
/replace="c"

BASE COUNT 200 a 489 c 443 g 221 t

ORIGIN

Query Match 100.0%; Score 41; DB 9; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTCCAGGGCCCCGACAGCCGAGCGCGTCCCGGGG 41
|||||
Db 910 CGGCTCCAGGGCCCCGACAGCCGAGCGCGTCCCGGGG 950

RESULT 5

HUMADRA HUMADRA 1521 bp DNA linear PRI 30-OCT-1994
LOCUS Human platelet alpha-2-adrenergic receptor gene, complete cds.
DEFINITION M18415
ACCESSION M18415.1 GI:178191
VERSION alpha-2-adrenergic receptor; alpha-adrenergic receptor.
KEYWORDS Human (lambda-EMBL 3 library) DNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1521)
AUTHORS Kobilka,B.K., Matsui,H., Kobilka,T.S., Yang-Feng,T.L., Francke,U.,
Caron,M.G., Lefkowitz,R.J. and Regan,J.W.
TITLE Cloning, sequencing, and expression of the gene coding for the
human platelet alpha 2-adrenergic receptor
JOURNAL Science 238 (4827), 650-656 (1987)
PUBMED 88042789
FEATURES 2823383

source

Location/Qualifiers
1. .1521
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="10q23-q25"
59. .1411
/gene="ZNF32"
59. .1411
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/note="alpha-2-adrenergic receptor old gene name 'ADRA2R'"
/codon_start=1
/protein_id="AAA51664.1"
/db_xref="GI:178192"
/db_xref="GDB:G00-125-339"
/translation="MGSLOPDAGNASWNGTEAPGGGARATPYSLOVTLTLVCLAGLLM
LITVFGNVLVIITAVFTSRALKAPQNLFLVSLASADILVATLVIPESLANEVMGYWYEG
KAWCEIYLADVLCTSSIVHLCAISLDRYWSITQAIENLKRTPRIKAIITVWVI
SAVISFPPLISIEKKGGGGGQPAEPCEINDQKWYISSCIGSEFAPCLIMILVYVR
TYTLTAVGCSVPRTLKFFFWFGYCNSSLNPVIYITIFNHDFRAFKKILCRGDRKRIY
"

IYQIAKRRTRVPPSRPGDAVAAPPGCTERRPNSLGPERSAGPGAEPPLPTQLNGA
PGEPAAGPRDITDALDLESSSSDHAERPPGRRPERGPRGKARASQVKPGDSLNG
AGRGRGSGRLQGRGSASGLPRRAGAGQNLKERTFTFYLAIVIGFVVCWCFPEFF
TYTLTAVGCSVPRTLKFFFWFGYCNSSLNPVIYITIFNHDFRAFKKILCRGDRKRIY
"

BASE COUNT 223 a 546 c 499 g 253 t

ORIGIN Chromosome 10q23-q25.

Query Match 100.0%; Score 41; DB 9; Length 1521;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTCCAGGGCCCCGACAGCCGAGCGCGTCCCGGGG 41
|||||
Db 968 CGGCTCCAGGGCCCCGACAGCCGAGCGCGTCCCGGGG 1008

RESULT 6

AF262016 AF262016 1941 bp DNA linear PRI 22-AUG-2000
LOCUS Homo sapiens adrenergic receptor alpha-2A gene, complete cds.
DEFINITION AF262016
ACCESSION AF262016
VERSION AF262016.2 GI:9864781
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1941)
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,
Beschi,M. and Agabiti Rosel,E.
TITLE A search for genetic variability in the human alpha-2 adrenergic
receptor on chromosome 10
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1941)
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,
Beschi,M. and Agabiti Rosel,E.
TITLE Direct Submission
JOURNAL Submitted (29-APR-2000) Medical and Surgical Sciences, University
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
REFERENCE 3 (bases 1 to 1941)
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,
Beschi,M. and Agabiti Rosel,E.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Medical and Surgical Sciences, University
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
REMARK Sequence update by submitter
COMMENT On Aug 22, 2000 this sequence version replaced gi:9837145.
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VERSION AX350513.1 GI:18616108
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Liggett,S.B. and Small,K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 25 25-OCT-2001;
Liggett, Stephen B. (US) ; Small, Kersten M. (US)
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DEFINITION cds.
ACCESSION AF281308
VERSION AF281308.1 GI:9652209
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1353)
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE An asn to lys polymorphism in the third intracellular loop of the
human alpha 2A-adrenergic receptor imparts enhanced
agonist-promoted Gi coupling

JOURNAL J. Biol. Chem. 275 (49), 38518-38523 (2000)
MEDLINE 20556293
PUBMED 10948191
REFERENCE 2 (bases 1 to 1353)
AUTHORS Small,K.M., Forbes,S.L., Bridges,K.M. and Liggett,S.B.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-2000) Internal Medicine, University of

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DEFINITION cds.
ACCESSION AF316894
VERSION AF316894.1 GI:12698667
KEYWORDS
SOURCE Homo sapiens.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1353)
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE An asn to lys polymorphism in the third intracellular loop of the
human alpha 2A-adrenergic receptor imparts enhanced
agonist-promoted Gi coupling

JOURNAL J. Biol. Chem. 275 (49), 38518-38523 (2000)
MEDLINE 20556293
PUBMED 10948191
REFERENCE 2 (bases 1 to 1353)
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-2000) Internal Medicine, University of
Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA
FEATURES location/Qualifiers
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ALIGNMENTS

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VERSION AX350512.1 GI:18616107
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
Ligett,S.B. and Small,K.M.
AUTHORS Alpha-2 adrenergic receptor polymorphisms
TITLE Patent: WO 0179561-A 24 25-OCT-2001;
JOURNAL

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; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
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; PRIOR FILING DATE: 2001-01-29
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OY 69 CAGCGTCGTATCCCTTCTCGCTGGCCAAAGAGTCAATGGGCTACTGTACTTGGCAA 128
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OY 129 GCGTTGGTGGAGATCTACCTGGCGCTGACGCTGCTCTTCTGACGTCGTCCTCATCGTGA 188
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QY 427 GGCTCTTCTTCCGCTTCCCTGCTCATCATGATCTGTGTACTGTGCGCATCTACAGATC 486
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 903 CTGAGTCTTCTTACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 962
QY 487 GCCAAGCGTGCACCGCGCTGCGCACCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 546
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 963 ATCCAGAGCGCGCACCGCGCTCGCGTGTGATGGGGCTCGAGAGCAGCGCGCGCGCGCGCG 1022
QY 547 CCGGGGGGCGACCGCGCGCAGGCGCGCAACCGGTG--GGCGCGAGCGCGCGCGCGCGCG 603
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Db 1023 CTTCCCGAGGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1082
QY 604 GGGGCGCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 663
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Db 1083 GGGCAGCGGGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1142
QY 664 CCGGCGCGCGG 672
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Db 1143 GAGGCGCGGG 1151

RESULT 11
US-09-350-206-1
; Sequence 1, Application US/09350206
; Patent No. US2002009199A1
;
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,206
;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
;
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNT-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
;
US-09-350-206-1

Query Match 11.4%; Score 133; DB 10; Length 2689;
Best Local Similarity 52.0%; Pred. No. 1.9e-18;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

QY 10 CTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 69
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Db 483 CTCCGACCGCAGAACCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 542
QY 70 ACCTCGTCATCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 129
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Db 543 GCGTCTGATCCACTGTATGTACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 602
QY 130 GCTTGTGCGAGATCTACCTGCGCGCTGCGACGTGCTTCTTCTTCTTCTTCTTCTTCTT 189
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Db 603 GCGCTTGTCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 562
QY 190 CTGTGCGCGCATCAGCGCTGACCGCGCTACTGTCTCATCACAGGCCATCGAGTAC--AAC 246
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Db 663 ATCGTGTCTATCAGCTACGACCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 722
QY 247 CTGAAGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 306
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Db 723 CAGCAGGGTGTACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 782
QY 307 GTCATCTCTTCCCGCGCGCTCATCTCTCATCGAGAAGAAGGGCGCGCGCGCGCGCGCGAG 366
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Db 783 CTGCTGTACGAGCAGCGCATCTGAGCTGGAGTACCTGTCTCGGGGGCAGCTCCATCCCC 842
QY 367 CCGGCGGAGCGCGCGCTGCGAGATCAACGACGAGAAGTGTGTACGTCTCTGTCTGTGATC 426
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 843 GAGGCGCACGTGTATGCGCGAGTCTTCTTCAACTGTGTACTTCTTCTTCTTCTTCTTCTT 902
QY 427 GGCTCTTCTTCCGCTTCCCTGCTCATCATGATCTGTGTACTGTGCGCATCTACAGATC 486
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 903 CTGAGTCTTCTTACGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 962
QY 487 GCCAAGCGTGCACCGCGCGCTGCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 546
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 963 ATCCAGAGCGCGCACCGCGCTCCGCGTGTGATGGGGCTCGAGAGGCGCGCGCGCGCGCG 1022
QY 547 CCGGGGGGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 603
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1023 CTTCCCGAGGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1082
QY 604 GGGGCGCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 663
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1083 GGGCAGCGGGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1142
QY 664 CCGGCGCGGG 672
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Db 1143 GAGGCGCGGG 1151

RESULT 12
US-10-005-010-1
; Sequence 1, Application US/10005010
; Patent No. US20020115149A1
;
; GENERAL INFORMATION:
; APPLICANT: weinshank et al, Richard L.
; TITLE OF INVENTION: Method of Obtaining A Composition Comprising A 5-HT1D
; FILE REFERENCE: 36536-BA
;
; CURRENT APPLICATION NUMBER: US/10/005,010
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,755
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/985,090
; FILING DATE: 04-DEC-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
;
; INFORMATION FOR SEQ ID NO: 1:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-349-755-1
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Query Match      11.4%; Score 133; DB 9; Length 2689;
Best Local Similarity 52.0%; Pred. No. 1.9e-18;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;
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OY 10 CTCAAGCGCGCCCAAAACCTCTTCCTGCTGCTGCTGCGCCCTCGCGGACATCCTGTGGCC 69
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DB 483 CTCGCGACCCAGAACACTTCTCTGCTCAACCTCGCCATCTCCGACTTCTCTGCTGGC 542
OY 70 ACGCTCGTCATCCCTTCTGCTGCGCCACGAGCTCATGGCTACTGCTACTTGGGCAAG 129
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 543 GCCTTCTGCATCCACCTGATATGTAACCTACGCTGACAGCGCGCTGAGACCTTGGCGCG 602
OY 130 GCTTGGTGGAGATCTACCTGGCGCTGACGCTGCTTCTGACAGTGCATCTGTCAC 189
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 603 GGCTCTGCAAGCTGTGCTGTAGTGACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
OY 190 CTGTGCGCATCAGCTGGAACCGCTACTGCTGCTATCACAACAGGCGCATGAGTAC--AAC 246
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DB 663 ATCGTCTCATCAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
OY 247 CTGAAGCGCGCGCGCGCGCATCAAGGCGCATCATCACCGTGTGGTTCATCTGGCC 306
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 723 CAGCAGGGTGACACCGCGCGCGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
OY 307 GTCATCTCTTCCCGCGCTCATCTCATGAGAAGAAGGCGCGCGCGCGCGCGCGCGAG 366
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 783 CTGCTGTACGACGACCATCTGAGCTGAGAGTACCTGTCCGGGGGAGCTCAATCCC 842
OY 367 CCGGCGGAGCGCGCTGAGATCAAGCAGACAGAGTGTAGCTATCTGCTGTCATC 426
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 843 GAGGGCCACTGTATGCGGAGTCTTCTCAACTGTACTTCTCATCACGGCTTCCACC 902
OY 427 GGTCTCTTCTGCTCTGCTGCTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 903 CTGAGTCTTACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 962
OY 487 GCCAAGCGTGCACCGCGCTGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 546
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 963 ATCAGAGGCGCACCGCGCTCGGCTGGATGGGCTCGAGAGGACGCGCGCGCGCGAGCCC 1022
OY 547 CCGGGGCGCAGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 603
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DB 1023 CCTCCGAGGCGCGCGCGCTCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 1082
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OY 604 GGGGCGCAGAGCGCGGACCGCTGCCACCCAGCTCAACGCGCGCCCTGGCGAGCCCGCG 663
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DB 1083 GGGCAGCGGGAGGCCATGCCCTGCACAGGATAGGGGTGGGTGAGGCGCGCGTAGCGGCT 1142
OY 664 CCGCGCGCGG 672
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DB 1143 GAGCGCGCGG 1151
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RESULT 10
US-09-166-334-1
; Sequence 1, Application US/09166334
; Patent No. US20020168708A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,334
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE:
; APPLICATION NUMBER: US 08/985,090
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
US-09-166-334-1
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Query Match      11.4%; Score 133; DB 9; Length 2689;
Best Local Similarity 52.0%; Pred. No. 1.9e-18;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;
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OY 10 CTCAAGCGCGCCCAAAACCTCTTCCTGCTGCTGCTGCGCCCTCGCGGACATCCTGTGGCC 69
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DB 483 CTCGCGACCCAGAACACTTCTCTGCTCAACCTCGCCATCTCCGACTTCTCTGCTGGC 542
OY 70 ACGCTCGTCATCCCTTCTGCTGCGCCACGAGTCAATGGCTACTGCTACTTGGGCAAG 129
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 543 GCCTTCTGCATCCACCTGATATGTAACCTACGCTGACAGCGCGCTGACCTTGGCGCG 602
OY 130 GCTTGGTGGAGATCTACCTGGCGCTGACGCTGCTTCTGACAGTGTCCATCTGTGAC 189
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DB 603 GGCTCTGCAAGCTGTGCTGTAGTGACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
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Db 493 CTGCTGTACGGACCAACCATCTGAGCTGGGAGTACCTGTCCGGGGGACAGCTCCATCCCC 552
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Db 553 GAGGCCACTGTATGCCAGTCTCTTACAACTGTACTCTTCATCAACGGCTTCCACC 612
QY 427 GGCTCTTCTTGGCTCCCTGCTCATATGATCTGTCTACGTGCGCATCTACAGATC 486
Db 613 CTGAGTCTTTACGCCCTTCTTCAAGCTTCTTTAACCCTCAGCATCTACCTGAAC 672
QY 487 GCCAAGCGTCGACCCCGCTGCGACCAACCCGCGGGGTCCGAGCGCGCTGCGCGCGCG 546
Db 673 ATCCAGAGGCGCACCCCGCTCCGCTGATGGGGCTCGAGAGCGACCGCGCGCGCGCG 732
QY 547 CCGGGGGGACCGAGCGCAGGCCCAACGGTCTG--GGCCCGAGCGCAGCGCGCGCG 603
Db 733 CCTCCCGAGGCCCGCCCTCACACCCCGCGCTGCTGCTGGGGCTGCTGGCAGAA 792
QY 604 GGGGGCGCAGAGCGCCGAACCGCTGCCCCACCCAGCTCAACGGCGCGCGCTGGCGAGCCCGCG 663
Db 793 GGGCAGCGGGAGGCCATGCCGCTGCACAGGATGGGGTGGGTGAGGCGCGCGCTAGCGCT 852
QY 664 CCGGCCGGG 672
Db 853 GAGGCCGGG 861

RESULT 8
US-09-350-206-3
; Sequence 3, Application US/09350206
; Patent No. US200209199A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,206
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNT-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-09-350-206-3

Query Match 11.4%; Score 133; DB 10; Length 1335;
Best Local Similarity 52.0%; Pred. No. 1.8e-18;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;
QY 10 CTCGAAGCGCCCCAAACCTTCTCCTGCTGTCTCTGCGCTGCGCGACATCTGTGGCC 69
Db 193 CTCGCCACCCAGAACACTTCTCTCTGCTCAACCTCGCCATCTCCGACTTCTCTCGCGC 252
QY 70 ACGTCTCATCCCTTTCCTGCTGGCCAACGAGGTGATGGCTACTGTACTTGGCAAG 129
Db 253 GCCTTCTGCATCCCACTGTATGTACCTACGTGCTGACAGCGCGCTGAGCTTGGCGCG 312
QY 130 GCTTGTGCGAGATCTACCTGGCGCTGACGTGCTCTTCTGACAGTCTCATCTGTCAC 189
Db 313 GGCCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGCACCTCTCTGCTTCAAC 372
QY 190 CTGTGCGCCATCAGCCTGACCGCTACTGTTCATCAACAGGCCATCGAGTAC--AAC 246
Db 373 ATCGTCTCATCAGCTACGACCGCTTCTCTGCTGCAACCGAGCGGTCTCATACCGGGCC 432
QY 247 CTGAAGCGCACCGCGCGCGCGCAATCAAGGCCATCATCAACCGTGTGGTCACTCTGGCC 306
Db 433 CAGCAGGGGTGACACGCGCGCGCGAGTGGGAAGATGCTGTGTGTGGGTGCTGGCTTTC 492
QY 307 GTCATCTCTTCCCGCGCTCATCTCCATCGAGAAGAGGGCGCGCGCGCGCGCGCGAG 366
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QY 367 CCGGCCGAGCCCGCTGCGAGATCAACGACCAAGAGTGTACGTATCTCTGTGATC 426
Db 553 GAGGCCACTGTATGCGGAGTTCTTCTACAACCTGTACTTCTCATACGGCTTCCACC 612
QY 427 GGCTCTTCTTGGCTCCCTGCTCATATGATCTCTGTCTTACGTGCGCATCTACAGATC 486
Db 613 CTGAGTCTTTACGCCCTTCTTCAAGCTTCACTCTTCTTAACTCAAGCATCTACTGAAC 672
QY 487 GCCAAGCGTCGACCCCGCTGCGACCAACCCGCGGGGTCCGAGCGCGCTGCGCGCGCG 546
Db 673 ATCCAGAGGCGCACCCCGCTCCGCTGATGGGGCTCGAGAGCGACCGCGCGCGCGCG 732
QY 547 CCGGGGGGACCGAGCGCAGGCCCAACGGTCTG--GGCCCGAGCGCAGCGCGCGCGCG 603
Db 733 CCTCCCGAGGCCCGCCCTCACACCCCGCGCTGCTGCTGGGGCTGCTGGCAGAA 792
QY 604 GGGGGCGCAGAGCGCCGAACCGCTGCCCCAACCAGCTCAACGGCGCGCGCTGGCGAGCCCGCG 663
Db 793 GGGCAGCGGGAGGCCATGCCGCTGCACAGGATGGGGTGGGTGAGGCGCGCGCTAGCGCT 852
QY 664 CCGGCCGGG 672
Db 853 GAGGCCGGG 861

RESULT 9
US-09-349-755-1
; Sequence 1, Application US/09349755
; Patent No. US2002016131A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; US-09-349-755-1

NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1335
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-349-755-3

Query Match 11.4%; Score 133; DB 9; Length 1335;
Best Local Similarity 52.0%; Pred. No. 1.8e-18;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

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QY 10 CTCAGGCGCCCAAAACCTCTCTGCTGTCTCTGCGCTCGCCGACATCCGTGGGCC 69
Db 193 CTCGCAACCCAGAACAACTCTCTGCTCAACCTCGCCATCTCCGACTCTCTGCGG 252
QY 70 ACCGTCGTATCCCTTCTGCTGCGCCAGAGGATGAGGCTACTGTACTTCCGCAAG 129
Db 253 GCCTTCTGCATCCCACTGTATGTACCTACGTGCTGACAGGCGGCTGACCTTCCGCG 312
QY 130 GCTTGGTGCAGATCTACCTGCGGCTCGACGTGCTCTTCTGCACGTCCTCATCTGTCAC 189
Db 313 GGCTTCTGCAAGCTGTGGTGTAGTGTGACTTCTGCTGTGACACCTCTCTGCTTCAAC 372
QY 190 CTGTGCGCCATCAGCCTTGACCGCTACTGTCTCATCACACAGGCCATCGAGTAC--AAC 246
Db 373 ATGCTGCTCATCAGCTACGACCGCTTCTCTGCTGCTACCCGAGCGGTCTCATACCGGGCC 432
QY 247 CTGAAGCGCACGCCGCGGCATCAAGGCCATCATCATCACCCTGTGGTCTATCTCGGCC 306
Db 433 CAGCAGGGTGACACGCGCGGCGAGTGGGAGATGCTGTGTGGTGTGCTGCGCTTC 492
QY 307 GTCATCTCTTCCCGGCTCATCTCTCATGAGAAAGGCGGCGCGCGGCCGCGCAG 366
Db 493 CTGCTGTACGACCAACCATCTGAGCTGGAGTACCTGTCCGGGGGAGCTCCATCCC 552
QY 367 CCGGCGGAGCGCGCTGCGAGATCAACGACCAAGTGTAGCTCATCTCTGCTGATC 426
Db 553 GAGGGCCACTGTATGCGAGTCTTCTTACACTGTACTTCTCATACAGGCTTCCACC 612
QY 427 GCGTCTTCTTCCCTGCTGCTCATCATGATCTCTGTCTACGTGCGCATCTACAGATC 486
Db 613 CTGAGTCTTCTTACGCTCTTCTCAGCGTACCTTCTTAACTCAGCATCTACCTGAAC 672
QY 487 GCCAAGCGTCGACCGCGCTGCCACCGCGCGCGGGGTCCGGACCGCTGCGCGCGC 546
Db 673 ATCCAGAGGCGCACCGCTCCGGCTGATGGGGCTCGAGAGGCGACCGCGCGCGCGC 732
QY 547 CCGGGGGCAGCGAGCGCAGGCCCAAGGCTG--GGCCCCGAGCGCAGCGGGGGCG 603
Db 733 CCTCCGAGGCGCACCGCTCACCACCGCCCTGCTGCTGTGGGGCTGCTGGCAGAG 792
QY 604 GGGGGCGCAGAGCGCAACCGCTGCGCCACCAAGCTCAACGGCGCGCGCTGCGAGCGCGC 663
Db 793 GGGCAGGCGGAGCGCATGCGCTGCAAGGATATGGGGTGTGAGGCGCGCGTAGGCGCT 852
QY 664 CCGGCGCGG 672
Db 853 GAGGCGCGG 861
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RESULT 7

US-09-166-334-3
Sequence 3, Application US/09166334
Patent No. US20020168708A1
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,334
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042,780
FILING DATE:
APPLICATION NUMBER: US 08/985,090
FILING DATE: 04-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1335
US-09-166-334-3

Query Match 11.4%; Score 133; DB 9; Length 1335;
Best Local Similarity 52.0%; Pred. No. 1.8e-18;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

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QY 10 CTCAGGCGCCCAAAACCTCTCTGCTGTCTCTGCGCTCGCCGACATCCGTGGGCC 69
Db 193 CTCGCAACCCAGAACAACTCTCTGCTCAACCTCGCCATCTCCGACTCTCTGCGG 252
QY 70 ACCGTCGTATCCCTTCTGCTGCGCCAGAGGATGAGGCTACTGTACTTCCGCAAG 129
Db 253 GCCTTCTGCATCCCACTGTATGTACCTACGTGCTGACAGGCGGCTGACCTTCCGCG 312
QY 130 GCTTGGTGCAGATCTACCTGCGGCTCGACGTGCTCTTCTGCACGTCGTCTCATCTGTCAC 189
Db 313 GGCTTCTGCAAGCTGTGGTGTAGTGTGACTTCTGCTGTGACACCTCTCTGCTTCAAC 372
QY 190 CTGTGCGCCATCAGCCTTGACCGCTACTGTCTCATCACACAGGCCATCGAGTAC--AAC 246
Db 373 ATGCTGCTCATCAGCTACGACCGCTTCTCTGCTGCTACCCGAGCGGTCTCATACCGGGCC 432
QY 247 CTGAAGCGCACGCCGCGGCATCAAGGCCATCATCATCACCCTGTGGTCTATCTCGGCC 306
Db 433 CAGCAGGGTGACACGCGCGGCGAGTGGGAGATGCTGTGTGGTGTGCTGCGCTTC 492
QY 307 GTCATCTCTTCCCGGCTCATCTCTCATGAGAAAGGCGCGCGCGCGCGCGCGCAG 366
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RESULT 5
US-09-954-531-995
; Sequence 995, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 995
; LENGTH: 2625
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
US-09-954-531-995

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Query Match	12.1%;	Score 141.4;	DB 9;	Length 2625;
Best Local Similarity	47.9%;	Pred. No. 3.9e-20;		
Matches 548; Conservative	0;	Mismatches 576;	Indels 21;	Gaps 4;

QY	/	GGGGTCAAGGCGCCCAAAACCTCTCTCTGGAGTCTCTGGCCCTGGCCGACATCTCTGGT	10
Db	355	GGCGTGCAGACCACCAACCACTACTGATCGTACGCCCTCGCAGTGGCCGCACTCCTCGTC	414
QY	67	GCCACGCTCGTCATCCCTTTCTCGCTGGCCCAACGAGGTCAATGGGCTACTGTCTCGGC	126
Db	415	GCCACACTGTGCATGCCCTGGTTGTCTACCTGGAGGTGTAGTGATGGAAATTCAGC	474
QY	127	AAGGTTGGTGCAGATCTACCTGGCGCTCGACGTGCTCTTCTGCAAGTGTCCATCGTG	186
Db	475	AGGATTCACCTGTGACATCTTCTGACTCTGGACGTGCATGATGTGACGGCGAGCATCCTG	534
QY	187	CACCTGTCCGCCATCAGCCTGAGCCGCTACTGTTCCATCACAACAGGCCATCGAGTACAAC	246
Db	535	AACCTGTGTGCCATCAGCATCGACAGGTACACAGCTGTGGCCATGCCCATGCTGTACAAT	594
QY	247	CTGAAGCGCACGCGCGCGCGCATCAAGGCCATCATCACCGTGTGGTCACTCGGCC	306
Db	595	ACGGCGTACAGCTCCAAAGCGCGGGTCAACCGTCATGATCTCCATCGTCTGGGCTCTGCC	654
QY	307	GTCATCTCTTCCCGCGCGCTCATCTCCATCGAGAAGAAGGGCGGGCGGGCCCCGCGAG	366
Db	655	TTACACATCTCTGCCCCACTCTCTTTCGACTCAATAACGACAGACCAGAACGATGCATC	714
QY	367	CCGGCCGAGCCGCGCTGCGAGATCAACGACAGAAAGTGGTACGTCACTCTCGTGCATC	426
Db	715	ATTGCCAACCCGGCCTTCTGTGTCTAC-----TCTTCATCGTCTCTTCTTAC	762
QY	427	GGCTCTTCTTCGCTCCCTGCCTCATCATGATCTGTCTACGTGCGCATCTACAGATC	486
Db	763	GTGCCCTTCAATTGTCAACCTGCTGTCTACATCAAGATCTACATTTGTCTCCGACGACGC	822
QY	487	GCCAAAGCTCGCACCCGCGTGCACACCAGCCGCGGGGTCCGGACGCGTCCGCGCGCG	546
Db	823	CGCAAGCGAGTTCACACCAACGACGACGCCGAGCTTTCAGGGCCACCTGAGGGCTCCA	882
QY	547	CCGGGGGGCACCGACCGCAGGCCCAACGGTCTGGCCCCCGAGCGCAGCGCGGGCCGGGG	606

Db	883	CTAAAGGGCAACTGTACTACACCCCGAGACATGAAACTCTGACCCGTTATCATGAAGTCT	942
QY	607	GGCGCAGAGGGCCGAACCGCTGCCCCACCCAGCTCAACGGCGCCCCCTGGCGAGCCCGCGG	666
Db	943	AATGGGAGTTTCCCACTGAACAGGCGAGAGTGGAGGCTGCCCCGGCGAGCCAGGAGGCTG	1002
QY	667	GGCGGGGGCGCCGACACCGACGGCGCTGACCTGGAGGAGAGTCTGTCTTCCGACACGCC	726
Db	1003	GAGATGAGATGCTCTTCCAGCACCAGCCACCCGAGAGGAGACCCGGTACAGCCCATCCCA	1062
QY	727	GAGCGGCTCCAGGGGCCCCCGACAGACCCGAGCGCGGTCCCGGGGCAAAAGCAAGGCCGA	786
Db	1063	CCCAGCCACCACCACTGACTCTCCCCGACCCGCTCCACACAGGTCTCCACAGCACTCCT	1122
QY	787	GCGAGCCAGGTGAAGCCGGGGCGACA---GCCCTGCCCGCGCGCGGGGGGGGGCGACGGG	842
Db	1123	GACAGCCCCCGCAACACAGAGAAATGGGCATGCCAAGAACCACCCAGATTGCCAAG	1182
QY	843	GATCGGGACGCGCGCTGCAGGGCGCGGGGAGAGAGCGCGTGGGGCTGCCAAGC--GTCG	900
Db	1183	ATCTTTGAGATCCAGACCACTGCCCAATGGCAAAACC CGGACCTCCCTCAAGACCATGAGC	1242
QY	901	CGCTGGCGCGGGCGGCAAGACCGAGAAAGCGCTTCACTGCTGCTGGCCGTGTCATC	960
Db	1243	CGTAGAAAGCTCTCCACAGCAAGAGAGAAAGAAAGCCACTCAGATGCTCGCCATTGTTCTC	1302
QY	961	GGAAGTGTTCGTGTGTGTGTTCCCTCTCTTCTTACCTACACGCT--CACGGCGCTC	1017
Db	1303	GGCGTGTTCATCATCTGCTGGCTGCCCTTCTTTCATCACACACATCTGAAACATACACTGT	1362
QY	1018	GGGTGCTCCGTGCCACGACGCTCTCAAAATCTTCTTCTTGGTTCGGCTACTGCAACAGC	1077
Db	1363	GACTGCAACATCCCGCGCTGTCTGTACAGCGCTTCAAGTGGCTGGGCTATGTCAACAGC	1422
QY	1078	TGCTTGAACCCGGTCACTTACACCATCTTCAACACGATTCGCGCGCCTTCAAGAG	1137
Db	1423	GCCGTGAACCCCATCATCTACACCACTTCAACATTGAGTTCGCAAGGCTTCTCTGAAG	1482
QY	1138	ATCCT 1142	
Db	1483	ATCCT 1487	

RESULT 6
US-09-349-755-3
; Sequence 3, Application US/09349755
; Patent No. US20020166131A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,755
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/985,090
; FILING DATE: 04-Dec-1997
; ATTORNEY/AGENT INFORMATION:
;

Db 1069 TGGCGTGCAGGGGCGGACGCTGACCGGGGAGAAGCGCTTACCTTCCGTGCTGCGTGTGTC 1128
QY 958 ATCGAGTGTTCGTGTGTGTGTTCCTTCCCTTCTTCTTCACTACACGCTACAGCGCCGTC 1017
Db 1129 ATTGGCGTTTGTGCTCTGCTGTGTTCCTTCCCTTCTTCTTCACTACAGCGCTGCGCCATC 1188
QY 1018 GGG-----TGCCTCGTGCACGACGCTCTTCAATTTCTTCTTGTGTTGCGCTAC 1068
Db 1189 TGCCCGAAGCACTGCAAGGTGCCCCATGGCCCTCTTCCAGTTCTTCTGTGATGCGCTAC 1248
QY 1069 TGCAACAGCTCGTTGAACCCGGTTCATCTACACCATCTTCAACCAAGATTTCGCGCGCC 1128
Db 1249 TGCAACAGCTCACTGAACCCGTGTATCTACACCATCTTCAACCAAGACTTCCGCGTGCC 1308
QY 1129 TTCAAGAAGATCCTCTGTGC 1148
Db 1309 TTCCGGAGGATCCTGTGCCG 1328

RESULT 4

US-09-825-923-3

; Sequence 3, Application US/09825923

; Patent No. US20010016338A1

; GENERAL INFORMATION:

; APPLICANT: Snapir, Amir

; APPLICANT: Helinonen, Paula

; APPLICANT: Alhopuro, Pia

; APPLICANT: Karvonen, Matti

; APPLICANT: Koulu, Markku

; APPLICANT: Pesonen, Ullamari

; APPLICANT: Scheinin, Mika

; APPLICANT: Tuomainen, Tomi-Pekka

; APPLICANT: Lakka, Timo A

; APPLICANT: Nyysanen, Kristina

; APPLICANT: Salonen, Riiita

; APPLICANT: Kauhanen, Jussi

; APPLICANT: Valkonen, Veli-Pekka

; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor

; FILE REFERENCE: protein, and uses thereof

; CURRENT APPLICATION NUMBER: US/09/825, 923

; PRIOR FILING DATE: 2001-04-05

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 1353

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1350)

; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor

; OTHER INFORMATION: protein

US-09-825-923-3

Query Match 34.3%; Score 400.8; DB 10; Length 1353;
Best Local Similarity 63.3%; Pred. No. 2.2e-72;
Matches 772; Conservative 0; Mismatches 367; Indels 81; Gaps 7;

QY 1 AGCCGGCGCTCAAGCGCCCAAAACCTCTTCTGTGTCTGTGCGCTGCGCGACATC 60
Db 118 AGCCGCTCGCTGCGCGCCCTCAGAACCTGTCTGTGTGCTGCGCGCGACATC 177
QY 61 CTGCTGGCCACGCTCGTATCCCTTCTCTGCTGGCCAAGGTCATGGGCTACTGTAC 120
Db 178 CTGCTGGCCACGCTCATCACTTCTCTGCTGGCCAAGGTCGCTGGCTACTGTAC 237
QY 121 TTCGGAAGGCTTGTGCGAGATCTACCTGCGCTGACGTGCTTCTGACAGTGTCC 180
Db 1309 TTCCGGAGGATCCTGTGCCG 1328

Db 238 TTCCGGCGCAGGTGTGCGAGGTGTACCTGGCGCTCGACGTGCTTCTGACACCTGTCC 297
QY 181 ATCGTACACCTGTGGCCATCAGCCTGAGCGCTACTGGTCCATCAGACAGCCATCAG 240
Db 298 ATCGTACACCTGTGGCCATCAGCCTGAGCGCTACTGGGCGGTGAGCGCGCTGAG 357
QY 241 TACAACCTGAAGCGCACCGCGCGCATCAAGCCATCATCATCAGGTGTGGTATC 300
Db 358 TACAACCTGAAGCGCACCGCGCGCATCAAGGTGTGGTATCAGGTGTGGTATC 417
QY 301 TCGCGCTCATCTCTTCCCGCGCTCATCTCATCAGAAAGAGCGCGCGCGCGC 360
Db 418 GCGCGCTCATCTCTGCTGCGCGCGCTCATCT-----ACAAGGCGAGCAGCGCGCC 468
QY 361 CCGCAGCGCGCGAGCGCGCTGCGAGATCAACGACAGAGAGGTAGCTATCTGTGC 420
Db 469 CAGCGCGCGCGCGCGCGCGCGAGTCAACGACAGAGCGCTGTATCATCTGTGCTCC 528
QY 421 TGCAATCGCTCTCTTCTGCTCCCTGCTCATCATGATCTGTGTACGTGCGCATCTAC 480
Db 529 AGCATCGATCTTCTTGTCTCTGCTCTGCTCATCATGATCTGTGTACGTGCGCATCTAC 588
QY 481 CAGATCGCAAGCGTGCACCGCGGTGCCACCA-----GCCGCG 521
Db 589 CTGATCGCAAGCGTGCACCGCGGTGCCACCAAGGCGCGCGCGCGCGCGCGCGT 648
QY 522 GGTCCGAGCGCGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 563
Db 649 GATCCAGAGCGT 708
QY 564 CAGCGCGAGCGTCTGCG 616
Db 709 CTGCGCTGTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
QY 617 CCGAACCGCTGCCACCGCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 676
Db 769 GAGGAGGCGGAGACCGCTGAAGTACTGGGACCGCGCGCGCGCGCGCGCGCGCGCGCG 828
QY 677 GCGACCGAGCGCGCTGAGCTGAGGAGAGAGTCTGCTTCCGACCGCGCGCGCGCTC 736
Db 829 CTTCCTCACTCAGCG 888
QY 737 CAGCGCGCGCGAGACCG 796
Db 889 GCTGAG 948
QY 797 TGAAGCGCGCGAGACGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 849
Db 949 GTGTCTCGCGCTCAGCTTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1008
QY 850 -----ACGCGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 897
Db 1009 GCCACCTACGTGCGCGAGGTCTCTCTGCGAGGCGCGGTGCTATAGTGGCGAGTGG 1068
QY 898 TCGCGCTGCGCGCGCGCGCGAGAACCGCGAGAACCGCTTACGTTGCTGCGCGCGTGC 957
Db 1069 TCGCGTGCAGCGCGCGCGCGAGAACCGCGAGAACCGCTTACCTTGTGCTGTGCTG 1128
QY 958 ATCGAGT 1017
Db 1129 ATTGGCGTTTGT 1188
QY 1018 GGG-----TGCCTCGTGCACGACGCTCTTCAATTTCTTCTTGTGTTGCGCTAC 1068
Db 1189 TGCCCGAAGCACTGCAAGGTGCCCCATGGCCCTCTTCCAGTTCTTCTGTGATGCGCTAC 1248
QY 1069 TGCAACAGCTCGTTGAACCCGGTTCATCTACACCATCTTCAACCAAGATTTCGCGCGCC 1128
Db 1249 TGCAACAGCTCACTGAACCCGTGTATCTACACCATCTTCAACCAAGACTTCCGCGTGCC 1308
QY 1129 TTCAAGAAGATCCTGTGTGC 1148
Db 1309 TTCCGGAGGATCCTGTGCCG 1328


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OY      481 CAGATCGCCAAAGCGTGCACCCGCGTGCACCCA-----GCCCGG 521
          ||||||| || ||| |||
Db      589 CTGATCGCCAAACGACGACCAACCGACAGAGTCCAGGGCCAAAGGGGGCCTGGCAGGGT 648
          ||||||| || ||| |||
OY      522 GGGTCCGGACGCCGTGCGCCGCGCCGCGGGGGGACCGAGCGCAGGCCCAACGGTCTG-- 579
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      649 GAGTCCAGCAGCCCCCGACCCGACCATGATGGGGCTTTGGCTCAGCCAACTGCCAGCC 708
          ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      580 -----GGCCCGAGCGCAGCGCGGGCCGGGGGCGCAGAG 615
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      709 CTGGCTCTGTGGCTTCTGCCAGAGAGGTCAACGACACTCGAAGTCCACTGGGAGAAAG 768
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      616 GCCGAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAGGCCCGCGCGGGCGG 675
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      769 GAGGAGGGGAGACCCCTGAAGATACTGGGACCGGGGCTTGCCACCCAGTTGGGCTGCC 828
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      676 CGCAGACCCGACGCGCTGGAAGAGAGAGAGAGTCTGCTCTCCGACCAAGCCGAGCGGCT 735
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      829 CTTCCCACTCAGGCCAGGGCCAGAAAGAGGGTGTGTTGGGGCATCTCCAGAGGATGAA 888
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      736 CCAGGGCCCCGACAGCCGAGCGCGTCCCCCGGGCAAAAGGCAAGGCCGAGCGAGCCAG 795
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      889 GCTGAAGAGAGAGAGAGAGAGAGAGAGTGTGAACCCAGGACAGTGCAGTGTCTCCG 948
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      796 GTGAAGCCGGCGACAGCGCTGCCCGCGCGCGCGCGCGCGCGCGAGGAGATCGGACGCCG 855
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      949 GCCTCAGCTTGACAGCCCCCGCTGTCAGCAGCCACAGGCGCTCCCGGTGCTGGCCACCTA 1008
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      856 GCTGCAGGGCGCGGGGAGAGAGCGCGTCCGGGCTGCCA-----AGCGTCCGCTGG 906
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1009 CGTGGCCAGGTGCTCCTGGGCAAGGGGCGTGGGTGCTATAGGTGGGACAGTGTGGCGTGA 1068
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      907 CGCGGGCGCGAGAACCGCGAGAGCGCTTCACGTTGCTGCTGGCCGTGCTCATCGGAGTG 966
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1069 CGGGCGCAGCTGACCCGGGAGAGCGCTTCACCTTCGCTGCTGCTGTGCTATGGCGTT 1128
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      967 TTCGTGTGCTGTGCTTCCCTCTTCTTCACCTACACGCTCACGGCCGTGCGG----- 1020
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1129 TTTGTGCTGTGCTGCTTCCCTCTTCTTCAGCTACAGCCTGGGCGCCATCTGCCGAAG 1188
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      1021 ---TGCTCGTGCACGACGACGCTCTCAAAATTCTTCTGTGCTGCGCTACTGCAACAGC 1077
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1189 CACTGCAAGGTGCCCATGCGCTCTTCCAGTCTTCTTGATCGGCTACTGCAACAGC 1248
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      1078 TCGTTGAACCGGTATCTACACCAATCTCAACACAGATTTCCGCGCGCTTCAAGAAG 1137
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1249 TCACTGAACCTGTATCTACACCAATCTCAACACAGAGACTTCCGCGCTTCCGGAGG 1308
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      1138 ATCCTCTGTCG 1148
          ||||| | | |
Db      1309 ATCCTGTGCCG 1319
          ||||| | | |

RESULT 3
US-10-077-870-3
; Sequence 3, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077, 870
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
;

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[illegible]

Db 298 ATCGTGCACCTGTGCGCCATCAGCCCTGAGCCGCTACTGGCGGTGAGCCGCGCTGAG 357
QY 241 TACAACCTGAAGCGACGCGCGCCGCAATCAAGCCATCATCATCACCGTGTGGTATC 300
Db 358 TACAACCTCAAGCGACCGCGCGCCGCAATCAAGTGCATCATCTCAGTGTGGTATC 417
QY 301 TCGGCCGTATCTCTTCCCGCGCTCATCTCCATCGAAGAAGGGCGGCGCGCGC 360
Db 418 GCCGCGTATCTCGCTGCGCGCCCTCATCT-----ACAAGGGCGACCAAGGGCCCC 468
QY 361 CCGCAGCGCGCGCGCGCGCGCTGCGAGATCAACGACCAAGAAGTGTACGTATCTCTG 420
Db 469 CAGCGCGCGCGCGCGCGCGCGCGAGTCAAGCTCAACGAGAGCGCTGTACATCTGCGCTCC 528
QY 421 TGCATCGGCTCTTCTTGGCTCCCTGCTCATCATGATCTGTGCTACGTGCGCATCTAC 480
Db 529 AGCATCGGATCTTCTTGTGCTCTGCTCATCATGATCTGTGCTACCTGCGCATCTAC 588
QY 481 CAGATCGCCAAAGCGTGCACCCCGCTGCCACCA-----GCCGCGG 521
Db 589 CTGATCGCCAAAGCGACGACCAAGGTCACAGGGGCCAAGGGGGGCGCTGGGCGAGGT 648
QY 522 GGGTCCGGACGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG-- 579
Db 649 GAGTCCAAAGCAGCG 708
QY 580 -----GGCG 615
Db 709 CTGGCCTCTGTGGCTTGTGCCAGAGAGGTCAACGAGACCTCGAAGTCCACTGGGAGAG 768
QY 616 GCGCAACCGCTGCGCCACCGCTCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 675
Db 769 GAGGAGGGGGAGAGACCGCTGAAGATACTGGGACCGCGCGCGCGCGCGCGCGCGCG 828
QY 676 CCGGACACCGACGCGCTGACCTGAGAGAGAGCTCTTCCGACCAAGCGCGCGCGCT 735
Db 829 CTTCCCAACTCAGGCG 888
QY 736 CCAGGGCG 795
Db 889 GCTGAAGAGGAGAGAGAGAGAGAGAGAGTGAACCCAGGAGTGCAGTGTCTCCG 948
QY 796 GTGAAGCG 855
Db 949 GCCTCAGCTTGACG 1008
QY 856 GCTGCAGGGCG 906
Db 1009 CGTGGCCAGGTGCTCTGGCGAGGGGCGGTGCTATAGTGGCGAGTGTGGCGTGA 1068
QY 907 CCG 966
Db 1069 CGGGCGCAGCTGACCG 1128
QY 967 TTCGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 1129 TTTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1188
QY 1021 ---TGCTCGTGCACGCGACGCTTTCAATTTCTTCTGCTGCTGCTGCTGCTGCTGCT 1077
Db 1189 CACTGCAAGGCG 1248
QY 1078 TCGTTGAACCGGCTCATCTACACCAATTTCAACCAAGATTTCCGCGCGCGCTCAAG 1137
Db 1249 TCACGTGAACCGCTTATCTACACCAATTTCAACCAAGACTTCCGCGCGCTTCCG 1308
QY 1138 ATCCTCTGTG 1148
Db 1309 ATCCTGTGCG 1319

RESULT 2
US-09-825-923-1

Sequence 1, Application US/09825923
Patent No. US20010016338A1
GENERAL INFORMATION:
APPLICANT: Snapir, Amir
APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Pia
APPLICANT: Karvonen, Matti
APPLICANT: Koulu, Markku
APPLICANT: Pesonen, Ullamari
APPLICANT: Scheinin, Mika
APPLICANT: Salonen, Jukka T
APPLICANT: Tuomainen, Tomi-Pekka
APPLICANT: Lakka, Timo A
APPLICANT: Myyrs'nen, Kristina
APPLICANT: Salonen, Riitta
APPLICANT: Kauhainen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825, 923
PRIORITY FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422, 985
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1

Query Match 34.4%; Score 402.6; DB 10; Length 1344;
Best Local Similarity 62.3%; Pred. No. 9.4e-73;
Matches 755; Conservative 0; Mismatches 384; Indels 72; Gaps 5;

QY 1 AGCGCGCGCTCAAGCG 60
Db 118 AGCGCGCTGCTGCG 177
QY 61 CTGTGCGCCACGCTGCTCATCTCTTCTGCTGCGCGCGCGCGCGCGCGCGCGCG 120
Db 178 CTGTGCGCCACGCTCATCTATCTTCTGCTGCGCGCGCGCGCGCGCGCGCGCG 237
QY 121 TTCGCGCAAGGCTTGTGCGAGATCTACCTGGCGCGCGCGCGCGCGCGCGCGCG 180
Db 238 TTCGCGCGCACGCTGTGCGAGGTGTACCTGGCGCGCGCGCGCGCGCGCGCGCG 297
QY 181 ATGCTGCACCTGTGCG 240
Db 298 ATGCTGCACCTGTGCG 357
QY 241 TACAACCTGAAGCG 300
Db 358 TACAACCTCAAGCG 417
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Db 529 AGCATCGGATCTTCTTGTGCTCTGCTCATCATGATCTGTGCTACCTGCGCATCTAC 588

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 06:22:49 ; Search time 80.4881 Seconds
(without alignments)
7403.688 Million cell updates/sec

Title: US-09-636-259B-1
Perfect score: 1170
Sequence: 1 agccgcgcgcgtcaagcgcc.....gggacaggaagcgatcgtg 1170

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	402.6	34.4	1344	10	US-09-825-923-1	Sequence 1, Appli
3	400.8	34.3	1353	9	US-10-077-870-3	Sequence 3, Appli
4	400.8	34.3	1353	10	US-09-825-923-3	Sequence 3, Appli
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6	133	11.4	1335	9	US-09-349-755-3	Sequence 3, Appli
7	133	11.4	1335	9	US-09-166-334-3	Sequence 3, Appli
8	133	11.4	1335	10	US-09-350-206-3	Sequence 3, Appli
9	133	11.4	2689	9	US-09-349-755-1	Sequence 1, Appli
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15	128	10.9	2140	9	US-10-185-991-1	Sequence 1, Appli
16	119.6	10.2	1356	10	US-09-993-844-12	Sequence 12, Appli
17	118	10.1	694	10	US-09-864-761-17258	Sequence 17258, A
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22	115.4	9.9	3683	10	US-09-895-211-1	Sequence 1, Appli
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25	107.4	9.2	1338	9	US-09-349-755-6	Sequence 6, Appli
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38	100	8.5	3451	10	US-09-990-596-2	Sequence 27, Appl
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ALIGNMENTS

RESULT 1
US-10-077-870-1
Sequence 1, Application US/10077870
Publication NO. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077, 870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
US-10-077-870-1

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Matches 755; Conservative 0; Mismatches 384; Indels 72; Gaps 5;

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DB	178	CTGTGGCCACGCTCATCATCCCTTCTCGCTGGCCAAGAGCTGTGGCTACTGTGCTAC	237
QY	121	TTCCGCAAGGCTTGTGCGAGATCTTACCTGGCGCTCGACGTGCTTCTTGACAGTCGTC	180
DB	238	TTCCGGCGGACGTGTGTGCGAGGTGTACCTGGCGCTCGACGTGCTTCTTGACACCTCGTC	297
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Best Local Similarity 48.0%; Pred. No. 6.3e-16;
Matches 559; Conservative 0; Mismatches 591; Indels 14; Gaps 6;
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Db 718 ACGCTGCTGTGACCTCTGGCTGGCCCTGAGCTATGTGCCAGCAATGCTCCG 777
QY 187 CACCTGTGGCCATCAGCCTGAGCCGCTACTGTTCCATCACAAGGCCATCGA 246
Db 778 AATCTGTGCTCATCAGCTTGAACGCTACTTCTCCGTGACTCGGCCCTGAGC 837
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QY 786 AGCGAGCCAGGTGAAGCGCGCGCAGACGCTGCGCGCGCGCGCGCGCGG 845
Db 1371 GGGCCCCACCAAGCAGCGCCCGACGAGCTCCCAATACAGTCAAGAGCG 1430
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QY 903 CTGCGCGCGCGCGCAGAACCGCGAGAAAGCGTTACGTTCTGCTGGCGT 962
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Db 1551 GGCCTTCACTCCTCACTGACACCGGTACAAATCATGCTGTGCTCACCT 1610
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Db 1611 GGACTGTGTTCGCCAGAGACCCGTGGGAGCTGGCTACTGCTGTGCTAC 1670
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Job time : 106.502 secs


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QY 127 AAGCTTGTGCGAGATCTACCTGGCGCTGAGCTGCTCTTCTGCACGCTGCTCATCTG 186
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RESULT 15

US-08-767-993-6
; Sequence 6, Application US/08767993
; Patent No. 6010885

GENERAL INFORMATION:

APPLICANT: TURNER, George J.
APPLICANT: BETLACH, Mary C.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS POLYPEPTIDES
TITLE OF INVENTION: IN HALOBACTERIA
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,993
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-57669/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 376..1812

FEATURE:
NAME/KEY: misc_feature
LOCATION: 376..414
OTHER INFORMATION: /note="Bacteriorhodopsin
OTHER INFORMATION: pre-sequence."

FEATURE:
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
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; LENGTH: 3335 base pairs
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; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 319..2124
; US-08-194-338-1

Query Match      11.3%; Score 132.4; DB 1; Length 3335;
Best Local Similarity 56.3%; Pred. No. 2.9e-16;
Matches 312; Conservative 0; Mismatches 231; Indels 11; Gaps 3;

QY 21 CCAAAACCTCTTCTGCTGCTGCTGCGCCGCGCCGACATCCTGTGGCCACGCTGTCAT 80
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 747 CCAGAACTTCTTCATAGTTTGGCTGGCGGTGGCCGATCTCAGCGGTGGCCCTTGTGCT 806
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 81 CCCTTCTCGCTGGCCACGAGCTATGGGCTTACTGTGTAATCTGGCAAGGCTTGGTCCGA 140
    || ||| || ||| || ||| || ||| || ||| || ||| || ||| || ||| ||
DB 807 GCCCTTCAACGTCGCTTACTGATCCTGGGGCGCTGGGAGTTCCGCATCCACCTGTGCAA 866
    || ||| || ||| || ||| || ||| || ||| || ||| || ||| || ||| ||
QY 141 GATCTACCTGGCGCTGACGTCCTCTCTGACAGTGTCCATCGTGCA-CCTGTGCGCCA 199
    || ||| || ||| || ||| || ||| || ||| || ||| || ||| || ||| ||
DB 867 GCTGTGCTCACTGCGACGTCGCTGTGCTGACCTAGCTCATCTGAACCCCTGTGTGCA 926
    || ||| || ||| || ||| || ||| || ||| || ||| || ||| || ||| ||
QY 200 TCAGCCTGACCGCTACTGTGTCATCACACAGGCCATCGAGTACACACCTGAAGCGCACGC 259
    || ||| || ||| || ||| || ||| || ||| || ||| || ||| || ||| ||
DB 927 TAGCCCTCGACCGGTACTGGGCCATTACGGA-CCCATCACTATGCCAGAAAGAGGACCG 985
    || ||| || ||| || ||| || ||| || ||| || ||| || ||| || ||| ||
QY 260 CGCGCCGATCAAGGCCATCATCACCGGTGGTGCATCTGCGCCGTCACTCTCTTCC 319
    || ||| || ||| || ||| || ||| || ||| || ||| || ||| || ||| ||
DB 986 TTGGTCGCTCCTCTCTCATCTCCGGGTGTGGTCTACTTTCGCTGTGATTAAGTAGTC 1045
    || ||| || ||| || ||| || ||| || ||| || ||| || ||| || ||| ||
QY 320 CGCCGCTCATCTCCATCGAAGAAGAGGGCGGGCGGGCGCCGACGCCGCGAGCCGC 379
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DB 1046 CGCCGTGATCGGCTGAA-----CGACTGGCCGACGAGTTTCAACAAGCGCCACGC 1096
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QY 380 GCTGCGAGATCAAGACCAAGAGTGTAGTCTCATCTCGTGTGATCGGCTCTCTTCC 439
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1097 CCTGCGAGCTGACCTCGACGAGGCTGATCTACTCTCTGCTGGGCTCTCTTTTA 1156
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 440 CTCCCTGCTCATCATGATCTGTGTACGTGCGCATCTACCAAGATGCCAAGCGTCCGA 499
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1157 TTCCGCTGGCCATCATGACGATGCTTACATCGAGATCTTGTGGCCACGCGCGCC 1216
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QY 500 CCGCGTGGCCACGAGCCCGCGGGTCCGAGCGCGCTGCGCGCGCGCGCGGGGACCCG 559
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1217 TAAGGAGCGAGCGAGGGCCACAACAGCTTAACAGATCGCTGTGAAGTCCACTGAGCTCG 1276
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 560 AGCGCAGGCCCAAC 573
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1277 AGCCGATGGCAAC 1290
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RESULT 14
US-08-313-553-6
; Sequence 6, Application us/08313553
; Patent No. 5641650
; GENERAL INFORMATION:
; APPLICANT: TURNER, George J.
; APPLICANT: BETLACH, Mary C.
; TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS POLYPEPTIDES
; TITLE OF INVENTION: IN HALOBACTERIA
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Walter H. Dregger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,553
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,662
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-57669/WHD
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1956 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 376..1812
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 376..414
; OTHER INFORMATION: /note= "Bacteriorhodopsin
; OTHER INFORMATION: pre-sequence."
; FEATURE:
; NAME/KEY: terminator
; LOCATION: 1864..1866
; OTHER INFORMATION: /note= "Bacteriorhodopsin stop
; OTHER INFORMATION: codon."
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(213, "")
; OTHER INFORMATION: /note= "G to T mutation removes
; OTHER INFORMATION: AlwNI restriction site."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 427..435
; OTHER INFORMATION: /note= "AlwNI cloning site."
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(930, "")
; OTHER INFORMATION: /note= "G to A mutation removes
; OTHER INFORMATION: AlwNI restriction site."
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(1179, "")
; OTHER INFORMATION: /note= "T to A mutation removes
; OTHER INFORMATION: AlwNI site."
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(1245, "")
; OTHER INFORMATION: /note= "G to A mutation removes
; OTHER INFORMATION: pstI restriction site."
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: 374
; OTHER INFORMATION: /note= "RNA start site."
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QY	547	CCGGGGGACCGACGCGCAGGCCCAACGGTCTG---GGCCCCGAGCGCAGCGCGGGCCCCG	603
Db	1031	CCTCCGAGGCGCCACCCCTCACACACCCCCACCGCCTGGCTGCTGGGGCTGCTGGCAGAAAG	1090
QY	604	GGGGGCGCAGAGCGCCGAACCGCTGCCACCCACAGCTCAACGGCGCCCTGGCGAGCCCGCG	663
Db	1091	GGGCACGGGGAGGCCATGCCGCTGCACACAGTATGGGGTGGGTGAGGCGGCGCGTGAAGCGCT	1150
QY	664	CCGGCCGGG	672
Db	1151	GAGGCCGGG	1159

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RESULT 10
US-09-642-855-5
; Sequence 5, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyatl, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-5

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Query Match	11.48;	Score 133;	DB 4;	Length 2699;
Best Local Similarity	52.08;	Pred. No. 2.2e-16;		
Matches 348; Conservative	0;	Mismatches 315;	Indels 6;	Gaps 2;

[illegible]

Db	911	CTGAGTTCTTTACGGCCCTTCCTCAGCGTCACCTCTTTAACTCAGCATCTACCTGAAC	970
QY	487	GCCAAGCGTCGACACCGCGGTGCCACCCAGCCGCCGGGCTCCGACGCCGTCGCCGCCG	546
Db	971	ATCCAGAGCGCACCCCGCTCCGCGTGGATGGGCTCGAGAGGACGCCGCCCGAGCCC	1030
QY	547	CCGGGGGGCACCGACGCGCAGGCCCAACGGTCTG--GGCCCCGAGCGCAGCGGGGCCG	603
Db	1031	CCTCCGAGGCCACAGCCCTCACCACCCCCACCGCGCTGGCTGGGCGCTGCTGGCAGAAG	1090
QY	604	GGGGGGCGCAGAGCGCCGAACCGCTGCCACCCAGCTCAACGGCGCGCCCTGGCGAGCCGCG	663
Db	1091	GGGCAAGGGGAGGCCATGCGCGCTGCACAGGTATGGGGTGGGTAGGCGCGCGT	1150
QY	664	CCGGCCGGG	672
Db	1151	GAGCGCGG	1159

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RESULT 11
US-09-642-514-5
; Sequence 5, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-514-5

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Query Match	11.4%;	Score 133;	DB 4;	Length 2699;
Best Local Similarity	52.08;	Pred. No. 2.2e-16;		
Matches 348;	Conservative	0;	Mismatches 315;	Indels 6;
				Gaps 2;

QY	10	CTCAAGGCGCCCAAACCTTCTTCCTGTGTCTTGCCCTGGCCGCATCCTGTGGCC	69
Db	491	CTCCGACCCAGAACACTTCTCTCTGCTCAACCTGGCATCTCCGACTTCTCTGGCC	550
QY	70	ACGCTCGTCATCCCTTTCTTCGCTGGCCAACGAGGTGATGGGCTACTGTACTTCGGCAAG	129
Db	551	GCCTTCTGCATCCCACTGATGTATACCCTACGTGCTGACAAGCCCGCTGGACCTTCGGCCGG	610
QY	130	GCTTGGTGCGAGATCTACCTGGCGCTGACGCTGCTCTTTCGACGTCGTCCATCGTGCAC	189
Db	611	GGCCTCTGCAAGCTGTGGCTGGTAGTGGA CTACCTGCTGTGCACCTCCTTGCCTTCAAC	670
QY	190	CTGTGCCCATCAGCCTGAGCCGCTACTGTCCATCACACAGCCATCGAGTAC--AAC	246
Db	671	ATCGTGCCTATCAGCTACGACCGCTTCTCTGCTCAGTCAACCCGAGCGGTCTCATACCGGGCC	730
QY	247	CTGAAGCGCACGCGCGCCGCATCAAGGCCATCATCAACCTGTGGTCACTCTCGGCC	306
Db	731	CAGCAGGGTGACACAGCGCGCGGCACTGCGGAAGATGCTGTGGTGTGGCTGCTGCGCTTC	790
QY	307	GTCATCTCTTCCCGCGCTCATCTCCATCGAAGAAGGGCGGCGCGCGCCGAC	366
Db	791	CTGCTGTACGACCAAGCCATCTTAAGCTGGGAGTACTCTGTCGGGGGCAAGCTCCATCCCC	850


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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-09-165-543-1

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```

Query Match      11.4%; Score 133; DB 3; Length 2689;
Best Local Similarity 52.0%; Pred. No. 2.2e-16;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

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QY 10 CTCAAGGCGGCCCAAAACCTCTTCGTGCTCTGCGCTGGCGGACATCCTGTGGCC 69
DB 483 CTCGGACCCCAACAACCTTCTCTGCTCAACCTCGCCATCTCCGACTTCTGCGGC 542
QY 70 ACGCTGCTATCCCTTCTCTGCTGCGCAAGAGTGCATGGGCTACTGTTACTTGGCAAG 129
DB 543 GCCTTCTGCAATCCCACTGATATGACCTGACGAGCGCGCTGACCTTGGCGCG 602
QY 130 GCTTGTGAGATCTACCTGGCGCTGACGTGCTCTTCTGCACTGCTCATCTGCGCAAG 189
DB 603 GGCTCTGCAAGCTGTGCTGTAGTGAGACTACCTGCTGTGACACTCTGCTGCTGCAAC 662
QY 190 CTGTGCGCATCAGCCTGACCGCTACTGCTCCATCACACAGGCCATCGAGTAC--AAC 246
DB 663 ATCGTGTCAATCAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 722
QY 247 CTGAAGCGCAGCGCGCGCGCATCAAGGCCATCATCATCAGCTGTGGTCACTTGGCC 306
DB 723 CAGCAGGCTGACACGCGCGCGCGCATGCGGAAGATGCTGCTGCTGCTGCTGCTGCTG 782
QY 307 GTCATCTCTTCCCGCGCTCATCTCATCGAAGAAAGGCGCGCGCGCGCGCGCGCGAG 366
DB 783 CTGCTGTACGGAACCAAGCCATCTGAGCTGGAGTACCTGTCCGGGCGAGCTCCATCCC 842
QY 367 CCGGCGGAGCGCGCGCTGCGAGATCAACGACGAGAGTGTGATCATCTCTGCTGCAATC 426
DB 843 GAGGGCCTACTGCTATGCGAGTCTTCTACAACTGTGACTTCTCATCACGGCTTCCACC 902
QY 427 GGCTCTTCTTCCCTGCTCATCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486
DB 903 CTGAGTCTTCTTACGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 962
QY 487 GCCAAGCTGCGACCGCGCTGCGCAACCGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 546
DB 963 ATCCAGAGGCGCACCGCGCTGCGCTGATGGGCTGAGAGGAGGAGCGCGCGCGCGAGCCC 1022
QY 547 CCGGCGGCGCACCGAGCGAGCGCAACGGTCTG--GCGCGCGAGCGCGAGCGCGCGCGCG 603
DB 1023 CTTTCCGAGGCGCACCGCTTCAACCAACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1082

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QY 604 GGGGCGAGAGGCCCAACCGCTGCGCCACCCAGCTCAACGCGCGCGCGCGCGCGCGCG 663
DB 1083 GGGCAGCGGAGAGGCCATGCCGCTGACACAGGTATGGGCTGAGGCGCGCGTAGCGGCT 1142
QY 664 CCGGCGCGG 672
DB 1143 GAGGCGCGG 1151

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RESULT 9
US-09-167-354-5
; Sequence 5, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyatt, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-167-354-5

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Query Match      11.4%; Score 133; DB 3; Length 2699;
Best Local Similarity 52.0%; Pred. No. 2.2e-16;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

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QY 10 CTCAAGGCGGCCCAAAACCTCTTCGTGCTCTGCGCTGGCGGACATCCTGTGGCC 69
DB 491 CTCGGACCCCAACAACCTTCTCTGCTCAACCTCGCCATCTCCGACTTCTGCGGC 550
QY 70 ACGCTGCTATCCCTTCTCTGCTGCGCAAGAGTGCATGGGCTACTGTTACTTGGCAAG 129
DB 551 GCCTTCTGCAATCCCACTGATATGACCTGACGAGCGCGCTGACACTTGGCGCG 610
QY 130 GCTTGTGCGAGATCTACCTGGCGCTGACGTGCTCTTCTGCACTGCTCATCTGCGCAAG 189
DB 611 GGCTCTGCAAGCTGTGCTGTAGTGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTG 670
QY 190 CTGTGCGCATCAGCCTGACCGCTACTGCTCCATCACACAGGCCATCGAGTAC--AAC 246
DB 671 ATCGTGTCAATCAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 730
QY 247 CTGAAGCGCAGCGCGCGCGCATCAAGGCCATCATCATCAGCTGTGGTCACTTGGCC 306
DB 731 CAGCAGGCTGACACGCGCGCGCGCATGCGGAAGATGCTGCTGCTGCTGCTGCTGCTG 790
QY 307 GTCATCTCTTCCCGCGCTCATCTCATCGAAGAAAGGCGCGCGCGCGCGCGCGCGAG 366
DB 791 CTGCTGTACGGAACCAAGCCATCTGAGCTGGAGTACCTGTCCGGGCGAGCTCCATCCC 850
QY 367 CCGGCGGAGCGCGCGCTGCGAGATCAACGACGAGAGTGTGATCATCTCTGCTGCAATC 426
DB 851 GAGGGCCTACTGCTATGCGAGTCTTCTTACAACTGTGACTTCTCATCACGGCTTCCACC 910
QY 427 GGCTCTTCTTCCCTGCTCATCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486
DB 911 CTGAGTCTTCTTACGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 970
QY 487 GCCAAGCTGCGACCGCGCTGCGCAACCGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 546
DB 971 ATCCAGAGGCGCACCGCGCTTCAACCAACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1030

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; NAME/KEY: CDS
; LOCATION: 291..1625
US-08-985-090-1
Query Match 11.4%; Score 133; DB 2; Length 2689;
Best Local Similarity 52.0%; Pred. No. 2.2e-16;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

QY 10 CTCGAAGCGCCCAAAACCTCTTCCCTGGTGTCTCTGGCCCTCGGCCGACATCCTGTGGCC 69
Db 483 CTCGCAACCCAGAAACAACCTTCTTCCCTGCTCAACCTCGCCATCTCCGACTTCTCGTGGC 542
QY 70 ACGCTGTCATCCCTTCTCTCGCTGCCCCAACGAGGTCATGGGCTACTGTACTTCGGCAAG 129
Db 543 GCCTTCTGCATCCCACTGTATGTATACCTTACGTCGTGACAGGCCGCTGGAACCTTCGGCCGG 602
QY 130 GCTTGGTGCGAGATCTACCTGGCGGCTGCAAGTCTCTTCTGCAAGTCGTCATCGTGAC 189
Db 603 GGCCCTCTGCAAGCTGTGGCTGTAGTGAAGTACCTGCTGTGACACCTCTCTGCTTCAAC 662
QY 190 CTGTGCGCATCAGCCTTGAGCCGCTACTGTGTCATCACACAGGCCATTCGAGTAC--AAC 246
Db 663 ATCGTGCTCATCAGCTACGACCGCTTCTGTCGCTCACCCGAGCGGCTCATACCGGGCC 722
QY 247 CTGAAGCGCAGCGCGCGCCGATCAAGGCCATCATCATCACCGGTGGGTATCTCGGCC 306
Db 723 CAGCAGGGTGACACGGCGCGGAGTGGAGAGATGCTGCTGTGGGTGCTGGCCCTTC 782
QY 307 GTCATCTCTTCCCGCGCTCATCTCCATGCAAGAAGAGGGCGCGCGCGCGCGCCAG 366
Db 783 CTGCTGTACGAGCAGCCATCTGAGCTGGAGTACCTGTCCGGGGGAGCTTCATCCCC 842
QY 367 CCGGCCGAGCCCGCGCTGGAGATCAACGACCAAGTGTGTACGTATCTGTGTGATC 426
Db 843 GAGGGCCACTGCTATGCGGAGTCTTCTACAACTGTACTTCTCTCATCAGGCTTCCACC 902
QY 427 GGTCTCTTCTTCCCTGCTGCTCATGATCTGTGTCTACGTGCGCATCTACAGATC 486
Db 903 CTGAGTCTTCTTACGCTTCTTCTTCAAGCTTCTTAACTCAAGATCTACCTGAAC 962
QY 487 GCCAAGCGTGCACCCCGGCTGCAACCCAGCTCAACGGCGCGCCCTGGCAGCCCGCG 663
Db 963 ATCCAGAGCGCAGCCCGCTTCCGCTGTGATGGGCTTGAAGAGCAGCCGCGCGAGCCC 1022
QY 547 CCGGGGGGACCGGAGCGCAGGCCCAACGGTCTG---GGCCCCGAGCGCAGCGGGCCG 603
Db 1023 CTTCCCGAGGCGCCAGCCCTTCAACCCACCCGCGCTGCTGTGGGCTGTGCGACAAG 1082
QY 604 GGGGGCGAGAGGCGGAACCGCTGCCCCACCCAGCTCAACGGCGCGCCCTGGCGAGCCCGG 663
Db 1083 GGGCAGGGGAGGCCATGCGCTGACACAGGTATGGGTGGGTGAGGCGGCGTAGGCGCT 1142
QY 664 CCGGCCGGG 672
Db 1143 GAGGCCGGG 1151
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RESULT 7

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US-08-985-090-1
; Sequence 1, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silverl
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: 291..1625
US-08-985-090-1
Query Match 11.4%; Score 133; DB 2; Length 2689;
Best Local Similarity 52.0%; Pred. No. 2.2e-16;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

QY 10 CTCGAAGCGCCCAAAACCTCTTCCCTGGTGTCTCTGGCCCTCGGCCGACATCCTGTGGCC 69
Db 483 CTCGCAACCCAGAAACAACCTTCTTCCCTGCTCAACCTCGCCATCTCCGACTTCTCGTGGC 542
QY 70 ACGCTGTCATCCCTTCTCTCGCTGCCCCAACGAGGTCATGGGCTACTGTACTTCGGCAAG 129
Db 543 GCCTTCTGCATCCCACTGTATGTATACCTTACGTCGTGACAGGCCGCTGGAACCTTCGGCCGG 602
QY 130 GCTTGGTGCGAGATCTACCTGGCGGCTGCAAGTCTCTTCTGCAAGTCGTCATCGTGAC 189
Db 603 GGCCCTCTGCAAGCTGTGGCTGTAGTGAAGTACCTGCTGTGACACCTCTCTGCTTCAAC 662
QY 190 CTGTGCGCATCAGCCTTGAGCCGCTACTGTGTCATCACACAGGCCATTCGAGTAC--AAC 246
Db 663 ATCGTGCTCATCAGCTACGACCGCTTCTGTCGCTCACCCGAGCGGCTCATACCGGGCC 722
QY 247 CTGAAGCGCAGCGCGCGCCGATCAAGGCCATCATCATCACCGGTGGGTATCTCGGCC 306
Db 723 CAGCAGGGTGACACGGCGCGGAGTGGAGAGATGCTGCTGTGGGTGCTGGCCCTTC 782
QY 307 GTCATCTCTTCCCGCGCTCATCTCCATGCAAGAAGAGGGCGCGCGCGCGCGCCAG 366
Db 783 CTGCTGTACGAGCAGCCATCTGAGCTGGAGTACCTGTCCGGGGGAGCTTCATCCCC 842
QY 367 CCGGCCGAGCCCGCGCTGGAGATCAACGACCAAGTGTGTACGTATCTGTGTGATC 426
Db 843 GAGGGCCACTGCTATGCGGAGTCTTCTACAACTGTACTTCTCTCATCAGGCTTCCACC 902
QY 427 GGTCTCTTCTTCCCTGCTGCTCATGATCTGTGTCTACGTGCGCATCTACAGATC 486
Db 903 CTGAGTCTTCTTACGCTTCTTCTTCAAGCTTCTTAACTCAAGATCTACCTGAAC 962
QY 487 GCCAAGCGTGCACCCCGGCTGCAACCCAGCTCAACGGCGCGCCCTGGCAGCCCGCG 663
Db 963 ATCCAGAGCGCAGCCCGCTTCCGCTGTGATGGGCTTGAAGAGCAGCCGCGCGAGCCC 1022
QY 547 CCGGGGGGACCGGAGCGCAGGCCCAACGGTCTG---GGCCCCGAGCGCAGCGGGCCG 603
Db 1023 CTTCCCGAGGCGCCAGCCCTTCAACCCACCCGCGCTGCTGTGGGCTGTGCGACAAG 1082
QY 604 GGGGGCGAGAGGCGGAACCGCTGCCCCACCCAGCTCAACGGCGCGCCCTGGCGAGCCCGG 663
Db 1083 GGGCAGGGGAGGCCATGCGCTGACACAGGTATGGGTGGGTGAGGCGGCGTAGGCGCT 1142
QY 664 CCGGCCGGG 672
Db 1143 GAGGCCGGG 1151
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RESULT 8

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US-09-165-543-1
; Sequence 1, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
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Db 613 CTGAGTTCTTTACGCCCTTCCAGCGCTACCTTCTTAACCTCAGCATCTACTGAAC 672
QY 487 GCCAAGCGTCGCACCCCGCGTGCACCCAGCCCGCGGGTCCGGAGCCCGTCCGCGCGG 546
Db 673 ATCCAGAGGGCGCACCCCGCTCCGGCTGGATGGGGCTCGAGAGGCGAGCCCGCCGAGCC 732
QY 547 CCGGGGGGACCGAGCGCGCAACGGTCTG--GGCCCCGAGCGAGCGCGCGCGCG 603
Db 733 CCTCCGAGGGCCAGCCCTCAACCCACCACCGCGCTGCTGGGGCTGCTGGCAGAGA 792
QY 604 GGGGCGCAGAGCGCCGAACCGCTGCCACCCAGCTCAACGGCGCGCCCTGGCGAGCCCGG 663
Db 793 GGGCAGGGGAGGCCATGCGCTGCACAGGTATGGGTGGGTGAGGCGCGCGTAAGCGCT 852
QY 664 CCGGCGCGGG 672
Db 853 GAGCGCGGG 861
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RESULT 5

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US-09-642-855-6
; Sequence 6, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-855-6
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Query Match 11.4%; Score 133; DB 4; Length 1335;
Best Local Similarity 52.0%; Pred. No. 2e-16;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;
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QY 10 CTCAGGCGGCCCAAAACCTTCTCCGTGTGTCTCTGGCGCTGGCGGACATCCTGTGCC 69
Db 193 CTCGGACCCAGAACACTTCTCTGCTCAACCTCGCCATCTCCGACTTCTCTGTGGC 252
QY 70 ACGCTGTCATCCCTTCTCCGTGCCCAACGAGGTCACTGAGCTACTGTACTTGGCAAG 129
Db 253 GCCTTCTGCATCCCACTGTATGTAACCTTACGTGCTGACAGGCCGCTGGACCTTGGCGG 312
QY 130 GCTTGTGCGAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGTGTCATCTGCAC 189
Db 313 GGCCTTGCAGAGCTGTGGCTGTAGTGACTACCTGCTGTGCACCTCTGCTTCAAC 372
QY 190 CTGTGCGCCATCAGCCTGAGCCGCTACTGTGCATCACAGGCCATCGAGTAC---AAC 246
Db 373 ATCGTGTCTATCAGCTACGACCGCTTCTCTGTGCTACCCGAGCGGTCTCATACGGGGC 432
QY 247 CTGAAGCGGACGCGCGCGCATCAAGGCCATCATCAACCGTGTGGGTCACTCGGCC 306
Db 433 CAGCAGGGTGACACGCGCGGGGAGTGCAGGAGATCTGTGTGGGTGGCTTTC 492
QY 307 GTGATCTCTTCCGCGCTCATCTCCATCGAAGAAGGGCGGCGCGCGCGCCGAG 366
Db 493 CTGCTGTACGAGCAGCATCTGAGTGGAGTACCTGTCCGGGGCAGCTCCATCC 552
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QY 367 CCGCGGAGCGCGCGTGGAGATCAACGACCAAGTGTGTACTCATCTCGTGTGATC 426
Db 553 GAGGGCACTGCTATGCCAGTTCTTTTACAACCTGTGTACTTCTTCATCACGGCTTCCAC 612
QY 427 GGCTCTTCTTCCCTCCCTGCTCATATGATCCTGTGTACGTGCGCATCTACAGATC 486
Db 613 CTGAGTTCTTTACGCCCTTCTCTCAGGCTACCTTCTTAACTCAGCATCTACTGAAC 672
QY 487 GCCAAGCGTCGACCCCGCGTGCACCCAGCCCGGGTCCGAGCCCGCTCGCGCGCG 546
Db 673 ATCCAGAGGCGCACCCCGCTCGGTGATGGGCTCGAGAGCGACCGCGCCGAGCC 732
QY 547 CCGGGGGGACCGAGCGCGACGCCCAACGGTCTG--GGCCCCGAGCGAGCGCGCGCG 603
Db 733 CCTCCGAGGCCAGCCCTCAACACCCACCACCGCTGCTGGGGCTGCTGGCAGAGA 792
QY 604 GGGGCGCAGAGCGCCGAACCGCTGCCACCCAGCTCAACGCGCGCCCTGGCGAGCCCGG 663
Db 793 GGGCAGGGGAGGCCATGCGCTGCACAGGTATGGGTGGGTGAGGCGCGCGTAAGCGCT 852
QY 664 CCGGCGCGGG 672
Db 853 GAGCGCGGG 861
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RESULT 6

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US-09-642-514-6
; Sequence 6, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-514-6
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Query Match 11.4%; Score 133; DB 4; Length 1335;
Best Local Similarity 52.0%; Pred. No. 2e-16;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;
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QY 10 CTCAGGCGGCCCAAAACCTTCTCCGTGTGTCTCTGGCGCTGGCGGACATCCTGTGCC 69
Db 193 CTCGGACCCAGAACACTTCTCTGCTCAACCTCGCCATCTCCGACTTCTCTGTGGC 252
QY 70 ACGCTGTCATCCCTTCTCCGTGCCCAACGAGGTCACTGAGCTACTGTACTTGGCAAG 129
Db 253 GCCTTCTGCATCCCACTGTATGTAACCTTACGTGCTGACAGGCCGCTGGACCTTGGCGG 312
QY 130 GCTTGTGCGAGATCTACCTGGCGCTCGACGTGCTCTTCTGCACGTGTCATCTGCAC 189
Db 313 GGCCTTGCAGAGCTGTGGCTGTAGTGACTACCTGTGTCACCTCTGCTTCAAC 372
QY 190 CTGTGCGCCATCAGCCTGAGCCGCTACTGTGCATCACAGGCCATCGAGTAC---AAC 246
Db 373 ATCGTGTCTATCAGCTACGACCGCTTCTGTGCTACCCGAGCGGTCTCATACGGGGC 432
QY 247 CTGAAGCGACGCGCGCGCATCAAGGCCATCATCAACCGTGTGGGTCACTTCGGCC 306
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; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-09-165-543-3

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Query Match      11.4%; Score 133; DB 3; Length 1335;
Best Local Similarity 52.0%; Pred. No. 2e-16;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

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QY 10 CTCGAAGGCGCCCAAAACCTCTTCCTGCTGCTCTGCGCTCGGCCGACATCCTGTGGCC 69
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Db 193 CTCGCGACCCAGAAACAATTCTCTCTGCTCAACCTCGCCATCTCCGACTTCCTGTCGGC 252

QY 70 ACGCTCGTCAATCCCTTTCTCTGCTGCGCCCAACGAGTCAATGGGCTACTGCTACTTCGGCAAG 129
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 253 GCCTTCTGATCCCACTGATGTATGATACCTGACTGCTGACAGGCGGCTGACCTTCGGCCGG 312

QY 130 GCTTGTGCGAGATCTACCTGGCGCTGACGCTGCTCTTCTGACAGCTGCTTCATCGTGAC 189
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 313 GGCTCTGCAAGCTGTGGCTGTAGTGACCTACTGCTGTGACACCTCTCTGCTTCAAC 372

QY 190 CTGTGCGCATCAGCCTTGAGCCGCTACTGTTCATCACACAGGCCCATCGAGTAC--AAC 246
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Db 373 ATCGTGCTCATCAGCTACGACCGCTTCTGCTGCTACCCGAGCGGTCTCATACCGGGCC 432

QY 247 CTGAAGCGCACGCGCGCGCATCAAGGCCATCATCACCGGTGGGTCACTCGGCC 306
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Db 433 CAGCAGGGTGACACGCGCGGCGAGTGCAGAAAGTCTGTGTGGTGTGGCTTTC 492

QY 307 GTCATCTCCTCCCGCGCTCATCTCCATCGAGAAAGGCGGCGGCGCGCGCCGCGAG 366
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 493 CTGCTGTACGGACCGCATCTGAGCTGGAGTACTGTCGGGGGCGAGCTTCATCCCC 552

QY 367 CCGGCGGAGCGCGCGCTGCGAGATCAAGCAGACGAGAGTGTAGCTCATCTGTCGTGATC 426
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Db 553 GAGGGCACTGCTATGCGGAGTCTTCTACAACTGTGACTTCTCATCACGGCTTCCACC 612

QY 427 GGCTCTCTCTTGGCTCCCTGCTCATCATGATCCTGTGCTACGTCGCGCATCAACGATC 486
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 613 CTGAGTCTTTTACGCGCTTCTCTCAGCGCTCACTTCTTAACCTCAGCATCTACGTAAC 672

QY 487 GCCAAGCGTGCACCCGCGTGCACCCAGCGCGCGGGGTCCGGAGCGCGCTCGCCGCGCCG 546

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Db 673 ATCCAGAGGCGCACCCGCTCCGGCTGAGATGGGGCTCGAGAGCGACCGGCCCGAGCCC 732
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QY 547 CCGGGGGCACCCGAGCGCAGGCGCCCAACGCTGTG---GGCCCCGAGCGCAGCGCGGCCG 603
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Db 733 CCTCCGAGGCGCCAGCCCTCACACACCCCGCCGCTGCTGCTGGGGCTGTGGCAGAG 792

QY 604 GGGGGCGCAGAGCGCCGAGCCGCTGCGCCACCCAGCTCAACGCGCGCCCTGCGAGCCGCG 663
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QY 664 CCGGCGCGG 672
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Db 853 GAGGCGCGG 861

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RESULT 4
US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cDNA
; US-09-167-354-6

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Query Match      11.4%; Score 133; DB 3; Length 1335;
Best Local Similarity 52.0%; Pred. No. 2e-16;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

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```

QY 10 CTCGAAGGCGCCCAAAACCTTCCTGCTGCTGCTCTGCGCTCGGCCGACATCCTGTGGCC 69
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Db 193 CTCGCGACCCAGAAACAATTCTCTCTGCTCAACCTCGCCATCTCCGACTTCCTGTCGGC 252

QY 70 ACGCTCGTCAATCCCTTTCTCTGCTGCGCCCAACGAGTCAATGGGCTACTGCTACTTCGGCAAG 129
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 253 GCCTTCTGATCCCACTGATGTATGATACCTGACTGCTGACAGGCGGCTGACCTTCGGCCGG 312

QY 130 GCTTGTGCGAGATCTACCTGGCGCTGACGCTGCTCTTCTGACAGCTGCTTCATCGTGAC 189
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 313 GGCTCTGCAAGCTGTGGCTGTAGTGAGCTACTGCTGTGACACCTCTCTGCTTCAAC 372

QY 190 CTGTGCGCATCAGCCTTGAGCCGCTACTGTTCATCACACAGGCCCATCGAGTAC--AAC 246
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
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QY 247 CTGAAGCGCACGCGCGCGCATCAAGGCCATCATCACCGGTGGGTCACTCGGCC 306
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 433 CAGCAGGGTGACACGCGCGGCGAGTGCAGAAAGTGTGTGGTGTGGCTTTC 492

QY 307 GTCATCTCCTCCCGCGCTCATCTCCATCGAGAAAGGCGGCGGCGCGCGCCGCGAG 366
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Db 493 CTGCTGTACGGACCGCATCTGAGCTGGAGTACCTGTCCGGGGGCGAGCTTCATCCCC 552

QY 367 CCGGCGGAGCGCGCGCTGCGAGATCAAGCAGACGAGAGTGTAGCTCATCTGTCGTGATC 426
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 553 GAGGGCACTGCTATGCGGAGTCTTCTTAACAAGTGTGACTTCTCATCACGGCTTCCACC 612

QY 427 GGCTCTCTTCTTGGCTCCCTGCTCATCATGATCCTGTGCTACGTCGCGCATCTACGAGATC 486

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OY 81 CCCTTCTCGCTGGCCAAAGAGTCAATGGGCTACTGTGCTACTTCGGCAAGCCTTGTCGA 140
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 807 GCCCTTCAACGTGGCTTACTGATCTGCGGCGCTGGAGTTCGGCATCCACCTGTGCAA 866
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OY 141 GATCTACCTGGCGCTGAGCTGCTCTTCTGCAAGCTGCTCCATCGTGCACTGTGGCCAT 200
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Db 867 GCTGTGGCTCACCTGGAGCTGTGTGTGCTAGCTTCCATCTTGAACCTGTGTGCCAT 926
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 201 CAGCCTGACCGCTACTGCTTCCATCACACAGCCCATCGAGTACACCTGAAGCGCACGCC 260
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    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 261 GCGCCGATCAAGGCCATCATCATCACCCTGTGGTCACTCGGCCGTCACTCTCTTCC 320
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OY 321 GCCGCTCATCTCCATCGAAGAAAGGGCGGGCGGGCGGCCGAGCCGCGAGCCGCG 380
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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OY 381 CTGCGAGATCAACGACCAAGAGTGTAGCTCATCTCGTGTGATCGGCTCTCTTCC 440
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1098 CTGCGAGCTGACCTGCGACGAGGCTGATCTACTCTGCTGGGCTCTCTTAT 1157
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OY 441 TCCCTGCTCATGATGATCTGTGTGCTGCGCATCTACAGATCGCCAAGCTGCGAC 500
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RESULT 2
US-08-985-090-3
; Sequence 3, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silverl
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
US-08-985-090-3
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Query Match 11.4%; Score 133; DB 2; Length 1335;
Best Local Similarity 52.0%; Pred. No. 2e-16;
Matches 348; Conservative 0; Mismatches 315; Indels 6; Gaps 2;
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OY 10 CTCAAGCGGCCCAAAACCTTCTGCTGTCTGTGCGCTCGGCCGACATCTGTGCCC 69
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Db 193 CTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGACTTCTCGTCCG 252
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OY 70 ACGCTGTATCCCTTCTCGCTGGCCCAAGAGTATGGGCTACTGTGTAATTGCGCAAG 129
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Db 253 GCCTTCTGATCCCACTGATATGACCCCTACGCTGCTGACAGGCCGCTGAGCTTCCGCGG 312
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OY 130 GCTTGTGGAGATCTACCTGGCGCTCGACGTCTTCTGACGTCGTCATCTGTCAC 189
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Db 313 GGCCCTGCAAGCTGTGGCTGTAGTGGACTACTGCTGTGACACCTCTCTGTGCTTCAAC 372
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OY 190 CTGTGCGCCATCAGCCTGACCGCTACTGTCTCATCACACAGGCCATCGAGTAC--AAC 246
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OY 247 CTGAAGCGCACGCGCGCGCATCAAGGCCATCATCACCGTGTGGTCTATCTCGGCC 306
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OY 307 GTCATCTCTTCCCGCGCTCATCTCATCGAAGAAAGGCGCGCGCGCGCGCGCGAG 366
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Db 493 CTGCTGTACGAGCAAGCATCTGAGCTGGAGTACCTGTCCGGGGCAGCTCCATCCCC 552
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OY 367 CCGCGCGAGCGCGCTGCGAGATCAACGACCAAGTGTAGCTCATCTCGTGTGATC 426
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OY 427 GGCTCTCTTCTCGCTCCCTGCTCATCATGATCTCTGTCTACGTGCGCATCTACAGATC 486
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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OY 487 GCCAAGCTGCGACCGCGGTGCCACCCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 546
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Db 673 ATCCAGAGGCGCACCGCGCTCCGGCTGTGATGGGCTCGAGAGCGACCGCGCGCGCGCG 732
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OY 547 CCGGGGGGCGACCGCGAGCGGCGCCCAACGCTGTG--GGCCCGAGCGCGCGCGCGCG 603
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 733 CTTCCGAGGCGCGGCGCTTACACACCGCGCGCGCTGTGCTGTGGGCTGTGCGAGAAG 792
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 604 GGGGGCGAGAGCGCGAACCCTGCGCCACCGCTCAACGCGCGCGCGCGCGCGCGCGCG 663
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 793 GGGCAGGGGAGGCGCATCGCTGACAGGATAGGGGTGAGGCGCGCGCGCGCGCGCT 852
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 664 CCGGCGCGG 672
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 853 GAGGCGGG 861
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 3
US-09-165-543-3
; Sequence 3, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
```

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 06:16:02 ; Search time 62.5019 seconds
(without alignments)
5740.812 Million cell updates/sec

Title: US-09-636-259B-1
Perfect score: 1170
Sequence: 1 agccgcgcgcgtcaagcgcc.....gggacacgaagcgatcgtg 1170

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155.4	13.3	3335	1 US-07-676-174A-1	Sequence 1, Appli
2	133	11.4	1335	2 US-08-985-090-3	Sequence 3, Appli
3	133	11.4	1335	3 US-09-165-543-3	Sequence 3, Appli
4	133	11.4	1335	3 US-09-167-354-6	Sequence 6, Appli
5	133	11.4	1335	4 US-09-642-855-6	Sequence 6, Appli
6	133	11.4	1335	4 US-09-642-514-6	Sequence 6, Appli
7	133	11.4	2689	2 US-08-985-090-1	Sequence 1, Appli
8	133	11.4	2689	3 US-09-165-543-1	Sequence 1, Appli
9	133	11.4	2699	3 US-09-167-354-5	Sequence 5, Appli
10	133	11.4	2699	4 US-09-642-855-5	Sequence 5, Appli
11	133	11.4	2699	4 US-09-642-514-5	Sequence 5, Appli
12	132.4	11.3	1645	2 US-08-461-812-1	Sequence 1, Appli
13	132.4	11.3	3335	1 US-08-194-338-1	Sequence 1, Appli
14	130.4	11.1	1956	1 US-08-313-553-6	Sequence 6, Appli
15	130.4	11.1	1956	3 US-08-767-993-6	Sequence 6, Appli
16	129	11.0	2428	3 US-08-475-742-15	Sequence 15, Appli
17	128	10.9	1621	1 US-08-722-001-13	Sequence 13, Appli
18	128	10.9	2140	1 US-08-334-698-1	Sequence 1, Appli
19	128	10.9	2140	1 US-08-228-932-1	Sequence 1, Appli
20	128	10.9	2140	1 US-08-468-939-1	Sequence 1, Appli
21	128	10.9	2140	2 US-08-406-855A-1	Sequence 1, Appli
22	128	10.9	2140	2 US-08-722-190-1	Sequence 1, Appli
23	128	10.9	2140	3 US-08-244-354-1	Sequence 1, Appli
24	128	10.9	2140	3 US-09-206-899-1	Sequence 1, Appli
25	128	10.9	2140	4 US-09-444-783-1	Sequence 1, Appli
26	128	10.9	2140	4 US-09-688-415-1	Sequence 1, Appli
27	128	10.9	2140	5 PCT-US95-04203-1	Sequence 1, Appli

28	127.8	10.9	1610	1 US-08-056-051-5	Sequence 5, Appli
29	127.8	10.9	1610	1 US-07-928-611-21	Sequence 21, Appl
30	127.8	10.9	1610	2 US-08-487-811A-21	Sequence 21, Appl
31	127.8	10.9	1610	4 US-09-060-694-21	Sequence 21, Appl
32	127.8	10.9	1610	4 US-09-378-074-21	Sequence 21, Appl
33	127.8	10.9	1610	5 PCT-US93-07370-21	Sequence 29, Appl
34	126.4	10.8	1776	1 US-08-722-001-29	Sequence 8, Appli
35	120.8	10.3	1581	1 US-08-313-553-8	Sequence 8, Appli
36	120.8	10.3	1581	3 US-08-767-993-8	Sequence 7, Appli
37	120	10.3	1601	1 US-08-722-001-7	Sequence 27, Appl
38	120	10.3	1997	1 US-08-722-001-27	Sequence 11, Appl
39	120	10.3	2004	1 US-08-722-001-11	Sequence 1, Appli
40	119.2	10.2	1673	1 US-07-791-936A-1	Sequence 1, Appli
41	119.2	10.2	1673	1 US-08-383-781B-1	Sequence 1, Appli
42	119.2	10.2	1771	2 US-07-969-267B-1	Sequence 1, Appli
43	119.2	10.2	1771	4 US-09-168-510-1	Sequence 1, Appli
44	119.2	10.2	2463	1 US-08-370-542-1	Sequence 1, Appli
45	119.2	10.2	2463	1 US-08-542-358-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-07-676-174A-1
; Sequence 1, Application US/07676174A
; Patent No. 5344776
; GENERAL INFORMATION:
; APPLICANT: Vantor, J. Craig
; TITLE OF INVENTION: Octopamine receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/676,174A
; FILING DATE: 19910328
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/79117/KIK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)861-3000
; TELEFAX: (202)822-8944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3335 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 319...2121
; US-07-676-174A-1

Query Match 13.3%; Score 155.4; DB 1; Length 3335;
Best Local Similarity 56.6%; Pred. No. 1.7e-20;
Matches 313; Conservative 0; Mismatches 231; Indels 9; Gaps 1;

QY 21 CCAAAACCTCTTCTGCTGCTCTGCGCCGACATCCTGTGCGCCACAGCTGCTCAT 80
Db 747 CCAGACTCTCTCATAGTTTCGCTGCGGTGGCCGATCTCACGGTGCCCTTCTGTGCT 806


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QY 433 TTCTTCGCTCCCTGCCCTCATCATGATCCTGGTCTAGTGCGCATCTACCAATCGCCAAG 492
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 TTCTTCGCGCCCTGCCCTCATCATGCTGTGGTGTACGCGCGCATCTACCACTCGTCAAG 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 493 CGTCCGACCCCGCGGTGCCACCCAGCCCGCGGGTCCGGACGCCGTCGCCGCGCGCGGGG 552
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 301 TGGAGGGGCGCCGAAGCTGCCGGCGAGACAAGAGAGCGGCCCATCATCGTCTGCCGCGCGATG 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 553 GGCACCGAGCGCGCAGCGCCCAACGGTCTGGGCCCCGAGCGCAGCGCGGCGCGCGCGCGCA 612
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 361 GAGTCCATCAGGATGAGCGGAGTGAACGGCAACGAGAGAGCGCGCGCGGCGAGGGGAACGGA 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 613 GAGGCCGAA 621
      | | | | |
Db 421 AACGGAGAA 429
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Search completed: February 15, 2003, 18:02:46
Job time : 2343.51 secs

Research 6:791-806, 1996)			
BASE COUNT	58 a	111 c	95 g
ORIGIN			86 t

Query Match	16.6%;	Score 194.2;	DB 10;	Length 350;
Best Local Similarity	88.3%;	Pred. No. 1.4e-26;		
Matches 211; Conservative	0;	Mismatches 28;	Indels 0.	Cane 0.

[illegible]

RESULT 14	
CNS03BQW	
LOCUS	
DEFINITION	
CNS03BQW	896 bp
Tetraodon nigroviridis genome survey sequence PUC-Or1 end of clone 012P03 of library G from Tetraodon nigroviridis, genomic survey sequence.	DNA linear GSS 15-MAY-2000

BASE COUNT	ORIGIN
163 a	276 c
295 g	157 t
	5 others

Query Match	16.4%;	Score 191.4;	DB 17;	Length 896;
Best Local Similarity	80.7%;	Pred. NO. 5.5e-26;		
Matches 222; Conservative	1;	Mismatches 52;	Indels 0.	Gaps 0.

OY	1	AGCCGGCGCTCAAGGCGCCCCAAAACCTTTCCTGTGTCTCTGACCCTCGGCCGACATC	60
Db	597	AGCCGGCGCTCAGAAGCGCCGACAACCTTTCCTGTGTCTCTGCCAACCGCGACATC	656
OY	61	CTGTGGCCACGCCTGTATCCCTTTCTGCGTGCCAAAGAGTGATGGGCTACTGGTAC	120
Db	657	CTGTGGCCACCCCTGTGATGCCCTTCTCCCTGGCCAAGACATGATGGGCTACTGGTAT	716
OY	121	TTCGGCAAGGCTTGTGCGAGATCTACCTGGCGCTCGACGCTCTTCTGCAAGCTGCTC	180
Db	717	TTCGGCAGAGTCTGTGCGGAGATTATCTGGCTCTGGATGTTTTAFTCTGCACCTGCTCG	776
OY	181	ATCGTGACACCTGTGCGCCATCAGCCCTGACCCGCTACTGTCATCACACAGGCCATCGAG	240
Db	777	ATCGTCCATCTGTGCGCATATAAGCTTGAACCGGCTACTGTGTGTCAAGGCGGCTCCAG	836
OY	241	TACAACCTGAAGCGCACGCGCGCGCGCATCAAAGC	275
Db	837	TACAACCTGAAGAGGACCCCTCAGCGCGTMAAGGC	871

RESULT	15		
LREA2AR			
LOCUS		777 bp	DNA
DEFINITION	LREA2AR Lamprey alpha2 adrenergic receptor gene fragment, sequence.		GSS 14-SEP-2001 genomic survey
ACCESSION	AL606561		
VERSION	AL606561.1	GI:15620571	
KEYWORDS	GSS; Alpha2 adrenergic receptor gene.		
SOURCE	Lethenteron reissneri.		
ORGANISM	Lethenteron reissneri		

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 777)
Hunter, C. and Elgar, G.
Alpha2 adrenergic receptor gene
Unpublished
2 (bases 1 to 777)
Hunter, C.
Direct Submission
Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource

FEATURES	Location/Qualifiers
source	1..777
	/organism="Lethenteron reissneri"
	/db_xref="taxon:7753"
BASE COUNT	169 a 237 c 241 g 130 t
ORIGIN	
Query Match	15.9%; Score 185.8; DB 17; Length 777;
Best Local Similarity	64.6%; Pred. No. 6e-25;
Matches 277; Conservative	0; Mismatches 152; Indels 0; Gaps 0

[illegible]

cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 98 a 315 c 286 g 143 t 25 others
ORIGIN

Query Match 24.28; Score 283.2; DB 9; Length 867;
Best Local Similarity 78.68; Pred. No. 4.4e-43;
Matches 346; Conservative 7; Mismatches 75; Indels 12; Gaps 1;

OY 15 GGGGCCCCAAACCTCTTCTGCTGCTGCTGCGCCGACATCCTGGCCAGCT 74
Db 440 GCGCCCAACAAACCTCTTCTGCTGCTGCTGCGCCGACATCCTGGCCAGCT 499
OY 75 CGTCATCCCTTTCGCTGGCCAAAGAGTCATGGGCTACTGCTACTTGGCAAGCTTG 134
Db 500 GGTATGCGCTTCTGCTGGCCAAAGAGTCATGGGCTACTGCTACTTGGGCAAGGTG 559
OY 135 GTGCGAGATCTACTGGCGCTGACGTGCTCTTGACAGCTGCTCATCGTGACCTGTG 194
Db 560 GTGCGGCGGTACTGGCGCTGATGATGCTGCTTGTGACACCTGCTGATCGTGTG 619
OY 195 CGCCATCAGCCTGGACCGCTACTGCTCATCACACAGGCCATCGAGTACAACCTGAAGCG 254
Db 620 TKCAACAGCCTGGACCGCTACTGCGGCTGACGACGAGCCGTCGAGTACAACCTGAAGCG 679
OY 255 CAGCGCGCGCGCATCAAGGCCATCATCACCGTGTGCTCATCTGCGCGCTCATCTC 314
Db 680 CACACACAGCGCGCTCAAGGCCATCATCTGCGCTGTGCTCAWCTCGCGCTCATCTC 739
OY 315 CTTCGCGCGCTCATCTCCATCGAAGAAAGGGCGCGCGCGCGCGCGAGCGCGCGA 374
Db 740 CTTCGCGCGCTGCTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 787
OY 375 GCGCGCGCTGCGAGATCAAGCAGACAGAGTGTGCTCATCTGCTGCTGCTGCTGCT 434
Db 788 CCGCAGTGGCGCTCAAGCAGACAGACCGGTACATCTGCTGCTGCTGCTGCTGCT 847
OY 435 CTTCGCTCCCTGCTCATCA 454
Db 848 CTTCGCGCGCTGCTCATCA 867

RESULT 11
BI459381 893 bp mRNA linear EST 21-AUG-2001
LOCUS 603200147F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5266354 5',
DEFINITION mRNA sequence.
ACCESSION BI459381
VERSION BI459381.1 GI:15250037
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 893)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

plate: LLAM1671 row: m column: 11
High quality sequence stop: 716.
Location/Qualifiers
1. 893

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5266354"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"

/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 149 a 303 c 290 g 151 t
ORIGIN

Query Match 19.7%; Score 230.6; DB 13; Length 893;
Best Local Similarity 81.0%; Pred. No. 2.8e-33;
Matches 406; Conservative 0; Mismatches 74; Indels 21; Gaps 11;
OY 1 AGCGCGCGCTCAAGCGCGCCCAAAACCTCTTCTGCTGCTGCTGCGCTCGG--CCGACA 58
Db 393 AGCGCGCGCTCAAGCGCGCCCAAAAGACTCTTCTGCTGCTGCTGCGCTCGGAGAAAT 452
OY 59 TCCGTGGGCGCACGCTCGT-CATCCCTTCTGCTGCGCCCAAGAGGTATGGGCTACTG 117
Db 453 TCCTGTGGCCACGCTCGTACATCCCTTCTGCTGCGCCCAAGAGGTATGGGCTACTG 512
OY 118 TACTTGGGCAA-GGCTTGTGCGG-AGATCTACTTGGCGCTGACGCTGCTTCTGACAGT 175
Db 513 TACTTGGGCAAAGGCTTGTGCGGAAGATCTACTTGGCGCTGACGCTGCTTCTGACAGT 572
OY 176 -CGTCATCTGTGACACCTGTGCGCCATCAGCCTGACCGCTACTGCTCATCACAGAGGC 234
Db 573 ACGTCCATCTGTGACACCTGTGCGCCATCAGCCTGACCGCTACTGCTCATCACAGAGGC 632
OY 235 ATCGAGTACAACCTGAAGCGCACGCGCGCGCGCGCGCATCAAGGCCATCATCACCGTGTG 294
Db 633 ATCGAGTACAACCTGAAGCGCACGCGCGCGCGCGCATCAAGGCCATCATCACCGTGTG 692
OY 295 GTC-ATCTCGGCGCTATCTCTCCG-----CCGCTCATCTCATCGAGAGAAGG 346
Db 693 GTCAATCTCGGCGTCACTCTCTCCGCGGCTTCACTCTCGAGAGAACAACGAGG 752
OY 347 GCGGCG 403
Db 753 CGGCAAGAGGCG 812
OY 404 GGTACGTCATCTGCTGTG--CATCGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 460
Db 813 GGTACGTAATTTGAGATCTGCAATGATTAATTGTTGCTGCTGCTGCTGCTGCTGCTGCT 872
OY 461 TGGTCTACGTGCGCATCTACC 481
Db 873 TGG-CAACGCGCGCATATACC 892

RESULT 12
AL544577/c 1135 bp mRNA linear EST 16-FEB-2001
LOCUS AL544577 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI021YC24 3
DEFINITION prime, mRNA sequence.
ACCESSION AL544577
VERSION AL544577.1 GI:12877057
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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QY      846  CCGGACGCGGCTGCAGGCGCGGGGAGAGACGCGTCCGGGCTGCCAAGCGTCGCGCTG  905
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Db      358  CCGGACGCGGCTGCAGGCGCGGGGAGAGAGCGGCTCGGGCTGCCAAGCGTCGCGCTG  299
QY      906  GCGCGGGCGGACAGACCGCGAGAGACGCGTTCACGTTGCTGCGCCGTGTCATCGGAGT  965
          |||
Db      298  GCGCGGGCGGACAGACCGCGAGAGACGCGTTCACGTTGCTGCTGGCGGTGTCATCGGAGT  239
QY      966  GTTCGTGTGTGCTGTGTTCCCTTCTTCTTTCACCTACACGCTACAGCGCGTCGGGTGCTC  1025
          |||
Db      238  GTTCGTGTGTGCTGTGTTCCCTTCTTCTTTCACCTACACGCTACAGCGCGTCGGGTGCTC  179
QY      1026 CGTGCCACGACGCGCTCTTCAAAATCTTCTGTGTTCCGCTACTGCAACAGCTCGTTGAA  1085
          |||
Db      178  CGTGCCACGACGCGCTCTTCAAAATCTTCTGTGTTCCGCTACTGCAACAGCTCGTTGAA  119
QY      1086 CCGCGTCATCTACACCATCTTCAACACGATTTCCGCCCGCCCTTCAAGAGATCCTCTG  1145
          |||
Db      118  CCGCGTCATCTACACCATCTTCAACACGATTTCCGCCCGCCCTTCAAGAGATCCTCTG  59
QY      1146 TCGGGGGGACAGGAAGCGGAT  1166
          |||
Db      58  TCGGGGGGACAGGAAGCGGAT  38
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RESULT 9
BO887729      988 bp      mRNA      linear      EST 16-AUG-2002
LOCUS      BO887729
DEFINITION  AGENCOURT_8764335 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313133
              5', mRNA sequence.
```

```
ACCESSION  BO887729
VERSION     BO887729.1
KEYWORDS    GI:22279743
SOURCE      house mouse.
```

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 988)

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: Susan L. Sullivan, PhD.

CDNA Library Preparation: Resgen, Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: LLM13739 row: m column: 06

High quality sequence start: 8

High quality sequence stop: 509.

Location/Qualifiers

FEATURES

source

1. 988

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:6313133"

/clone_1ib="NIH_MGC_129"

/lab_host="DH10B (phage-resistant)"

/note="Organ: olfactory epithelium; Vector:

pcmv-SPORT6.1.cdb; Site_1: EcoRV; Site_2: NotI; Cloned

unidirectionally. Primer: Oligo dT. Average insert size

2.2 kb. Constructed by Resgen, Invitrogen Corp. Note: this

is a NIH_MGC Library."

BASE COUNT 158 a 349 c 300 g 181 t

ORIGIN

Query Match 26.5%; Score 310.2; DB 14; Length 988;
Best Local Similarity 74.3%; Pred. No. 4,2e-48;
Matches 423; Conservative 0; Mismatches 133; Indels 13; Gaps 2;

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QY      1  AGCCGCGGCTCAAGCGCGCCCAAAACCTCTTCCTGTGTCTCTGGCCTCGGCCG-ACAT  59
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Db      31  AGCCGAGCACTGCGCGCGCCCGCAGAACCTCTTCCTGTGTCTCTGGCCCTACACAT  90
QY      60  CCTGTGGCCACGCTCGTCAATCCCTTCTCCTGTGGCCAAAGAGTCAATGGGCTACTGTGTA  119
          |||
Db      91  CCTGTGGCCACACTGGTCAATGCCCTTTCTCTGTGGCCAAATGAGCTCATGGCCCTACTGTGTA  150
QY      120 CTTGCGCAAGGCTTGTGTGCGAGATCTACCTGGCGGCTCGACGTGCTCTTCTGACGTGTC  179
          |||
Db      151 CTTGCGCAAGTGTGTGTGTGTATACCTGGCAGCTGAGCTGCTCTTCTGACCTGTC  210
QY      180 CATCGTGACCTGTGCGCCATACGCTTGACCGGCTACTGTCCATCACACAGGCCATCGA  239
          |||
Db      211 CATCGTGACCTGTGTGCCATTAATGTGACCGCTACTGTGGGTGACGCAAGCGGTAGA  270
QY      240 GTACAACCTGAAGCGACGCGCGCGCGCATCAAGGCCATCATCAACGCTGTGGTCAAT  299
          |||
Db      271 GTACAACCTGAAGCGACGCGCGCGCGGTGCAAGGCCACCATCGTGGCGGTGCTCAT  330
QY      300 CTCGGCGGTCAATCTCTTCCCGCGGCTCATCTCCATCGAGAAGAGGGCGGCGGCGG  359
          |||
Db      331 CTCGGGTGCAATCTCTTCCCGCGGCTCATCTCCATCGAGAAGAGGGCGGCGGCGGCGG  388
QY      360 CCGCGACCGCGCGGACGCGGCTGCGAGATCAACGACAGAGAGTGTACGTCTCTGTC  419
          |||
Db      389 -----GCCATACCGCAGTGGCGGCTCAACGATGAGACCTGTATCATCTGTCTCTC  438
QY      420 GTGATCGGCTCTCTTCCGCTCCCTGCTCATCATGATCTGTGTACGTGGCATCTA  479
          |||
Db      439 CTGATAGGCTCTCTTCTTCCGCGGCTGCTCATCATGAGGCTGTGTATGCGGCATCTA  498
QY      480 CCAGATCGCCCAAGCGTCGACACCGCGGTCGACACCCAGCCGCGGGTCCGGACGCGTCCG  539
          |||
Db      499 CCGCGTGCCCAAGCTGCGCACGCGTACGCTCAGCGAAGAACGCGGCGCGCGCGCGCA  558
QY      540 CCGCGCGCGCGGGGCGACCGAGCGCAGGC  568
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Db      559 CCGCGCGTCCCGGACACAGAGATGGGC  587
```

RESULT 10

AL530418 867 bp mRNA linear EST 13-FEB-2001

LOCUS

DEFINITION

AL530418 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD007YE02 5

prime, mRNA sequence.

AL530418

AL530418.1 GI:12793911

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 867

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DD007YE02"

/clone_1ib="LTI_NFL001_NBC4"

/sex="male"

/tissue_type="neuroblastoma cells"

/lab_host="DH10B"

/note="Organ: brain; Vector: pcMWSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

REFERENCE 1 Phasianinae; Gallus.
AUTHORS 1 (bases 1 to 855)
TITLE Hunter,C. and Elgar,G.
JOURNAL Alpha2 adrenergic receptor gene
REFERENCE 2 Unpublished
AUTHORS 2 (bases 1 to 855)
TITLE Hunter,C.
JOURNAL Direct Submission
Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hgmrc.mrc.ac.uk
FEATURES
source location/Qualifiers
1..855
BASE COUNT 201 a 248 c 245 g 161 t
ORIGIN
Query Match 27.4%; Score 320.2; DB 17; Length 855;
Best Local Similarity 65.8%; Pred. No. 5.6e-50;
Matches 626; Conservative 0; Mismatches 223; Indels 102; Gaps 7;
QY 106 ATGGCTACTGTGTAATTCGGCAAGCGTGGTGGAGATCTACTTGGCGCTGAGCTGCTC 165
Db 1 ATGGGTTATGTGTAATTCGGCAAGCTGTGGTGGAGATCTACTTGGCGCTGAGCTGCTG 60
QY 166 TTCTGCACGTGCTGCATCGTGCACCTGTGGCCCATCAGCCTGGACCGCTACTGTGCATC 225
Db 61 TTCTGCACCTCTCCATCGTGCATCTGTGGCCCATCAGCCTGGACCGCTACTGTGCATC 120
QY 226 ACACAGGCCATGAGTACACACTGAAGCGGACAGCGCGCGCCGATCAAGGCCATCATCATC 285
Db 121 ACACAGGCCATGAGTACACACTGAAGCGGACAGCGCGCGCCGATCAAGGCCATCATCATC 180
QY 286 ACCGTGTGGTCAATCTCGCGCGTCAATCTCTCCCGCGCTCATCTCCATGAGAGAAG 345
Db 181 ATCGTCTGGTCAATCTCGCGCGTCAATCTCTCTCCCGCGCTCATCTCCATGAGAGAAG 240
QY 346 GCGGCG 405
Db 241 AGTGGCGAGAGGTGAGCAGTGGGC---GGCAGGATGCAAGATCAATGACGAGAAGTGG 297
QY 406 TACGTCAATCTGCTGCTGATCGGCTCTCTTCTGCTCCCTGCTCATCATGATCCTGGTC 465
Db 298 TACATCAATCTGCTGCTGATCGGCTCTCTTCTTCAACCCGCTGCTCATCATGATCCTGGTC 357
QY 466 TACGTGCGCATCTACAGATGCCAAGCGTGCACCGCGTGCACCCAGCCGCGCGGT 525
Db 358 TACGTGCGCATCTATCAGATGCCAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 413
QY 526 CCGGAGCGCGTGCAGCG 585
Db 414 -----GCCAGAGCG 453
QY 586 GAGCGAGCG 645
Db 454 AAGGAGGAGCGCT-----CCTGCTCAGGCCAGCTCAATGAGAGA 493
QY 646 GCCCTGGCGAGCG 705
Db 494 AAGCGCGCGGAGCTGGCGATGGGCGAGG-AGGAGAGGTTCAACGGTATAGACATGAGGAA 552
QY 706 AGCTGCTCTCCGACCAAGCG 765
Db 553 ACCTCCTCTCTGAGCAGCAGGAGAACACAC---AGCCCAAGAAATCAGAGAGACCCCTG 609
QY 766 CGGGGCAAGGCAAGCG 825
Db 610 CGGGGAAAGACCAAGCTAAGCTGAGCCAGATTAAAGCTTGGGACACTTTGCCAGAGAG 669
QY 826 GGGCGGGGGCGAGCGGGGATCGGAGCGCGCGCTGACGGCGCGGAGAGAGCGCGTGGG 885
Db 670 ACGGAGGAGGAGA-----GG 684

QY 886 CTGCGCAAGCGCTCGCGCTGGCGCGCGCGCGCGAGAACCGCGGAGAACGGCTTCACGTTGCTG 945
Db 685 AACACCAAGAGGTCCCGGTGGAGGGGCGAGAACCGCGGAGAACGTTTCACGTTGCTG 744
QY 946 CTGGCGGTGTCATCGGAGTGTTCGTGTGTGCTGTGTTCCCTTCTTCTTACCTACAGC 1005
Db 745 CTGGCGGTGTCATGTTGGGCTTCTGTCATCTGCTGTGTTCCCATTTCTTCTTACCTACAGC 804
QY 1006 CTCACGGCGCTGGG-----TGCTCCGTGCCACGACGCTCTTCAAAATTC 1050
Db 805 CTGACCGCGGTCTGCAAGAGCTGCTGTGCTCCCTCCACCTCTTCAAGTTTC 855

RESULT 8
BM352981/c 358 bp mRNA linear EST 07-JAN-2002
LOCUS
DEFINITION
1969h02.y1 HR85 1stlet Homo sapiens cDNA 5' similar to SW:A2AA_HUMAN
P08913 ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.
ACCESSION
BM352981
VERSION
BM352981.1 GI:18085339
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 358)
AUTHORS
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Maira,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T.,
, Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: 1969h02.x1
COMMENT
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 342.
location/Qualifiers
1..358

FEATURES
source
1..358
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HR85 1stlet"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

BASE COUNT 76 a 114 c 115 g 53 t
ORIGIN
Query Match 27.3%; Score 319.4; DB 13; Length 358;
Best Local Similarity 99.7%; Pred. No. 7e-50;
Matches 320; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ACCESSION mRNA sequence.
 VERSION B1838282
 KEYWORDS B1838282.1 GI:15949832
 SOURCE EST.
 ORGANISM human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 740)
 AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM11559 row: 1 column: 04
 High quality sequence stop: 740.
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 1..740
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 /db_xref="taxon:9606"
 /clone="IMAGE:5222475"
 /clone_lib="NIH_MGC_120"
 /lab_host="DH10B"
 /note="Organ: pooled pancreas and spleen; Vector:
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 source anonymous pool of spleen and pancreas from 28 yo
 male. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 1.5 kb, insert size range 1-2.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 025. Note: this is a NIH_MGC library."
 BASE COUNT 115 a 240 c 235 g 150 t
 ORIGIN
 Query Match 33.8%; Score 395; DB 13; Length 740;
 Best Local Similarity 100.0%; Pred. No. 6.5e-64;
 Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 776 GCAAGGCCGAGCGAGCCAGGTGAAGCCGGCGACAGCCTGCGCGCGCGCGGGG 835
 Db 1 GCAAGGCCGAGCGAGCCAGGTGAAGCCGGCGACAGCCTGCGCGCGCGGGG 60
 OY 836 CGACGGGATCGGACGCCGCGTCAGAGCGCGGGGAGAGCGCGTGGGCGCTGCCAAGG 895
 Db 61 CGACGGGATCGGACGCCGCGTCAGAGCGCGGGGAGAGCGCGTGGGCGCTGCCAAGG 120
 OY 896 CGTCGGCTGGCGGGCGGCGAGAACCGCGAGAGCGCTTCACGTTCTGCTGGCCGTGG 955
 Db 121 CGTCGGCTGGCGGGCGGCGAGAACCGCGAGAGCGCTTCACGTTCTGCTGGCCGTGG 180
 OY 956 TCATCGGAGTGTTCGTGGTGTGCTGTTCCCTCTCTTCTTACCTACACGCTCAGGCCG 1015
 Db 181 TCATCGGAGTGTTCGTGGTGTGCTGTTCCCTCTCTTCTTACCTACACGCTCAGGCCG 240
 OY 1016 TCGGCTGCTCCGTGACGACGAGCTCTTCAAAATCTTCTTCTGTTCCGCTACTGCAACA 1075
 Db 241 TCGGCTGCTCCGTGACGACGAGCTCTTCAAAATCTTCTTCTGTTCCGCTACTGCAACA 300
 OY 1076 GCTCGTTGAACCCGGTCACTTACACCATCTTCAACACGATTTCCGCGCGCTTCAAGA 1135
 Db 301 GCTCGTTGAACCCGGTCACTTACACCATCTTCAACACGATTTCCGCGCGCTTCAAGA 360
 OY 1136 AGATCCTCTGTGCGGGGACAGAGCGGATCGTG 1170
 Db 361 AGATCCTCTGTGCGGGGACAGAGCGGATCGTG 395

RESULT 5
 LOCUS BB643669/c
 DEFINITION BB643669
 ACCESSION BB643669
 VERSION BB643669
 KEYWORDS BB643669.1 GI:16478370
 SOURCE EST.
 ORGANISM house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 691)
 AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
 Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,
 M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
 Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,
 D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
 Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
 Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 Unpublished (2001)
 COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gscl.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,
 M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
 Watanahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,
 S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
 Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,
 Y. and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaoka,I., Aizawa,
 K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
 Hayashizaki,Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 e mouse tissues.

FEATURES

source

Location/Qualifiers
 1..691
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="B230352011"
 /clone_lib="RIKEN full-length enriched, adult male corpora
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 /sex="male"
 /tissue_type="corpora quadrigemina"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Site_1: SalI; Site_2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in

Query Match 41.9%; Score 490.4; DB 14; Length 492;
Best Local Similarity 99.8%; Pred. No. 1e-81;
Matches 491; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 499 ACCCGCGTGCACCCAGCCGCGGGGTCCGAGACCCGCTGCCGCGCGCCGCGGGGGGCACACC 558
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Db 492 ACCCGCGTGCACCCAGCCGCGGGGTCCGAGACCCGCTGCCGCGCGCCGCGGGGGGCACACC 433
QY 559 GAGCGCAGGGCCCAACGGTCTGGCCCCCGAGCGCGACCGCGGGGGGGGGGGGCAGAGGCC 618
|||||
Db 432 GAGCGCAGGGCCCAACGGTCTGGGGCCCCGAGCGCGCGGGGGGGGGGGGCAGAGAGGCC 373
QY 619 GAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAGACCCGCGCGCGCGGGGGCGCGC 678
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Db 372 GAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAGACCCGCGCGCGGGGGCGCGC 313
QY 679 GACACCGACGCGCTGAGCTGGAGGAGAGCTGCTTCCGACACGCGCGAGCGGCTCCA 738
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Db 312 GACACCGACGCGCTGAGCTGGAGGAGAGCTGCTTCCGACACGCGCGAGCGGCTCCA 253
QY 739 GGGCCCCGACAGCCGAGCGCGGTCCCGGGGCAAGGCAAGGCCCGAGCGAGCCAGGTG 798
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Db 252 GGGCCCCGACAGCCGAGCGCGGTCCCGGGGCAAGGCAAGGCCCGAGCGAGCCAGGTG 193
QY 799 AAGCCGGCGACAGCCTGCGCGCGCGCGGGCGCGGGGCGAGCGGGATCGGAGCGCGGCT 858
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Db 192 AAGCCGGCGACAGCCTGCGCGCGCGCGGGCGCGGGGCGAGCGGGATCGGAGCGCGGCT 133
QY 859 GCAGGGCGGGGGAGGAGCGCGTGGGGGCTGCCAAGCGCTGCCGCTGGCGCGGGCGGCGAG 918
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Db 132 GCAGGGCGGGGGAGGAGCGCGTGGGGGCTGCCAAGCGCTGCCGCTGGCGCGGGCGGCGAG 73
QY 919 AACCGCGAGACCGCTTCACGTTCTGCTGGCCGTGTATCGAGTGTTCGTGTGTC 978
|||||
Db 72 AACCGCGAGACCGCTTCACGTTCTGCTGGCCGTGTATCGAGTGTTCGTGTGTCGA 13
QY 979 TGGTTCCTCTTC 990
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Db 12 TGGTTCCTCTTC 1

RESULT 3 453 bp mRNA linear EST 29-APR-2002
BQ129312/c 1j34d05.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
LOCUS cdNA clone IMAGE:6136736 5' similar to SW:A2AA_HUMAN P08913
DEFINITION ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.

ACCESSION BQ129312
VERSION BQ129312.1 GI:20203223
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 453)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: 1j34d05.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

TITLE
JOURNAL
COMMENT
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:

Washington University Genome Sequencing Center This clone is
available royalty-free through LNL; please contact the IMAGE
consortium (info@image.lnl.gov) for further information
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco.

FEATURES
source

1..453
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/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoI of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 41 a 189 c 164 g 59 t
ORIGIN

Query Match 38.7%; Score 453; DB 14; Length 453;
Best Local Similarity 100.0%; Pred. No. 9.5e-75;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 538 GCCGCGCGCGCGGGGCAACCGAGCGCAGCGCCCAACGGTGTGGGCCCGAGCGCAGCGCG 597
|||||
Db 453 GCCGCGCGCGCGGGGCAACCGAGCGCAGCGCCCAACGGTGTGGGCCCGAGCGCAGCGCG 394
QY 598 GGGCCGGGGGGGGCGCAGAGCGCCGAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAG 657
|||||
Db 393 GGGCCGGGGGGGGCGCAGAGCGCCGAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAG 334
QY 658 CCGCGCGCGCGCGCGCGCGCGCGCAGACCGCGCGTGGAGACTGGAGAGAGACTGCTTCC 717
|||||
Db 333 CCGCGCGCGCGCGCGCGCGCGCGCAGACCGCGCGTGGAGACTGGAGAGAGACTGCTTCC 274
QY 718 GACCACGCGGAGCGGCTCCAGGGCCCCCGCAGACCCGAGCGCGGCTCCCGGGGCAAAAGGC 777
|||||
Db 273 GACCACGCGGAGCGGCTCCAGGGCCCCCGCAGACCCGAGCGCGGCTCCCGGGGCAAAAGGC 214
QY 778 AAGCGCCGAGCGAGCCAGGTAAAGCCGGGGCGACAGCCTGCCGCGCGCGGGGGGGCG 837
|||||
Db 213 AAGCGCCGAGCGAGCCAGGTAAAGCCGGGGCGACAGCCTGCCGCGCGGGGGGGGGCG 154
QY 838 ACGGGGATCGGGAGCGCGCGCTCGAGGGCGCGGGGAGAGAGCGCGTGGGGCTGCCAAGCGG 897
|||||
Db 153 ACGGGGATCGGGAGCGCGCGCTCGAGGGCGCGGGGAGAGAGCGCGTGGGGCTGCCAAGCGG 94
QY 898 TCGCGCTGGCGCGGGCGCAGAACCGCGAGAGCGCTTCAGTGTGCTGGCCGTGGTGC 957
|||||
Db 93 TCGCGCTGGCGCGGGCGCAGAACCGCGAGAGCGCTTCAGTGTGCTGGCCGTGGTGC 34
QY 958 ATCGAGTGTTCGTGTGTGCTGTCCCTTC 990
|||||
Db 33 ATCGAGTGTTCGTGTGTGCTGTCCCTTC 1

RESULT 4 740 bp mRNA linear EST 04-OCT-2001
BI838282
LOCUS BI838282
DEFINITION 603083213F1 NIH_MGC_120 Homo sapiens cdNA clone IMAGE:5222475 5',

Fax: 617-495-8557
Email: dmeltone@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)

Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 445.

FEATURES

source

1.561
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/db_xref="taxon:9606"
/clone="IMAGE:6136374"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 63 a 215 c 210 g 73 t
ORIGIN

Query Match 47.9%; Score 561; DB 14; Length 561;
Best Local Similarity 100.0%; Pred.No. 7.5e-95;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 430 TCCTTCTTGGCTCCCTGCTCATCATGATCTGTCTACGTGGCATCTACCAATCGCC 489
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OY 490 AAGCGTGGACCCGCGTGGCCACCCAGCCGCGGGTCCGACGCCGTGCGCCGCCGCCG 549
Db 501 AAGCGTGGACCCGCGTGGCCACCCAGCCGCGGGTCCGACGCCGTGCGCCGCCGCCG 442
OY 550 GGGGGCACCGAGCCGAGGCCCAACGGTCTGGCCCCGACGCCAGCGCGGGCGGGGGGC 609
Db 441 GGGGGCACCGAGCCGAGGCCCAACGGTCTGGCCCCGACGCCAGCGCGGGCGGGGGGC 382
OY 610 GCAGAGCGCAACCGCTGCCCCACCCAGCTCAACGGCGCCCCCTGGAGCCCCCGCGGCC 669
Db 381 GCAGAGCGCAACCGCTGCCCCACCCAGCTCAACGGCGCCCCCTGGAGCCCCCGCGGCC 322
OY 670 GGGCGCGCGACACCGACCGCGCTGGACCTGGAGGAGAGCTGCTTCCGACCAAGCCGAG 729
Db 321 GGGCGCGCGACACCGACCGCGCTGGACCTGGAGGAGAGCTGCTTCCGACCAAGCCGAG 262
OY 730 CGGCTTCAGGGGGCCCCGACAGCCGAGCGGTCGCCGGGGCAAGGCAAGCCCGAGCG 789
Db 261 CGGCTTCAGGGGGCCCCGACAGCCGAGCGGTCGCCGGGGCAAGGCAAGCCCGAGCG 202
OY 790 AGCCAGGTGAAGCCGGGGCAGACCTGCGCGCGCGGGCGGGGGCGAGGGGATCGGG 849
Db 201 AGCCAGGTGAAGCCGGGGCAGACCTGCGCGCGCGGGCGGGGGCGAGGGGATCGGG 142
OY 850 ACGCCGGCTGCAGGGCGCGGGGAGAGAGCGGTCGGGGCTGCCAAGCGCTGCGCTGGCGC 909
Db 141 ACGCCGGCTGCAGGGCGCGGGGAGAGAGCGGTCGGGGCTGCCAAGCGCTGCGCTGGCGC 82
OY 910 GGGCGCGCAAGCCGCGAGAAAGCGCTTACGTTCTGCTGGCCGCTGTCATCGAGTGTTC 969

Db 81 GGGCGCGCAAGCCGCGAGAAAGCGCTTACGTTCTGCTGGCCGCTGTCATCGAGTGTTC 22
OY 970 GTGCTGTGCTGTTCCCTTC 990
Db 21 GTGCTGTGCTGTTCCCTTC 1

RESULT 2

BM967243/c 492 bp mRNA linear EST 29-APR-2002

LOCUS

1j32c09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens

DEFINITION

CDNA clone IMAGE:6136336 5' similar to SW:A2AA_HUMAN P08913

ACCESSION

BM967243 ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.

VERSION

BM967243.1 GI:19561038

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

1 (bases 1 to 492)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T., Jackson,Y. and Bowers,Y.

TITLE

Endocrine Pancreas Consortium

JOURNAL

unpublished (2000)

COMMENT

Other ESTs: 1j32c09.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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Tel: 617-495-1812
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Email: dmeltone@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 455.

FEATURES

source

1.492

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6136336"

/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"

/sex="Both"

/tissue_type="Islets of Langerhans"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 44 a 202 c 182 g 64 t
ORIGIN

Gencore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 12:34:42 ; Search time 2326.51 Seconds
(without alignments)
8144.696 Million cell updates/sec

Title: US-09-636-259B-1
Perfect score: 1170
Sequence: 1 agccgcgcgcctcaaggcgcc.....gggacaggaagcgatcgtg 1170

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estmu:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	561	47.9	561	14	BM967248	BM967248 ij32d04.y
C 2	490.4	41.9	492	14	BM967243	BM967243 ij32c09.y
C 3	453	38.7	453	14	BQ129312	BQ129312 ij34d05.y
C 4	395	33.8	740	13	BI838282	BI838282 603083213
C 5	373	31.9	691	10	BB643669	BB643669 BB643669
C 6	322.6	27.6	1077	9	AL544609	AL544609 AL544609

C	7	320.2	27.4	855	17	GGA2AAR	AL606540 Chicken a
C	8	319.4	27.3	358	13	BM352981	BM352981 1g69h02.y
C	9	310.2	26.5	988	14	BQ887729	BQ887729 AGENCOURT
C	10	283.2	24.2	867	9	AL530418	AL530418 AL530418
C	11	230.6	19.7	893	13	BI459381	BI459381 603200147
C	12	199.8	17.1	1135	9	AL544577	AL544577 AL544577
C	13	194.2	16.6	350	10	BE648878	BE648878 UI-M-BH2.
C	14	191.4	16.4	896	17	CNS03BQW	AL236849 Tetraodon
C	15	185.8	15.9	777	17	LREA2AR	AL606561 Lamprey a
C	16	185.6	15.5	801	17	GGA2CAR	AL606541 Chicken a
C	17	181.2	15.3	966	17	CNS02NV2	AL205895 Tetraodon
C	18	179.4	15.3	1010	17	CNS04CMO	AL284651 Tetraodon
C	19	175.8	15.0	921	17	CCLA2BAR	AL606559 Herring a
C	20	173.4	14.8	691	17	HIPAA2AAR	AL606565 Sea Horse
C	21	172.6	14.8	774	17	AGAA2C2AR	AL606580 Toothcarp
C	22	172.2	14.7	882	17	HIPAA2C2AR	AL606551 Frog alph
C	23	171.4	14.6	697	17	RESA2AAR	AL606560 Horse alp
C	24	169.6	14.5	872	17	ECAA2BAR	AL606576 Sturgeon
C	25	167.8	14.3	825	17	ARUA2BAR	AL217170 Tetraodon
C	26	166.8	14.3	890	17	CNS02WK9	AL606574 Sturgeon
C	27	164.8	14.1	693	17	ARUA2AAR	AL606581 Toothcarp
C	28	163.4	14.0	723	17	AGAA2A2AR	AL549866 AL549866
C	29	161.8	13.8	829	9	AL549866	AL606570 Shark alp
C	30	160.6	13.7	705	17	HGRA2AAR	AL237702 Tetraodon
C	31	160.2	13.7	805	17	CNS03CEL	AL606564 Ostrich a
C	32	160	13.7	753	17	SCAA2CAR	AL606584 Zebrafish
C	33	159.4	13.6	788	17	DREA2CAR	AL606553 Gar alpha
C	34	158.6	13.6	699	17	LOSA2AAR	AL606569 Sea Horse
C	35	154.4	13.2	981	17	HIPAA2BAR	AL573897 AL573897
C	36	151.4	12.9	872	9	AL573897	AL244403 Tetraodon
C	37	151	12.9	860	17	CNS03HKO	AL606557 Herring a
C	38	148.8	12.7	780	17	CCLA2CAR	T39448 ya06a09.r2
C	39	146.4	12.5	301	14	T39448	BM6447571 170006873
C	40	143.4	12.3	535	13	BM647571	AI461341 fb43d01.x
C	41	141.8	12.1	451	9	AI461341	BI836679 603089610
C	42	141.4	12.1	702	13	BI836679	AL606579 Toothcarp
C	43	141.4	12.1	798	17	AGAA2C1AR	AK018378 Mus muscu
C	44	140.8	12.0	2146	11	AK018378	AL234292 Tetraodon
C	45	140.4	12.0	975	17	CNS039RV	

ALIGNMENTS

RESULT 1
BM967248/c 561 bp mRNA linear EST 29-APR-2002
LOCUS ij32d04.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
DEFINITION cDNA clone IMAGE:6136374 5' similar to SW:A2AA.HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ; mRNA sequence.

ACCESSION BM967248
VERSION BM967248.1 GI:19561047
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 561)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)

TITLE
JOURNAL
COMMENT
Other_ESTS: ij32d04.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept Of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812

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Db 1249 TCACGTGAACCCGTGTATCTACACATCTCAACAGGACTTCGCGCTGCTTCCGAGG 1308
OY 1138 ATCCTCTGTGCG 1148
Db 1309 ATCCTGTGCGG 1319
RESULT 15
AAI99906
ID AAI99906 standard; DNA; 1344 BP.
XX AAI99906;
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2BAR third intracellular loop variant encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1344
FT /*tag= a
FT /product= "alpha-2BAR"
FT /note= "sequence is deleted for a 9 nucleotide
FT polymorphic site found at nucleotides 901-909
FT of the wildtype alpha-2BAR protein (AAI99905)"
XX
PN WO200179561-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US12575.
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMAL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
DR P-PSDB; AAM52118.
XX
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site .
XX
PS Claim 5; Page 144-145; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (ggggcggggcg) or (B) (ggggcggctgag) at
CC positions 961-972 of (IIIV). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,

CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolficine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the third intracellular loop of
CC the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide
CC polymorphic site found at nucleotides 901-909 of the wildtype gene
CC (AAI99905).
XX
SQ Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 other;
Query Match 34.4%; Score 402.2; DB 23; Length 1344;
Best Local Similarity 63.4%; Pred. No. 1.4e-57;
Matches 769; Conservative 0; Mismatches 368; Indels 76; Gaps 7;
OY 1 AGCGCGCGCTCAAGCGCGCCCAAAACCTCTCTGCTGTCTCTGGCCCTGCGCCGACATC 60
Db 118 AGCGGCTGCTGCGCGCCCTCAAGACCTGTCTGCTGCTGCGCCGCGCCGACATC 177
OY 61 CTGCTGCCACGCTCGTCATCCCTTTCTCGCTGCGCCCAAGGTCATGCGCTACTGTGTC 120
Db 178 CTGCTGCCACGCTCGTCATCCCTTTCTCGCTGCGCCCAAGGTCATGCTGCTGCTGTC 237
OY 121 TTCGCAAGGCTTGTGCGAGATCTACCTGCGGCTGCACGCTGCTCTTCTGCACGTGTC 180
Db 238 TTCGCGCGCACGCTGTGCGAGGTACTGCGGCTGCACGCTGCTCTTCTGCACCTGTC 297
OY 181 ATCGTGACCTGTGCGCATGACCTTGACCGCTACTGCTGCTACACAGGCCATCGAG 240
Db 298 ATCGTGACCTGTGCGCATGACCTTGACCGCTACTGCGGCTGCAGCGCGGCTGAG 357
OY 241 TACAACCTGAAGCGCACGCGCGCGCCGATCAAGCCATCATCATCAGCTGTGGTCATC 300
Db 358 TACAACCTGAAGCGCACGCGCGCGCCGATCAAGCTCATCATCTCTGCTGTGCTCATC 417
OY 301 TCGCGCTCATCTCTTCCCGCGCTCATCTCTGATCGAAGAGGCGCGCGCGCGCG 360
Db 418 GCGCGCTCATCTCTGCTGCGCGCGCGCGCTCATCT-----ACAAGGCGCACGAGGCGCC 468
OY 361 CCGGAGCGCGCGCGAGCGCGCGCTGCGAGTCAACGACGAGAGTGTGATCTCTGTCG 420
Db 469 CAGCGCGCGCGCGCGCGCGCGAGTCAACGAGGAGGCTGTGATCTCTGCGCTTC 528
OY 421 TGCATCGGCTCTCTTCTGCTCCCTGCTCATGATCTCTGCTCACTGCGCATCTAC 480
Db 529 AGCATCGGATCTTCTTCTGCTCTGCTCATGATCTCTGCTCACTGCGCATCTAC 588
OY 481 CAGATCGCCAAAGCGTCGCAACCGGCTGCGACCGCGCGCGGCTCGGAGCGCTGCGC 540
Db 589 CTGATCGCCAAAGCGTCGCAACCGGAGGTCAGAGGCGCAAGG--GGGCTGCGGAGG 646
OY 541 GCGCGCGCGCGCGAGCGCGGCGCAAGGCTGTGCGCGCGCGCGAGCGAGCGGCGG 600
Db 647 GTGAGTCCAAGCAGCGCGCGAGCGAGCATGTGCGGCTTGTGCGCTCAAGCAACTGCCAG 706
OY 601 CCGGGG-----GGCGAGAGGCGGAACCGCTGCCACCGCTCAACGGCGCGCTGCGG 655
Db 707 CCCTGCGCTCTGTGCGCTTCTGCGAGAGGTCAACGAGCATCGAAGTCCACTGGGAGA 766
OY 656 AGCGCGCGCGCGCGCGCGCGCGCGAGCAGCGCGCTGACCTGAGAGAGCTGCTT 715
Db 767 AGGAGGAGGAGAGAGCCCTGAAGATACTGGAGCCCGGCGCTTGCACCCAGTTGGGCTG 826
OY 716 CCGAGCAGCGCGAGCGG-----CTCCAGGGCC 743
Db 827 CCCTTCCCAACTCAGGCCAGGCGCAGAAGAGGCTTTGTGGGCGATCTCCAGAGGATG 886
OY 744 CCGCAGACCGAGCGCGCTCCCGCGGCGCAAGGCAAGCGCGCGAGCGAGGTAAGCC 803
Db 887 AAGCTGAAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 946

AAD04761
ID AAD04761 standard; DNA; 1344 BP.
XX
AC AAD04761;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human alpha2B-adrenoceptor (alpha2B-AR) variant gene.
XX
KW Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
KW norepinephrine; ephrine; therapy; vascular contraction; variant;
KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
KW acute myocardial infarction; AMI; Prinzmetal's variant; ds.
XX
OS Homo sapiens.
FH
FT Key Location/Qualifiers
FT CDS 1..1344
FT /tag= a
FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
FT variant protein"
XX
PA WO200129082-A1.
XX
PD 26-APR-2001.
XX
PF 20-OCT-2000; 2000WO-FI00913.
XX
PR 22-OCT-1999; 99US-0422985.
XX
PI (JUVA-) JUVANTIA PHARMA LTD OY.
XX
PI Snapir A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
PI Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Nyssönen K;
PI Salonen R, Kaunanen J, Valkonen V;
XX
DR WPI; 2001-300318/31.
DR P-PSDB; AAE00989.
XX
PT New DNA molecule encoding variant specific adrenoceptor protein with
PT deletion of specific amino acids located in the third intracellular
PT loop of the polypeptide, for treating vascular contraction of coronary
PT arteries -
XX
PS Claim 3; Page 24-26; 37pp; English.
XX
CC The present sequence is a gene encoding human alpha2B-adrenoceptor
CC (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat
CC element (amino acids 298-309) of 12 glutamates, in an acidic stretch of
CC 18 amino acids (amino acids 294-311), located in the third intracellular
CC loop of the receptor polypeptide. The variant is obtained by deletion of
CC three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR
CC gene is located on chromosome 2. Alpha2-AR mediate many of the
CC physiological effects of the catecholamines, norepinephrine and
CC epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating
CC a mammal suffering from vascular contraction of coronary arteries and a
CC disease involving vascular contraction of coronary arteries which is
CC clinically expressed as coronary heart disease (CHD), unstable chronic
CC angina pectoris which is clinically expressed as Prinzmetal's variant
CC form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
CC gene therapy.
XX
SQ Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;
Query Match 34.4%; Score 402.6; DB 22; Length 1344;
Best Local Similarity 62.3%; Pred. No. 1.2e-57;
Matches 755; Conservative 0; Mismatches 384; Indels 72; Gaps 5;

QY 61 CTGGTGGCCACGCTCGTCATCCCTTCTCGCTGGCCAAAGAGTCTAGGCTACTGTAC 120
DB 178 CTGGTGGCCACGCTCGTCATCCCTTCTCGCTGGCCAAAGAGTCTAGGCTACTGTAC 237
QY 121 TTCGGCAAGGCTTGGTGGAGATCTACCTGGCGCTGACGTCTTCTGCAAGTCTCC 180
DB 238 TTCGGCGGACGCTGGTGGAGGTGTACCTGGCGCTGACGTCTTCTGCAAGTCTCC 297
QY 181 ATCGTGACCTGTGCGCAATCAGCCTGGACCGCTACTGTGTCATCACAGGCAATCGAG 240
DB 298 ATCGTGACCTGTGCGCAATCAGCCTGGACCGCTACTGTGCGCTGAGCGCGCTGAG 357
QY 241 TACAACCTGAAGCGCACGCGCGCGCGCATCAAGGCCATCATCATCACCCTGTGGTATC 300
DB 358 TACAACCTGAAGCGCACGCGCGCGCATCAAGGTGATCATCTCATCTGTGTGCTCATC 417
QY 301 TCGGCGGTATCTCTCTTCCCGCGCTCATCTCATCATCAGAGAAGGCGCGCGCGGCG 360
DB 418 GCGGCGGTATCTCTCTTCCCGCGCTCATCTCATCATCAGAGAAGGCGCGCGGCGG 468
QY 361 CCGCAGCGCGCGCGAGCGCGCGCGAGATCAACAGCAGAGAGTGTACGTATCTGTGCG 420
DB 469 CAGCGCGCGCGCGCGCGCGCGAGTCAACAGCAGAGAGTGTACGTATCTGTGCGTCC 528
QY 421 TGCAATCGGCTCTCTCTTCTGCTCCCTGCTCATCATCATCATCATCATCATCATCAT 480
DB 529 AGCATCGGATCTTCTTCTTCTGCTCTCTGCTCATCATCATCATCATCATCATCATCAT 588
QY 481 CAGATCGGCAAGCGTGCACACCGCGGTGCCACCA-----GCGCGCG 521
DB 589 CTGATCGGCAAGCGCAGCAACCGCAGAGTCCAGGCGCAAGGCGCGCGCGCGCGAGGT 648
QY 522 GGGTCCGAGCGCGCGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 579
DB 649 GAGTCCAAAGCAGCG 708
QY 580 -----GCG 615
DB 709 CTGGCTCTGTGGCTTCTGCGCAGAGAGGTCAACGCGACACTGGAATCCACTGGGAGAAG 768
QY 616 GCCGAACCGCTGCCACCCAGCTCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 675
DB 769 GAGCAGGCGGAGACCGCTGAAGATCTGGGACCGCGCGCGCGCGCGCGCGCGCGCGCG 828
QY 676 CGCGACACCGACCGCTGAGCCTGGAGGAGAGCTCTTCCGACCGCGCGCGCGCGCGCT 735
DB 829 CTTCCTCAACTCAGCG 888
QY 736 CCAGGCGCGCGCGCAGACCG 795
DB 889 GCTGAAG 948
QY 796 GTGAAGCGCGCGCGCAGACCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 855
DB 949 GCGTCAGCTTGCAGCG 1008
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DB 1009 CGTGCGCAGGTGCTCTCTGGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1068
QY 907 CCGCGCGCGCGCAGAACCGCGCGAGAGCGCTTCAAGTCTGCTGCGCGCGCGCGCGCGCG 966
DB 1069 CGGGCGCAGCTGACCGCGGAGAGAGCGCTTCACTCTGCTGCTGCTGCTGCTGCTGCT 1128
QY 967 TTGCTGTGTCTGTGTTCCCTCTTCTTCACTTACAGGCTCAGCGCGCTCGG----- 1020
DB 1129 TTGCTGTGTCTGTGTTCCCTCTTCTTCACTTACAGGCTGCGCGCGCGCGCGCGAG 1188
QY 1021 ---TGTCTGT 1077
DB 1189 CACTGCAAGGTGCG 1248
QY 1078 TCGTTGAACCGCGGTCTATCTACACCACTTCAACCAAGATTTCGCGCGCGCGCGCGCG 1137

RESULT 13
AAQ64890
ID AAQ64890 standard; DNA; 1382 BP.
XX
AC AAQ64890;
XX
DT 01-FEB-1995 (first entry)
XX
DE Human derived adrenaline alpha 2CII receptor DNA.
XX
KW adrenaline receptor; alpha CII; screening; detection; pharmacology;
KM drugs; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..2
FT /tag= a
FT /note= "5'-non translated region"
FT CDS 3..1376
FT /tag= b
FT /product= adrenaline alpha CII receptor
FT misc_feature 3..5
FT /tag= b
FT /note= "encodes Met; this codon may or may not be present, but can only be present if nucleotides 6-53 are also present"
FT misc_feature 6..53
FT /tag= c
FT /note= "this sequence may or may not be present"
FT 3'UTR 1377..1382
FT /tag= c
FT /note= "3'-non-translated region"
XX
PN JP06121686-A.
XX
PD 06-MAY-1994.
XX
PF 12-OCT-1992; 92JP-0272744.
XX
PR 12-OCT-1992; 92JP-0272744.
XX
PA (ASAH) ASAH KASEI KOGYO KK.
XX
DR WPI; 1994-185923/23.
DR P-PSDB; AAR54834.
XX
PT Adrenaline receptor gene encoding alpha 2CII receptor - for
PT screening drugs reactive to the alpha 2CII receptor
XX
PS Claim 1; Page 9-11; 13pp; Japanese.
XX
CC This sequence encodes the amino acid sequence of a polypeptide
CC (AAR54834) that constitutes human derived adrenaline alpha 2CII
CC receptor. this can be used for the study of the pharmacological
CC importance of the gene expression in humans.
XX
SQ Sequence 1382 BP; 165 A; 480 C; 497 G; 240 T; 0 other;

Query Match 40.1%; Score 468.8; DB 15; Length 1382;
Best Local Similarity 66.2%; Pred. No. 1.6e-68;
Matches 778; Conservative 0; Mismatches 347; Indels 51; Gaps 5;

Db 357 TTCGGGACAGTGTGGTGGGGCGGTGTACCTGGCGCTCGATGTGCTTTTGCACCTCTCG 416
QY 181 ATCGTGACACTGTGGCCATCAGCCTGGACCGCTACTGTTCATCACAGGCCATCGAG 240
Db 417 ATCGTGACATCTGTGTCCATCAGCCTTGACCGCTACTGTGTGATGACGAGCGCGTGA 476
QY 241 TACAACCTGAAGCGCAGCGCGCGCATCAAGCCATCATCAACCGTGTGGTCAATC 300
Db 477 TACAACCTGAAGCGCAGCAGCGCGCGTCAAGCCATCATCAACCGTGTGGTCAATC 536
QY 301 TCGGCGTCACTCTCTTCCGCGCTCATCTCATCGAAGAGGCGCGCGCGCGCG 360
Db 537 TCGGCGTCACTCTCTTCCGCGCGTGTCTCGCTTACCGCCAGCGCGCGCGCGCGCG 593
QY 361 CCGCAGCGCGCGCGCGCGCTGCGAGATCAACGACAGAGTGTGTACGTCTCTCG 420
Db 594 -----GCCCTACCGCGAGTGGCGGCTCAACGACGAGACCTGTACATCTCTCTCC 644
QY 421 TGCATCGGCTCTCTTCTCGCTCCCTGCTCATCATGATCTGTCTACGTGCGCATCTAC 480
Db 645 TGCATCGGCTCTCTTCTCGGCGCGCTCATCATGATGCGCTGTCTACGCGCGCATCTAC 704
QY 481 CAGATCGGCAAGCGTGGACCGCGCGTGGCACCCAGCGCGCGCGCGCGCGCGCGCG 540
Db 705 CGAGTGGCGCAAGCTGGCGACCGCGCGCTCAGCGAGAGCGCGCGCGCGCGCGCGAC 764
QY 541 GCG 600
Db 765 GGTGCGTCCCCGACTACCGA-----AAACGGCTGGCGCGCGCGCGCGCGCGCGAG 815
QY 601 CCGGGGCGCGCAGAGGCGCGCAACCGCTGCCACCGCTCAACGCGCGCGCGCGCGAG 660
Db 816 GAGAACGGG-----CACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGCA 862
QY 661 GCG 720
Db 863 GAGCAGCGCAGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 922
QY 721 CACGCGAGCGCGCTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 923 GCGAGCGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 982
QY 781 GCCCGAGCGAGCGAGTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Db 983 GCGCGTGAACGCTCCAGGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1042
QY 841 GGGATCGGGAGCGCGCGTGCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 1043 CTCCGTGAGTCTCTCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1094
QY 901 CGCTGGCGCGCGCGCGAGAACCGCGAGAACCGCTTACGTTCTGTGCTGGCGTGTGATC 960
Db 1095 CGCCGCAAGGTGGCG 1154
QY 961 GAGTGTCTGT 1017
Db 1155 GGTGTGTCTGT 1214
QY 1018 -----GGGTGCTCCGTGCGACGCGCGCTTCAAAATCTTCTGTGTGTGTGTGTGT 1071
Db 1215 CGCGAGCGCGCGCGAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1274
QY 1072 AACAGCTCGTTGAACCGCGTCAATCAACCATCTTCAACCAAGATTTCGCGCGCGCTTC 1131
Db 1275 AACAGCTCGTTGAACCGCGTCAATCAACCGTCTTCAACCAAGATTTCGCGCGCGCTTC 1334
QY 1132 AAGAAGATCTCTGTGTGGGGGAGAGGAAGCGGATC 1167
Db 1335 AAGCACATCTCTTCCGACGAGAGGAAGGGGCTTC 1370

RESULT 14

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1371
FT /*tag= a
FT /product= "alpha-2CAR"
FT /note= "sequence is deleted for a 12 nucleotide
polymorphic site at nucleotides 961-972 of the
wildtype sequence (AA199931)"
FT
XX
PN WO200179561-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US12575.
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
DR P-PSDB; AAM52126.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
determining whether an individual is at increased risk of developing a
disease associated with the corresponding receptor comprises detecting
a polymorphic site -
PT
XX
PS Claim 103; Page 158; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
alpha-2A or alpha-2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
or a site comprising (A) (ggggcgggcg) or (B) (ggggcgctgag) at
positions 961-972 of (III). The method may be used for genotyping an
alpha-2B, alpha-2A or alpha-2C receptor gene and further used to determine
whether an individual is at increased risk of developing a disease
associated with alpha-2B, alpha-2A or alpha-2, comprising detecting a
polymorphic site which correlate to disease selected from cardiovascular
disease, central nervous system disease and combinations of these. In
addition, the technique may be used to predict an individual's response
to an alpha-2B, alpha-2A, or alpha-2C agonist (e.g. epinephrine,
norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
rauwolscine, idazoxan, tolazoline, phenolamine and combinations of
these) by detecting the polymorphic site and correlating the site to a
predetermined response (where the response is correlated to adenylyl
cyclase, MAP kinase activity, phosphorylation or inositol phosphate
levels). The present sequence is that of the human alpha-2CAR variant,
the sequence is deleted for a 12 nucleotide polymorphic site at
nucleotides 961-972 of the wildtype gene (AA199931).
XX
SQ Sequence 1371 BP; 164 A; 479 C; 491 G; 237 T; 0 other;
Query Match 40.4%; Score 472.4; DB 23; Length 1371;
Best Local Similarity 66.4%; Pred. No. 4.1e-69;
Matches 781; Conservative 0; Mismatches 341; Indels 54; Gaps 5;
QY 1 AGCGCGCGCTCAAGCGCGCCCAAAACCTCTTCGTGGTGTCTCTGGCCTCGCGGACATC 60
DB 235 AGCGCGCGCTGCGCGCGCCACAGAACCTCTTCGTGGTGTCTGGCCTCGCGGACATC 294
QY 61 CTGGTGCCACGCTGCTATCCCTTCTCGCTGGCCCAAGAGTCAATGGGCTACTGTGAC 120
DB 295 CTGGTGCCACGCTGCTATGCCCTTCTCTGTGGCCCAAGAGTCAATGGGCTACTGTGAC 354

QY 121 TTCGGCAAGCCTTGTCGCGAATCTACCTGGCGCTCGACGTGCTCTTTCGACGTGCTCC 180
DB 355 TTCGGGCAAGGTGTGTGTCGCGGTGTACCTGGCGCTGATGTGCTGTTTTCGACCTCGTCG 414
QY 181 ATCGTCACCTGTGCGCCATCAGCCTTGAGCCGCTACTGTCCATCACAACAGGCCATCGAG 240
DB 415 ATCGTCATCTGTGTGCCATCAGCCTTGAGCCGCTACTGTGCTGACGACGCGCTCGAG 474
QY 241 TACAACCTGAAGCGCAGCCCGCGCCGCATCAAGGCCATCATCATCACCCTGTGCTCATC 300
DB 475 TACAACCTGAAGCGCAGCAGCCCGCGCTCAAGGCCACCATCGTCGCTGTGCTCATC 534
QY 301 TCGGCGCTCATCTCTCTCCCGCGCTCATCTCCATCGAAGAAGGGCGGCGGCGGCG 360
DB 535 TCGGCGCTCATCTCTCTCCCGCGCTCTCCCGCTGCTCTGCTCTACCGCCAGCCGCGCGCC 591
QY 361 CCGCAGCGCGCGAGCGCGCGCTGCGAGATCAACGACCAAGAGTGTACGTATCTGTGCG 420
DB 592 -----GCCTACCGCAGTGGCGCTCAACGACGAGACCTGTACATCTGTCTCC 642
QY 421 TGCATCGGCT 480
DB 643 TGCATCGGCT 702
QY 481 CAGATCGCCAAAGCTGCGACCCCGCTGCCACCCAGCCCGCGGCTCCGAGCGCTGCGC 540
DB 703 CGAGTGCCAAAGCTGCGACCGCGCAGCTCAGCGAGAGAGCGCGCGCGCGCGCGCG 762
QY 541 GCG 600
DB 763 GGTGCTGCCCGACTACCGAAGAGGGGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 822
QY 601 CCGGGGGCGCAGAGCGCGAAGCGCTGCCACCCAGCTCAACGCGCGCGCGCGCGCGCG 660
DB 823 ACTG-----CG 869
QY 661 GCG 720
DB 870 GCGCGCGAGAGCG 921
QY 721 CACGCGAGCGGCTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
DB 922 ----GCGGCGCGGAGGCG 977
QY 781 GCCCGAGCGAGCGAGTGAAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
DB 978 GCGCGTGAACGCTCCAGGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1037
QY 841 GGGATCGGAGCG 900
DB 1038 CTCCGTGAGTCT 1089
QY 901 CGCTGCG 960
DB 1090 CGCCGCAAGGTGGCG 1149
QY 961 GGAGTGTCTGT 1020
DB 1150 GCGGTGTCTGT 1209
QY 1021 -----TGCTCCGTGCCACGCGCTCTCAATTTCTTCTGTGCTGCTGCTGCTGCTG 1071
DB 1210 CGCGAGGCTGCGCAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1269
QY 1072 AACAGCTGCTGAACCCCGGTCTATCAACCATCTTCAACCAAGATTTCCGCGCGCTTC 1131
DB 1270 AACAGCTGCTGAACCCCGGTCTATCAACCGGTCTTCAACCAAGATTTCCGCGCATCTTC 1329
QY 1132 AAGAAGATCTCTGTGCGGGGAGACAGAGCGGATC 1167
DB 1330 AAGCACATCTCTTCCGACGAGAGAGAGGGGCTTC 1365

PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
PI Llggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
DR P-PSDB; AAM52124.
XX

PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX

PS Example 15; Page 157; 163pp; English.

XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIV)
CC or a site comprising (A) (999g999g99) or (B) (999g99g99g) at
CC positions 961-972 of (IIV). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2CAR, the
CC sequence includes a 12 nucleotide polymorphic site at nucleotides
CC 961-972, absent in the alpha-2CAR variant (AAI99933).
XX

XX
SQ Sequence 1383 BP; 164 A; 482 C; 500 G; 237 T; 0 other;

Query Match 41.5%; Score 485.4; DB 23; Length 1383;
Best Local Similarity 66.9%; Pred. NO. 3e-71;
Matches 787; Conservative 0; Mismatches 346; Indels 44; Gaps 5;

OY 1 AGCCGCGGCTCAAGGCGCCCAAAACCTCTTCTGCTGCTCTGCGCTCGCGGACATC 60
Db 235 AGCCGCGGCTCGCGCGCCACAGAACCTCTTCTGCTGCTCGCTCGCGGACATC 294
OY 61 CTGTGGCCACGCTGCTATTCCTTCTGCTGCGGCCAACAGAGTCAATGGCTACTGTAC 120
Db 295 CTGTGGCCACGCTGCTATTCCTTCTGCTGCGGCCAACAGAGTCAATGGCTACTGTAC 354
OY 121 TTCGCAAGGCTTGTGCGAGATCTACCTGGCGCTGACGTGCTTCTGACAGTCTCC 180
Db 355 TTCGCGCAGGTGTGTGCGGCGTGTACCTGGCGCTGATGTGCTGTTTTCACCTCGTCG 414
OY 181 ATCGTGACCTGTGCGGCATCAGCTTGACCCCTACTGTCCATCACAAGGCCATCGAG 240
Db 415 ATCGTGACCTGTGTGCATCAGCTTGACCCCTACTGTGCGTGACGACGCGCTCGAG 474
OY 241 TACAACCTGAAGCGACGCGCGCCGATCAAGGCCATCATCACCCTGTGGTCAATC 300
Db 475 TACAACCTGAAGCGACACACGCGCGGTCAAGGCCACCATCGTCGCGGTGCTCAATC 534
OY 301 TCGGCCGTCATCTCTTCCCGCGCTCATCTCCATCGAAGAAAGGGCGGCGGCGGC 360
Db 535 TCGGCCGTCATCTCTTCCCGCGCTCGTCTACCGCGCCGACGCGGCGCGCG-- 592

OY 361 CCGCAGCCGCGGACCGCGCTGCGAGATCAACGACAGAAAGTGTACGTACTCTGTCG 420
Db 593 -----CCTACCCGAGTGGCGCTCAACGACAGACCTGGTACATCTCTCTCC 642
OY 421 TGCATCGGCTCTTCTTCTGCTCCCTGCTCATCATGATCTGCTTACGTGGCATCTAC 480
Db 643 TGCATCGGCTCTTCTTCTGCGCCCTGCTCATCATGAGGCTGTCTACGCGGCATCTAC 702
OY 481 CAGATCGCAAGCGTGCACCCGCTGCCACCCAGCCCGGGGTCCGAGCCCTGCGC 540
Db 703 CGAGTGGCCAGCGTGCACCGCCGCTCAGCGAGAAAGCGCCCGCGTGGGCCCGGAC 762
OY 541 GCGCCGCGGGGGGACCGAGCCGAGCCCAACGCTTGGGCCCCGAGCGAGCGCGGC 600
Db 763 GGTGCGTCCCGACTACCGAAGAAAGCGGCTGGGCGCGGCGAGCGAGAAAGGCG 822
OY 601 CCGGGGGCGCAGAGGCGCGAACCCTGCCCCACCTCAACGCGCCCTGGCGAGC-C 659
Db 823 ACTGCGCGC-----CCCCGCGCGAGCTGAGCGGACGAGAGCAG 865
OY 660 CGCGCCGCGCGGCGCGCGGACCGAGCGGCTGAGACTTGAGAGAGAGTCTTCCGA 719
Db 866 CGCAGCGCGCGAGAGGCGGCGCGCGCGGCGGCTTGGCGCGGCGCGCGCGAGCGG 925
OY 720 CCACGCGGAGCGGCTTCCAGGCGCGCGAGACCGAGCGGCTCCGCGGCGCAAGGCAA 779
Db 926 GCGCGGAGGGGGCGCGGCGGCTGCGAGCGGAGGGGGCGGCGGCGGCGGCTGAGT 985
OY 780 GGGCGGAGCGAGCGCAGTGAACCGGGGAGACAGCTTCCGCGGCGCGCGCGGCGGAG 839
Db 986 CGGGGCGGCTGACCGGCTTCCAGGTTCCCGGGCGCGGCTGCGCGCGCGCAGCT 1045
OY 840 GGGATCGGAGCGCGGCTGAGGCGCGGCGGAGGAGCGGCTGCGGCGTCCAGAGCGTC 899
Db 1046 CGGCTCGCTGAGTTCCTTCTGCGCGCGCGCGCGCGCGGCGGCGAG-----CAGCGTGTG 1100
OY 900 GCGCTGCGCGGCGCGGCGGAGAACCGGAGAGCGCTTCAAGTTCGCTGCGGCTGCTAT 959
Db 1101 CCGCGGCAAGGTGCGGCGGAGGCGCGGAGAGGCGTTCACCTTGTGCTGCTGCTGCTAT 1160
OY 960 CGAGTGTCTGCTGCTGCTGCTGCTTCCCTTCTTCTTCACTTACAGCTCAGGCGCTC-- 1017
Db 1161 GGGCGTGTCTGCTGCTGCTGCTGCTTCCCTTCTTCTTCACTTACAGCTTACGCGCTG 1220
OY 1018 -----GGTGTCTGCTGCGCAGCGACGCTCTTCAATTCCTTCTGCTGCGGCTACTG 1070
Db 1221 CCGGAGGCGCTGCGAGGTGCGCGCGCGCTTCAAGTTCCTTCTTCTGAGTGGCTACTG 1280
OY 1071 CAACAGCTCGTTGAACCCGGGTATCTTACACCATCTTCAACACGAGTTTCGCGCGCTT 1130
Db 1281 CAACAGCTCGTTGAACCCGGGTATCTTACACCGGTTTCAACACGAGTTTCGCGCAATCTT 1340
OY 1131 CAAGAAGATCTCTGTCGGGGGAGACGAGAAAGCGGATC 1167
Db 1341 CAAGCATCTCTTCTTCCGAGGAGAGAAAGGGGCTTC 1377

RESULT 12
AAI99933
ID AAI99933 standard; DNA; 1371 BP.
XX
AC AAI99933;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2CAR variant encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2CAR; chromosome 4; ds.
XX

```
XX (EPiG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2002-154759/20.
DR
XX
PT Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT gene -
XX
XX Claim 1; Page 32-36; 190pp; English.
PS
XX
XX The invention relates to nucleic acids comprising a segment of chemically
XX pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
XX relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
XX useful for detecting cytosine methylations. The pretreated DNA is useful
XX for the diagnosis or therapy of behavioural disorders, neurological
XX disorders and cancer, in particular major depressive disorder, Tourette's
XX syndrome, schizophrenia, psychiatric traits, compulsive gambling, human
XX drug abuse, alcoholism, personality traits, behaviours in schizophrenic
XX immunodeficiency virus dementia, migraine, behaviours in schizophrenic
XX and schizoaffective patients, and suicidal behaviour in patients with
XX schizophrenia. The nucleic acid is useful for detecting the methylation
XX state of all CpG dinucleotides and/or single nucleotide polymorphisms
XX (SNPs). The present sequence is human chemically treated genomic DNA.
XX
XX Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;
SQ
Query Match 62.0%; Score 725.2; DB 24; Length 7353;
Best Local Similarity 76.2%; Pred. No. 1.3e-110;
Matches 892; Conservative 0; Mismatches 278; Indels 0; Gaps 0;
QY 1 AGCCGCGCGCTCAAGGCGCCCAAAACCTCTTCCTGGTGCTCTGGCCTCGGCGGACATC 60
Db 5181 AGTCGCGCGCTTAAAGCGTTTAAATTTTTCCTTTTGGTGTTTTCGTCGATATT 5240
QY 61 CTGGTGCCACGCGTCGTCATCCCTTCTCGCTGGCCCAACGAGTCATGGGCTACTGTTAC 120
Db 5241 TTGGTGTTACGTTGCTTATTTTTCGTTGTTAACGAGGTTATGGGTTATGGTAT 5300
QY 121 TTGCGCAGGCTTGGTGCAGATCTACCTGGCGCTCGACGTGCTCTCTGCACGTCGCC 180
Db 5301 TTGCGTAAGGTTGGTGCAGATTTATTTGGCGTTCGACGTGTTTTTTGTACGTCGTT 5360
QY 181 ATCGTCACCTGTGCGGCATCAAGCCTGACTGCTACTGCTCCATCACAGGCCATCGAG 240
Db 5361 ATCGTGTATTGTGCGTATTAGTTTGGATCGTTATGCTTATATAGGTTATCGAG 5420
QY 241 TACAACCTGAAGCGCAGCGCGCGGCATCAAGGCCATCATCATCACCCTGGGTATC 300
Db 5421 TATAATTTGAACGCTACGTCGCGCTGATTAAGGTTATTTATATATCGTGGGTTATT 5480
QY 301 TCGCGCGTCACTCTTCCCGCGCTCATCTCCATCGAGAGAAGGGCGGCGCGCGGC 360
Db 5481 TCGTGTATTATTTTTCGTCGTTATTATTTTATCGAAGAGAGGGCGGCGCGCGGT 5540
QY 361 CCGCAGCGCGCGAGCGCGCTGCGAGATCAACGACAGACGAAGTGTACGTACTCTGTCG 420
Db 5541 TCGTAGTCGCTGAGATCGCGTGCAGAGATTAAAGATTAGAAAGTGTACGTTATTTCCGTCG 5600
QY 421 TGCATCGGCTCTTCTGCTCCCTGCCATCATGATCCTGCTACGTACGTGCGCATCTAC 480
Db 5601 TGTATCGGTTTTTTTTCGTTTTTGTATTATATGATTTTGTTCGTTACGTCGATTTAT 5660
QY 481 CAGATCGCCAAGCGTCGCAACCGCGCTGCCAACCAGCCGCGGGTCCGGACGCGCTCGCC 540
Db 5661 TAGATCGTTAAGCGTCGTAATTCGCGGTATTATAGTCGTCGGGTCGAGACGTCGTCGTC 5720
QY 541 GCGCGCGCGGGGGGACCGAGCGCAGGCCCAACGCTCTGGCCCCGAGCGCAGCGCGGC 600
Db 5721 GCGTCGTCGGGGGGTATCGAGCGTAGGTTTAAACGGTTTGGGTTTCAGCGTAGCGCGGT 5780
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QY 601 CCGGGGGCGCAGAGGCCGAACCGCTGCCCAACCCAGCTCAACGCGCCCGCTGGCAGCCC 660
Db 5781 TCGGGGGCGGTAGAGTCAATCGTTGTTATTTAGTTTAAACGCGCTTTTGGCAGGTTG 5840
QY 661 GCGCGCGCGCGCGCGCGCAGACCCGACGCGCTGGAACCTGAGAGAGAGCTGCTTCCGAC 720
Db 5841 GCGTCGTCGCGTCCGCGCATATCGACGCGTTGGATTGGAGAGAGATTTCGTTTTTCGAT 5900
QY 721 CACGCCGAGCGGCTTCAGAGGGCCCCGACAGCCGAGCGCGGTCCCGGGCCAAAGCAAG 780
Db 5901 TACGTCGAGCGGTTTTTAGGGTTTCGTAGATTGACGCGCGGTTTTTCGGGGTAAAGTTAAG 5960
QY 781 GCGCGAGCGAGCGAGGTGAAGCCGGGCGACAGCCTGCCGCGCGCGCGCGCGCGCGGAGC 840
Db 5961 GTTCGAGCGAGTTAGGTGAGTCGCGCGATAGTTGTGCGGCGCGCGGTCCGGGGCGAGC 6020
QY 841 GGGATCGGGACGCGCGCTGACAGGGCGGGGAGAGAGCGGCTCGGGCTGCCAAGCGCTCG 900
Db 6021 GGGATCGGGACGTCGCTGTGTAAGGCTCGGGGAGAGAGCGGCTCGGTTGTTAAGCGCTCG 6080
QY 901 CGCTGCGCGCGCGCGCGCAGAACCGCGAGAACGCGTTCAAGTTCGTGCGCGGTGTCATC 960
Db 6081 CGTTGCGCGCGCGCGGTAGAAATCGCAGAAAGCGTTTACGTTGCTGTCGCGGTATC 6140
QY 961 GGAGTTTCTGTTGTTGTTGTTCCCTTCTTCTTCACTACAGCTCACGCGCGCGCTCGGG 1020
Db 6141 GGAGTTTCTGTTGTTGTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 6200
QY 1021 TGCTCCGTCACGACGACGCTCTTCAAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 1080
Db 6201 TGTTTCGTTTACGTTACGTTTCTTCAAAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 6260
QY 1081 TTGAACCCGCTCATCTACACCATCTTCAACCAAGATTTCGCGCGCGCTTCAAGAGATC 1140
Db 6261 TTGAATTCGTTATTATATTATTATTATTATTATTATTATTATTATTATTATTATTATT 6320
QY 1141 CTCTGTCGGGGGACAGGAAGCGGATCGTG 1170
Db 6321 TTTTGTGCGGGGATAGGAAGCGGATCGTG 6350
```

```
RESULT 11
AAI99931
ID AAI99931 standard; DNA; 1383 BP.
XX
AC AAI99931;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2CAR encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2CAR; chromosome 4; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1.1386
FT CDS
FT /*tag= a
FT /product= "alpha-2CAR"
FT /note= "sequence includes a 12 nucleotide polymorphic
FT site at nucleotides 961-972 absent in the
FT alpha-2CAR variant (AAI99933)"
XX
XX WO200179561-A2.
XX
XX 25-OCT-2001.
XX
XX 17-APR-2001; 2001WO-US12575.
XX
```

XX Homo sapiens.
OS
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
PS Claim 1; SEQ ID NO 45; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;

Query Match 62.0%; Score 725.2; DB 24; Length 7353;
Best Local Similarity 76.2%; Pred. No. 1.3e-110;
Matches 892; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

OY 1 AGCGGCGGCTCAAGGCGCCCAAAACCTCTCTCGTGTCTCTGGCCTCGGCCGACATC 60
DB 5181 AGTCGCGCGTTTAAAGCGTTTAAATTTTTCGTTTGGTTCGTTTCGGTCGATATT 5240
OY 61 CTGTGGCAGCGCTGTCATCCCTTCTCGCTGGCCAAGGTCATGGGCTACTGTAC 120
DB 5241 TTGTGTGTACGTTGTTATTTTTCGTTGTTAACGAGGTTATGGTTATTTGGTAT 5300
OY 121 TTGCGCAAGGCTTGTGCGAGATCTACCTGGCCCTCGACGTCCTTTCGACGTCGCC 180
DB 5301 TTGCGTAAGGTTTGTGCGAGATTATTGGCGTTTCGACGTCGTTTTCGACGTCGTT 5360
OY 181 ATGTGCACCTGTGCGCATCAGCCCTGACCGCTACTGTCATCAGAGGCCATCGAG 240
DB 5361 ATGTGTATTGTGCGTATTAGTTTGATCGTTATTTGTTATTATATAGGTTATCGAG 5420
OY 241 TACAACCTGAAGCGCAGCGCCGCCCATCAAGGCCATCATCACCGTGGTCAATC 300
DB 5421 TATTAATTGAAGCGTACGTCGCGTCGTAATTAAGTTATTATTAATTCGTGGTATT 5480
OY 301 TCGGCGGTCATCTCTTCCCGCGCTCATCTCCATCGAAGAAGCGCGCGCGCGC 360
DB 5481 TCGGTCGTATTATTTTTCGTCGTTTATTTTATCGAAGAAGCGCGCGCGCGGT 5540
OY 361 CCGCAGCGCGCGCAGCGCGCTGCGAGATCAAGCAGAAAGTGTACGTATCTGTCG 420
DB 5541 TCGTAGTCGTCAGTCGCGTTCGAGATTAAACGATTAGAAAGTGTACGTATTTCGTCG 5600
OY 421 TGCATCGGCTCTCTTCTGCTCCCTGCTCATCATGATCCGTCTACGTGCGCATCTAC 480
DB 5601 TGTATCGGTTTATTTTTCGTTTTCGTTTATATGATTTGTTTACGTGCGTATTAT 5660
OY 481 CAGATCGCCAAGCGTCGACACCGCGTCGACACCGCGCGCGGTCCGAGCGCGTCGCC 540
||||| ||||||| | ||||| | || ||||||| ||||||| |||||||

DB 5661 TAGATCGTTAAGCGTCCGATATTCGCGTGTATTATTAGTCGTCGGGGTTCGGACGTCGCTC 5720
OY 541 GCGCCGCGGGGGGCGACCGAGCGCAGGCCCAACGGTCTGGGCCCGGAGCGGCGGGC 600
DB 5721 GCGTCGTCGGGGGATTTCGAGCGGTAGCTTTTAAACGGTTTGGGTTTCGAGCGTACGCGGT 5780
OY 601 CCGGGGGGCGCAGAGCGCCGAACCGCTGCCCAACCACTCAACGGCGCCCTGCGAGCCC 660
DB 5781 TCGGGGGGCGTAGAGGTCGAATCGTTGTTTATTATTAGTTTAAACGGCGGTTTTCGAGCTTC 5840
OY 661 GCGCCGCGCGCGCGCGCGCAGACCGCAGCGCTGAGCCTGAGAGAGAGCTGCTTCCGAC 720
DB 5841 GCGTCGTCGGGTCGCGCGCATATTCAGCGCGTTGATTTGAGAGAGAGATTCTGTTTCGAT 5900
OY 721 CAGCGCAGCGGCTCCAGGGCCCCGACAGCCGAGCGCGGTCCCGGGCAAGCAAG 780
DB 5901 TACGTCAGCGGTTTATTAGGTTTCGTAGATTTCAGCGCGGTTTTCGGGGTAAAGGTAAG 5960
OY 781 GCGCGAGCGCAGCGAGTGAAGCGGGCGACAGCCTGCGCGCGCGCGCGCGCGCGGCGAGC 840
DB 5961 GTTCGAGCGAGTTAGTGAAGTCGGCGCATAGTTGTCGGCGCGCGGTCGGGGCGAGC 6020
OY 841 GGGATCGGAGCGCGCGCTGCAGGCGCGGGGAGAGCGCGTCCGGGCTCCCAAGCGCTCG 900
DB 6021 GGGATCGGAGCGCTCGGTTGTAAGGTCGGGGAGAGCGCGCTCGGGTTGTTAAGCGCTCG 6080
OY 901 CGTCGCGCGCGCGCGCGCAGAACCGCGAGAAAGCGTTACGTTCTGTCGCGCGCTGTCATC 960
DB 6081 CGTTGCGCGCGCGCGGTAGAAATCGCGAGAAAGCGTTTACGTTCTGTCGTCGTCGTTATC 6140
OY 961 GGAGTGTCTGTGTGCTGCTGCCCTTCCTTCCTTCAACCTTACACGCTCACAGCGCCGTCGG 1020
DB 6141 GGAGTGTCTGTGTGCTGCTGCCCTTCCTTCCTTATATTATACGTTTACGCTGTCGG 6200
OY 1021 TGTCTCGTGCACGCGCCTCTCAAAATTCCTTCTGTGTTGCGTACTGCAACAGCTCG 1080
DB 6201 TGTTCGTGTACGTAAGTTTAAATTTTTCGTTTTCGTTTCGTTTATGTAATAGTTCG 6260
OY 1081 TTGAACCGGTCAATACACCATCTTCAACCAAGATTTCCGCGCGCCCTTCAAGAAATC 1140
DB 6261 TTGAATTCGTTATTATATTATTATTAAATTTTTCGTTTCGTTTCGTTTAAAGAAATT 6320
OY 1141 CTCTGTGGGGGAGCAAGCGGATCGTG 1170
DB 6321 TTTTGTGGGGGATAGGAACGCGATCGTG 6350
RESULT 10
AAD28362
ID AAD28362 standard; DNA; 7353 BP.
XX
AC AAD28362;
XX
DT 22-APR-2002 (first entry)
XX
DE Human chemically treated genomic DNA #3.
XX
KW Human; cytosolic; antidepressant; neuroleptic; nootropic; antiaddictive;
KW adrenergic alpha-1c-receptor; cytosine methylation; therapy; alcoholism;
KW behavioural disorder; neurological; psychiatric; cancer; schizophrenia;
KW Tourette's syndrome; smoking; human immunodeficiency virus dementia;
KW drug abuse; migraine; ds.
XX
OS Homo sapiens.
XX
PN WO200202809-A2.
XX
PD 10-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07540.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.

XX 07-MAR-2002.
PD
XX
XX 01-SEP-2001; 2001WO-EP10074.
PF
XX 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
PR
XX
PA (EPiG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
XX WPI; 2002-371829/40.
DR
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
PS
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
CC
XX
SQ Sequence 1733 BP; 685 A; 585 C; 211 G; 252 T; 0 other;
Query Match 62.0%; Score 725.2; DB 24; Length 1733;
Best Local Similarity 76.2%; Pred. No. 1.4e-110;
Matches 892; Conservative 0; Mismatches 278; Indels 0; Gaps 0;
QY 1 AGCCGCGCGCTCAAGCGCCGCCAAACCTCTCTCTGCTGCTCTGCGCTCGCGGACATC 60
Db 1293 AGTCGCGCGCTTAAAGCGCTTAAATTTTGTGCTTTGCTTTCGTCGATAT 1234
QY 61 CTGCTGGCAGCGCTGTCATCCCTTCTCTGCTGCGCACAGAGTCATGGGCTACTGCTAC 120
Db 1233 TTGCTGTACGTTCTGTTATTTTTCGTTTGTAAACGAGTTATGGGTATTGGTAT 1174
QY 121 TTCGGCAAGGCTTGTCGAGATCTACCTGGCGCTCGACGTGCTCTCTGACGTCGTC 180
Db 1173 TTCGTAAGGTTGGTGCAGATTATTGGCGTTCGACGTGTTTTTTGTACGTCGTT 1114
QY 181 ATCGTGACCTGTGGCCATCAGCCCTGACCGCTACTGTCCTCATCACACAGCCATCGAG 240
Db 1113 ATCGTATTTGGCGTTATTTAGTTGGATCGTTATTTGTTATATAGGTTATCGAG 1054
QY 241 TACAACCTGAAGCGACGCCGCCGACATCAAGCCATCATCATACCGTGTGGTCATC 300
Db 1053 TATAATTGAAGCGTACGTCGCGTGTATTAAGGTTATTATTATTCGTGTGGTTATT 994
QY 301 TCGGCGCTCATCTCCTTCCCGCGCTCATCTCCATCGAGAGAAGGCGCGCGCGCGGC 360
Db 993 TCGGTCGTATATTTTTCGTCGTTATTATTATTCGAGAAGAGGCGCGCGCGGT 934
QY 361 CCGCAGCCGCGCGAGCGCGCTGCGAGATCAACGACCAAGAGTGTACGTCATCTCGTCG 420
Db 1113 CCGCAGCCGCGCGAGCGCGCTGCGAGATCAACGACCAAGAGTGTACGTCATCTCGTCG 420

Db 933 TCGTAGTCGGTCGAGTCGCGCTTGCGAGATTACGATTAGAGTGTACGTTATTTCCGTCG 874
QY 421 TGCATCGGCTCCCTTCTTCGCTCCCTGCGCATCATGATCTGTCTACGTGCGCATCTAC 480
Db 873 TGTATCGGTTTTTTTTCGTTTTTTTGTATTATATGATTTTGGTTACGTCGATTTAT 814
QY 481 CAGATCGCCACAGCGTCGCACCCCGCTGCGCACCCAGCCCGCGGGTCCGAGCCGTCGCC 540
Db 813 TAGATCGTTAAGCGTCGTTATTCGCGTGTATTAGTCGTCGGGGTTCGACGTCGTCGTC 754
QY 541 GCGCCCGCGGGGCGACCGCAGCGGACGCCCAACGCTGTGGCCCCGAGCGCAGCGCGGC 600
Db 753 GCGTCGTCGGGGGATTCGAGCGCTAGGTTAACGCTTTGGGTTTCGAGCGTAGCGCGGT 694
QY 601 CCGGGGGCGCAGAGCGCCGAACCGCTGCCACCCACCTCAACGCGCGCCCTGGCGAGCCC 660
Db 693 TCGGGGGCGCTAGAGGTCGAATCGTTGTTATTAGTTTAACGCGCTTTTGGCGAGTTC 634
QY 661 GCGCCCGCGCGCGCGCGCAGACCGCAGCGCTGACCTGAGAGAGAGCTCTCTCCGAC 720
Db 633 GCGTCGTCGGGTCGCGCGCATCGACGCGTTGATTTGAGAGAGAGTTCGTTTTTCGAT 574
QY 721 CAGCGCAGCGGCTCCAGGCGCCCGCAGACCCGAGCGCGGTCCCGGGCGCAAGGCAAG 780
Db 573 TACGTCGAGCGGTTTTTAGGGTTTCGATATTCGAGCGCGGTTTTCCGGGTAAGGTTAAG 514
QY 781 GCGCCGAGCGAGCCAGGTGAAGCGCGGCGACAGCCTGCGCGCGCGCGCGCGCGCGACG 840
Db 513 GTTCGAGCGAGTTAGTGAAGTCGCGCGATAGTTTTCGCGCGCGCGCGCGCGCGCGACG 454
QY 841 GGGATCGGAGCGCCGCGCTGCAGGCGCGGGGAGAGAGCGCGCTCGGCCAAGCGCTCG 900
Db 453 GGGATCGGAGCGCTCGGTGTAGGGTCGGGGGAGAGAGCGCGCTCGGGTGTAAAGCGCTCG 394
QY 901 CGCTGGCGCGCGCGCGCAGAACCGCGAGAACGCTTACGTTCTGCTGCGCGCTGTCATC 960
Db 393 CGTTGGCGCGCGCGGTAGAAATCGCGAGAACGCTTACGTTCTGCTGCTGCTGCTATC 334
QY 961 GGAGTGTTCGTGCTGTGCTGCTGCTTCCCTTCTTCTTACCTACAGCTCACGCGCGTCGG 1020
Db 333 GGAGTGTTCGTGCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 274
QY 1021 TGCTCCGTGCGCACGACGCTCTTCAAAATCTTCTTCTGTTGCGCTACTGCAACAGCTCG 1080
Db 273 TGTTCGTGTACGTAACGTTTCTTCAAAATTTTTTTTGTGTCGTTATGTAATAGTTTCG 214
QY 1081 TTGAACCGGTCATCTACACCATCTTCAACACGATTTCCGCGCGCTTCAAGAGATC 1140
Db 213 TTGAATTCGTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 154
QY 1141 CTCTGTCGGGGGAGCAGGAAGCGGATCGTG 1170
Db 153 TTTTTCGCGGGGATAGGAAGCGGATCGTG 124
RESULT 9
ABL32072
ID ABL32072 standard; DNA; 7353 BP.
XX ABL32072;
AC
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 45.
XX
XX Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytosinatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.

XX 07-MAR-2002.
PD
XX
PF 01-SEP-2001; 2001WO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Plepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA
XX
PS Claim 12; 56pp + sequence listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 1733 BP; 252 A; 211 C; 585 G; 685 T; 0 other;

Query Match 62.0%; Score 725.2; DB 24; Length 1733;
Best Local Similarity 76.2%; Pred. No. 1.4e-110;
Matches 892; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

QY 1 AGCCGGCGCTCAAGGCGCCCAAACTCTTCTGTGTCTGTGGCTCGGCCGACATC 60
Db ||||||| ||||||| ||||| ||||||| ||||| ||||| ||||| ||||| |||||
441 AGTCGGCGCTTAAAGCGTTTAAATTTTGTGTTTGGTTTGGTTCGGTCATATT 500
QY 61 CTGGTGGCCAGCTCGTCATCCCTTCTCGCTGGCCACAGAGCTCATGGCTACTGTAC 120
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
501 TTGGTGGTTACGTTCTTATTTTCTGTGTTACGAGAGTTATGGTTATTGGTAT 560
QY 121 TTCGGCAAGGCTTGTGCGAGATCTACCTGGCGCTGACGTGCTCTTTCGACGTGTC 180
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
561 TTCGTAAGTTTGTGCGAGATTATTGGCGTTCGACGTGTTTTCGTAAGTTTTCG 620
QY 181 ATGTGCACTGTGCGCATGAGCTTGACCGCTACTGTGTCATCACACAGCCATCGAG 240
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
621 ATGTGTATTGCGTTATTTGATTCGTTATTTGTTATTTATATAGTTATCGAG 680
QY 241 TACAACCTGAAGCGACGCGCGCCGATCAAGGCCATCATCACCGTGTGGTATC 300
Db || || ||||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
681 TATAATTGAAGCGTACGTCGCGCTGTTAAGTTATTATTATTCGTGGTTATT 740
QY 301 TCGCCGCTCATCTCTCCCGCCGCTCATCTCCATCGAAGAAGGCGCGCGCGC 360
Db ||||| ||||| || ||||| || ||||| || ||||| ||||| ||||| ||||| ||||| |||||
741 TCGGTGCTTATTTTTCGTCGTTTATTTATCGAAGAAGGCGCGCGCGGT 800
QY 361 CCGCAGCCGCGCGAGCGCGCTGCGAGATCAACGACGAGAGTGTACGTCTCGTCG 420
|| || ||||| ||||| ||||||| ||||| ||||||| ||||| ||||| ||||| |||||

Db 801 TCGTAGTCGCTCGAGTCGCGTTGGCAGATTACGATTAGAACTGGTACGTTATTTCGTG 860
QY 421 TGCATCGGCTCCTTCTTCGCTCCCTGCTCATCATGATCTGTCTACGTCCGATCTAC 480
Db || ||||| || ||||| || ||||| || ||||| ||||| ||||| ||||| ||||| |||||
861 TGTATCGGTTTTCGTTTCGTTTTCGTTTTCGTTTATATGATTTTGGTTACGTGCGTATTAT 920
QY 481 CAGATCGCCAAAGCGTCGCACCCCGCTGCCACCCCGCGGGTCCGACGCCGTGCGC 540
Db ||||||| ||||||| ||||||| ||||||| || ||||| ||||| ||||| ||||| |||||
921 TAGATCGTTAAGCGTCGTTATTCGCGTTTATTTAGTCGTGGGGTTCGACGTCGTGTC 980
QY 541 GCGCCGCGGGGGGCGCACCGCAGCGCCCAACGCTGTGGCCCGCAGCGCAGCGCGGC 600
Db || || ||||||| || ||||||| || ||||||| ||||| ||||| ||||| ||||| |||||
981 GCGTCGTCGGGGGATATCGACCGTAGGTTTAACGGTTTGGTTTCGACGTCAGCGCGGT 1040
QY 601 CCGGGGGCGCAGAGCGCGAACCCTGCCACCCAGCTCAACGCGCGCCCTGGCAGCC 660
Db ||||||| ||||||| ||||| ||||| || ||||| || ||||| ||||| ||||| |||||
1041 TCGGGGGCGGTAGAGGTCGATCGTTGTTTATTAGTTTAACGGCGTTTTCGCGAGTTC 1100
QY 661 GCGCCGCGCGCGCGCGACACCGACGCGCTGACCTGAGAGAGCTCGTCTTCGAC 720
Db || || ||||| ||||||| ||||||| ||||| ||||||| ||||| ||||| ||||| |||||
1101 GCGTCGCTCGGCTCGCGCGATATCGACGCGTTGATTTGAGAGAGATTGTTTTCGAT 1160
QY 721 CACGCCAGCGGCTCCAGGGCGCCCGCAGACCCGAGCGCGGTCCCGGGGCAAGGCAAG 780
Db ||||| ||||||| || ||||| || ||||| ||||| ||||| ||||| ||||| |||||
1161 TACGTGAGCGGTTTAAAGGTTTCGTAAGTTCGAGCGCGGTTTTCGGGGTAAGGTAAG 1220
QY 781 GCCCGAGCGACGAGTGAAGCCGCGGACAGCTGCGCGCGCGCGCGCGCGCGCGAGC 840
Db || ||||||| ||||||| ||||||| || ||||| ||||| ||||| ||||| ||||| |||||
1221 GTTCGAGCGAGTTAAGTGAAGTCGCGCGATAGTTGTGCGCGCGCGCGCGCGAGC 1280
QY 841 GGGATCGGGAGCGCGGCTGCAGGGCGGGGAGAGAGCGCGCTCGGAGCGCTCGCAAGCGCTCG 900
Db ||||||| ||||| || ||||| ||||||| ||||||| ||||||| ||||| ||||| |||||
1281 GGGATCGGAGCTCGGTTGTAGGTCGCGGGAGAGAGCGCGCTCGGAGCGCTCG 1340
QY 901 CGCTGGCGCGCGCGCGCAGAACCGGAGAAAGCGTTACGTTGCTGCGCGCTGTCATC 960
Db || ||||||| ||||||| ||||| ||||||| || ||||||| || ||||||| ||||| |||||
1341 CGTTGGCGCGCGCGGTAGAAATCGGAGAAAGCGTTTACGTTGCTGCTGCTGCTATC 1400
QY 961 GGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db ||||||| ||||||| ||||| || ||||| || ||||| || ||||| ||||| ||||| |||||
1401 GGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1460
QY 1021 TGCTCGTCCACGACGCGCTTCAAAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| |||||
1461 TGTTCGTTGCTACGTAAGTTTAAATTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCG 1520
QY 1081 TTGAACCGGTCATCTACACATCTTCAACACGATTTCCGCCCGCTTCAAGAGATC 1140
Db ||||| ||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| |||||
1521 TTGAATTCGTTATTATATATTTTAAATTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCG 1580
QY 1141 CTCTGTGGGGGGGACAGAGCGGATCGTG 1170
Db || ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1581 TTTTGTGCGGGGATAGGAAGCGGATCGTG 1610

RESULT 8
ABQ47499/C
ID ABQ47499 standard; DNA; 1733 BP.
XX
AC ABQ47499;
XX
DT 12-JUL-2002 (first entry)
XX
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 34090.
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.

[illegible]

Db	1813	CCGCAACCGAACCGAACCGCGCTACGAAATCAACGACCAGAAAAATTAATACGTATCTCGTCG	1754
QY	421	TGCATCGGCTCCTTCTTCGCTCCCTGCCTCATCATGATCTGTGCTAGCTGCGCATCTAC	480
Db	1753	TACATCGACTCTTCTTCGCTCCCTACCTCATCATATCTTAATCTAATCTACGTACGCATCTAC	1694
QY	481	CAGATCGCCCAAGCGTTCGCACCCCGCGTGCACACCCAGCCGCGGGGTCCGGACGCCGTGCGC	540
Db	1693	CAAAATCGCCAAACGTTCGCACCCCGGTACCCACCCCAACCGCGAAATCCGAACGCCGTGCGC	1634
QY	541	GCGCCGCCGGGGGCGACCCGAGCGCAGAGGCCCAACGCTCTGGGCCCGAGCGACGCGGCG	600
Db	1633	GCGCCGCCGAAAAAACACCGAACCGCAAAACCAAGATCTAAACCCCGAAGCGCAACGCGAAC	1574
QY	601	CCGGGGGGCGCAGAGCGCCGAACCGCTGCCCCACCCAGCTCAACGGCGCCCTTGCGAGCCC	660
Db	1573	CCGAAAAACGCAAAAAACCGAACCGCTACCCACCACTCAACGACAGCCCCCTAACGAACCC	1514
QY	661	GGCGCGCCCGGGCGCGCGGACACCGACGCGCGCTGGACCTGGAGGAGAGCTCGTCTCCGAC	720
Db	1513	GGCGCGGACCGAACCGCGGACACCGACGCGCGCTAAACCTAAAAAAAACCTCGTCTCCGAC	1454
QY	721	CACGCGGAGCGCGCTCCAGGGCCCCCGCAGACCCCGACGCGGTCCCCGGGGCAAAAGCAAG	780
Db	1453	CACGCGGAGCGACCTCCAAAAACCCCGCAACCCGAAACGCGATCCCCGGAACAAAAACAAA	1394
QY	781	GCCCGAGCGAGCCAGGTGAACCGCGGGCGACAGCCTGCCCGCGGGCGCGGGGGCGAGC	840
Db	1393	ACCGGAGCGAACCAATAAAAACCGAACGACAACTACCGGACGCGAACCAGAAAAACGACG	1334
QY	841	GGGATCGGGAACGCCGCTGACGGGCGCGGGGAGGAGCGCGTGGGGCTGCCAAGCGCTCG	900
Db	1333	AAATTCGAACAGCGCGACTACAAAAACGAAAAAAGCGGTCGAAACTACCAAAAAAGTCCG	1274
QY	901	CGCTGGCGCGGGCGGAGAACCGCGAGAAAGCGCTTACGTTGCTGCGCGGTGTCATC	960
Db	1273	CGCTAACCGGAACGACAAAAACCGGAAAAAAGCTTACGTTGCTACTAACCGTAATCATC	1214
QY	961	GGAGTGTTCGTGTGTGCTGTGTTCCCTTCTTCACTACACGCTCACGGCGCTCGGG	1020
Db	1213	GAAATATTCGTAATATATCTAATTCCTTCTTCACTACACGCTCACGACGCTCAGACCGTCGAA	1154
QY	1021	TGCTCCGTGCGACGACGCTCTTCAAAATCTTCTTCTGTGTTGCGCTACTGCAACAGCTCG	1080
Db	1153	TACTCCGTACCGACGACGCTCTTCAAAATCTTCTTCTAATTCGACTACTACAAACAGCTCG	1094
QY	1081	TTGAACCCCGTCACTATACACCATCTTCAACCAAGATTTCCGCGCGCTTCAAGAAAGATC	1140
Db	1093	TTAAACCCGATCATCTACACCATCTTCAACCAAGATTTCCGCGCGCTTCAAAAAAATC	1034
QY	1141	CTCTGTGCGGGGAGGAAAGCGGATCGT	1169
Db	1033	CTCTATCGAAAAAACAAAAACGAATCGT	1005
RESULT 7			
ABQ47498			
ID	ABQ47498	standard; DNA; 1733 BP.	
XX	ABQ47498;		
AC			
XX			
DT	12-JUL-2002	(first entry)	
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 34089.		
XX			
KW	Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;		
KW	drug; side effect; cancer; central nervous system; cardiovascular;		
KW	gastrointestinal; respiratory system; single nucleotide polymorphism;		
KW	SNP; cell differentiation; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200218632-A2.		

XX 26-MAR-2002 (first entry)
DT
XX
DE Human immune system associated gene SEQ ID NO: 46.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; anti-HIV; anticonvulsant; ophthalmological;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
PS Claim 1; SEQ ID NO 46; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;

Query Match 68.7%; Score 804.2; DB 24; Length 7353;
Best Local Similarity 80.5%; Pred. No. 1.4e-123;
Matches 941; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

QY 1 AGCCGCGCGCTCAAGCGCCCAAAACCTTCTGCTGCTGCTGCGCTGCGCGACATC 60
DB 2173 AACCGCGCGCTCAAAACGCCCCAAACCTTCTTAATATCTTAACTGACGACATC 2114
QY 61 CTGCTGGCCAGCTGCTATCCCTTCTGCTGCGCAAGAGGTCATGGGCTACTGTAC 120
DB 2113 CTAATAACCAAGCTGTCATCCCTTCTGCTAACCAGAAATCATAACTAATAATAC 2054
QY 121 TTCGGCAAGGCTTGGTGAGATCTACCTGGCGCTGACGTGCTTCTGACGTCGTC 180
DB 2053 TTCGACAAACTTAATAGAAATCTAACGCTGACGTACTCTTCTACAGTCGTC 1994
QY 181 ATGCTGCACTGTGCGCATGACCTGACCGCTACTGTGTCATCACACAGCCATCGAG 240
DB 1993 ATCGTACACTTATAGCCATCACTAAACCGCTACTAATCCATCACACAAACCATCGAA 1934
QY 241 TACAACCTGAAGCGCAGCGCCGCGCATCAAGCGCATCATCACCGTGTGGTCATC 300
DB 1933 TACAACCTGAAGCGCAGCGCCGCGCATCAAAACCATCATCATCACCGTATAATCATC 1874
QY 301 TCGGCGGTATCTCTTCCGCGCGCTCATCTCCATCGAGAAGAGGCGCGCGCGCGC 360

DB 1873 TCGACGTCATCTCTTCCCGCGCTCATCTCATCGAAAAAAGACGACGACGAC 1814
QY 361 CCGCAGCCGCGGAGCGCGCTGCGAGATCAACGACGAGAAAGTGTACGTCTCTGTCG 420
DB 1813 CCGCAACGACCGAAGCGCGCTACGAAATCAACGACGACAAATAATATACGTATCTCTGTCG 1754
QY 421 TGCATCGGCTCTTCTTCTGCTCCCTGCTCATCATGATTCCTGTACTGCGCATCTAC 480
DB 1753 TACATCGACTCTTCTTCTGCTCCCTACCTCATCATATFCTAATCTACGTACGCATCTAC 1694
QY 481 CAGATGCGCAAGCGTTCGACCGCGCTGCCACCCAGCCGCGGGGTCCGACGCGCTCGCC 540
DB 1693 CAAATGCGCAACGTCGACCGCGGTACCAACCCAGCCGAATCCGAACGCGCTCGCC 1634
QY 541 GCGCGCGCGGGGCGACCGAGCGGACGCGCAACGCTTGGGCCCGCGAGCGCGCGGC 600
DB 1633 GCGCGCGCGAAAAAACACCGAAGCGCAACCCAGCATCTAAACCCCGCAACGCGGAAC 1574
QY 601 CCGGCGGCGCGCAGAGCGCGAACCCTGCGCCACCAAGCTCAACGCGCGCGCTGCGAGCC 660
DB 1573 CCGAAAAACGCAAAACCGAACCGCTACCCACCACTCAACGACGCGCGCTAACGAACC 1514
QY 661 GCGCGCGCGCGCGCGCGACACCGCGCTGACCTGAGAGAGAGCTGCTTCTCGAC 720
DB 1513 GCGCGCGACCGACCGCGCGACACCGCGCTAAACCTAAAAAAACCTGCTTCTCGAC 1454
QY 721 CACGCGGAGCGGCTTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 780
DB 1453 CACGCGGAGCGACTTCCAAAAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 1394
QY 781 GCGCGGAGCGAGCGAGTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 840
DB 1393 ACCCGAAGCAACCAATTAACCGAAGCAACCTACCGCGCGCGCGCGCGCGCGCGCGCGAG 1334
QY 841 GGGATCGGAGCGCGCTGACG 900
DB 1333 AAAATCGAAACCGCGACTCAAAACCGGAAAAAACCGCGCGCGCGCGCGCGCGCGCGCGCG 1274
QY 901 CGCTGCGCGCGCGCGCGCGAGAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
DB 1273 CGTACGCGCGAGCAACAAACCGCGGAAAAACCGCTTACGCTTACTAACCGTAATCATC 1214
QY 961 GGAGTGTCTGCTGTGCTGCTGCTTCTTCTTCACTACAGCGCTACGCGCGCGCGCGG 1020
DB 1213 GAAATATCTGTAATATATTAATTCCTTCTTCACTACAGCGCTACGCGCGCGCGCGAA 1154
QY 1021 TGCTCCGTGCGCAGCGCGCTTCAAAATCTTCTGCTGCGCTACGCGCGCGCGCGCGCG 1080
DB 1153 TACTCCGTACCAAGCGCGCTTCAAAATCTTCTTCAATTCGACTACACAACTCG 1094
QY 1081 TTGAACCGCGCTATCTACACATCTTCAACACAGATTCGCGCGCGCGCGCGCGCGCGCG 1140
DB 1093 TTAACCGCGATCATCTACACATCTTCAACACAGATTCGCGCGCGCGCGCGCGCGCGCG 1034
QY 1141 CTCTGTGCGGGGAGCAGAGCGGATCGT 1169
DB 1033 CTCTATCGAAAAAACAACGAATCGT 1005

RESULT 6
AAD28363/C
ID AAD28363 standard; DNA: 7353 BP.
AC AAD28363;
XX
DT 22-APR-2002 (first entry)
XX
DE Human chemically treated genomic DNA #4.
XX
KW Human; cytosine; antidepressant; neuroleptic; nootropic; antiaddictive;
KW adrenergic alpha-1c-receptor; cytosine methylation; therapy; alcoholism;
KW behavioural disorder; neurological; psychiatric; cancer; schizophrenia;

XX 12-JUL-2002 (first entry)
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 34092.
DE
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX Homo sapiens.
XX WO200218632-A2.
XX 07-MAR-2002.
XX 01-SEP-2001; 2001WO-EP10074.
XX 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K, Guetly D;
XX WPI; 2002-371829/40.
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
XX Sequence 1733 BP; 626 A; 625 C; 211 G; 271 T; 0 other;
SQ
Query Match 68.7%; Score 804.2; DB 24; Length 1733;
Best Local Similarity 80.5%; Pred. 1.5e-123; Indels 0; Gaps 0;
Matches 941; Conservative 0; Mismatches 228;
QY 1 AGCCGGCGGCTCAAGCGCCGCCAAACCTCTTCTGCTGTCTCTGGCCCTCGGCGACATC 60
DB 441 AACCGCGCGCTCAAAACGCCCAAAACCTCTTCTAATATCTTAACCTCGACGACATC 500
QY 61 CTGGTGGCCACGCTGTCATCCCTTCTCGCTGGCAACGAGGTGATGGGCTACTGTAC 120
DB 501 CTAATAACCAAGCTGTCATCCCTTCTCGCTAACCAAGAAATCATAACTACTAATAC 560
QY 121 TTGCGCAAGGCTTGTCGAGATCTACCTGGCGTCGACGTGCTCTTGACAGTGTCC 180
DB 561 TTCGAAAACTTAATACGAATCTACCTAACGCTCGACGTACTCTTACACGCTGCC 620
QY 181 ATCGTGACCTGTGCGCAATCAAGCTGGAACCGCTACTGTGTCATCACAAGGCCATCGAG 240

DB 621 ATCGTACACCTATACGCCGATCAACCTAAACCGCTACTAATCCATCACACAACCATCGAA 680
QY 241 TACAACCTGAAGCGCAGCGCCGCCGCATCAAGGCCATCATCATCACCGTGTGGTATC 300
DB 681 TACAACCTAAACGACGCGCGCGCGCATCAAAACCATCATCATCACCGTGTAAATCATC 740
QY 301 TCGGCGGTATCTCTCTTCCCGCGCTCATCTCCATCGAGAAAGAGGCGCGCGCGGC 360
DB 741 TCGACCGTATCTCTCTTCCCGCGCTCATCTCCATCGAATAAAAAACGACGACGAC 800
QY 361 CCGCAGCGCGCGGAGCGCGCGCTGCGAGATCAACGACCAAGAGTGTACGTACTCTGTCG 420
DB 801 CCGCAACCGACCGAAACCGCGCTACGAAATCAACGACCAAAATAATACGTACTCTGTCG 860
QY 421 TGCAATCGGCTCTCTCTGCTGCTCCCTGCTCATCATGATCCTGCTACGTGCGCATCTAC 480
DB 861 TACATCGACTCTCTCTGCTGCTCCCTTACCTCATCATTAATCTAATCTACGTACGATCTAC 920
QY 481 CAGATCGCAAGCGTTCGACCCCGCTGCGCAACCCAGCCGCGCGGTCCGACGCGTCCGC 540
DB 921 CAATCGCCAAACGTTCGACCCCGCTTACCAACCCAGCCGCGGAAATCCGAACGCGTCCGC 980
QY 541 GCGCGCGCGGCGGCGACCGAGCGCGAGCGCCCAACGCTGTGGGCCCGCGAGCGCGGCG 600
DB 981 GCGCGCGCGGAAACACCGAACCGCAACCCCAACGATCTAAACCCCGAAGCGAACCGAAC 1040
QY 601 CCGGGGCGCAGAGCGCGCAACCGCTGCGCCCAACCCAGCTCAACGCGCGCCCTGGCAGCGCC 660
DB 1041 CCGAAAAACGCAAAAAACCGAACCGCTTACCCCACTCAACGACGCGCCCTAACGAACCC 1100
QY 661 GCGCGCGCGCGCGCGCGACACCGACCGCGCTGGAACCTGGAGAGAGCTGCTTCCGAC 720
DB 1101 GCGCGACCGAACCGCGCGACACCGACCGCGCTTAAACCTAAAAAAAACCTGCTTCCGAC 1160
QY 721 CACGCGAGCGCGCTCCAGGGCGCGCGCAGACCGCGAGCGCGGTCCCGCGCGCAAGGCAAG 780
DB 1161 CACGCGAGCAGACTTCAAAAAACCGCGCAACCGCGAGCGGATCCCGCAACCAAAAAACAA 1220
QY 781 GCGCGAGCGAGCGAGTGAACCGCGCGCGACAGCTGCGCGCGCGCGCGCGCGCGCGAGC 840
DB 1221 ACCGGAACGAAACCAATTAACCGAACGACCACTACCGGACGCGAACCGAAGAACGACG 1280
QY 841 GGGATCGGAGCGCGCGTCCAGGGCGCGCGGAGAGCGCGTGGGGCTGCCAAGCGCTCG 900
DB 1281 AAATCGAAACCGCGAGTCAAAAAACGAAAAAAAACGCGTGAACCTTACCAAAAAACGTCG 1340
QY 901 CGTGGCGCGCGCGCGCAGAACCGCGAGAGCGCTTCAAGCTGCTGCTGCGCGCTGCTCATC 960
DB 1341 CGCTAACGCGAACGACAAACCGCGAAAAACGCTTCAAGTCTGCTACTAACCGTAAATCATC 1400
QY 961 GGAGTGTGCTGTGTGTGCTGCTTCCCTTCTTCACTTACAGCTACAGCTACGCGCGTCCGG 1020
DB 1401 GAAATATTCGTAATATATATTAATTCCTTCTTACCTAACAGCTACAGCGCTCAGCGCTCGAA 1460
QY 1021 TGCTCCGTGCGCAGCAGCGCTTCAAAATCTTCTGCTGCTGCTACTGCAACAGCTCG 1080
DB 1461 TACTCCGTACCAAGCAGCGCTTCAAAATCTTCTTAAATTCGACTACTACAACTACTCG 1520
QY 1081 TTGAACCCCGGTATCTTACACCATCTTCAACGAGATTTCCGCGCGCTTCAAGAGATC 1140
DB 1521 TTAACCCCGATCATCTACACCATCTTCAACGAGATTTCCGCGCGCTTCAAAAAAATC 1580
QY 1141 CTCTGTGCGGGGAGACAGGAAGCGGATCGT 1169
DB 1581 CTCTATCGAAAAAACAAAAACGAATCGT 1609
RESULT 5
ABL32073/c
ID ABL32073 standard; DNA; 7353 BP.
XX
AC ABL32073;

XX 12-JUL-2002 (first entry)
DT
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34091.
XX
KW Human; cytosine methylation; 5'-Cpg-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KM SNP; cell differentiation; ds.
XX
OS Homo sapiens.
PN MO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
XX (EPiG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
DR
XX
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
PS Claim 12: 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-Cpg-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers.
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (1) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP/s); and (11) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 1733 BP; 271 A; 211 C; 625 G; 626 T; 0 other;

Query Match 68.7%; Score 804.2; DB 24; Length 1733;
Best Local Similarity 80.5%; Pred. No. 1.5e-123;
Matches 941; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

QY 1 AGCCGGCGCTCAAGGCGCCCAAAACCTCTTCCTGGTGTCTCTGGCCTCGCGCCGACATC 60
Db 1293 AACCGCGCTCAAAACGCCCAAAACCTCTCTTAATATCTCTAACCTCGACCGACATC 1234
QY 61 CTGTGGCCACGCTGCTATCCCTTTCTCGTCGCGCAACGAGTCAATGGCTACTGTGATC 120
Db 1233 CTAAATAACACGCTGCTATCCCTTTCTCGCTAACCAACGAAATCATTAATACTACTAATAC 1174
QY 121 TTCGGCAAGGCTTGTGCGAGATCTACCTGGCGCTGACGTGCTTTCTGCAGCTGCTCC 180
Db 1173 TTCGACAAACTTAATACGAATCTACCTAACGCTGACGTACTTCTTACACAGTCTGTC 1114
QY 181 ATCGTGACCTGTGGCCATCAGCCTGACCCCTACTGTCCATCACACAGGCGCATCGAG 240

Db 1113 ATCGTACACCTATACGCCATCAACCTAAACCGTACTAATCATCATCACACAAACATCGAA 1054
QY 241 TACAACCTGAAGCGACCGCGCGCGCATCAAGGCATCATCACCGTGTGGTTCATC 300
Db 1053 TACAACCTAAACGACGCGCGCGCGCATCAAAACCATCATCATCACCGTATTAATCATC 994
QY 301 TCGGCGGTATCTCTCTCCCGCGCTCATCTCATCGAGAAGAAGGCGCGCGCGCG 360
Db 993 TCGACCGTATCTCTCTCCCGCGCTCATCTCATCGAAAAAAGAAAGACGACGACGAC 934
QY 361 CCGCACCCGCGCGCGCGCTGCGAGATCAAGACGACGAAAGTGTACGTCATCTGTCG 420
Db 933 CCGCAACCGACCGAAACCGCGCTACGAAATCAAGACGACCAAAATTAATACGTCATCTGTCG 874
QY 421 TGCATCGGCT 480
Db 873 TACATCGACT 814
QY 481 CAGATCGCCAAAGCTGCGACCGCGCTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Db 813 CAATCGCCAAACGTCGACCGCGCTACCGACCGCAACCGCGCAATFCGACGCGCTGCGC 754
QY 541 GCG 600
Db 753 GCG 694
QY 601 CCGGGGCG 660
Db 693 CCGAAAAACGCAAAACCGAACCGCTACCCACCGCACTCAACGACGCGCGCGCGCGCGCG 634
QY 661 GCG 720
Db 633 GCG 574
QY 721 CAGCGCGAGCGCGCTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 573 CAGCGCGAGCGACTCCAAAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 514
QY 781 GCGCGAGCG 840
Db 513 ACCGAGCGAGCG 454
QY 841 GCGATCG 900
Db 453 AAAATCGAAACG 394
QY 901 CGCTGCG 960
Db 393 CGCTAACCGCGAGCG 334
QY 961 GGAGTGTCTGT 1020
Db 333 GAAATATTCGTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 274
QY 1021 TGCTCCGTGCG 1080
Db 273 TACTCCGTACCG 214
QY 1081 TTGAACCGCGGTATCTACACCATCTTCAACCAAGATTTCCGCGCGCGCGCGCGCGCG 1140
Db 213 TTAAACCGCGATCTATCAACCATCTTCAACCAAGATTTCCGCGCGCGCGCGCGCGCG 154
QY 1141 CTCTGTGCG 1169
Db 153 CTCTATCGAAAAAACAACCAAGATCGT 125

RESULT 4
ABQ47501
ID ABQ47501 standard; DNA; 1733 BP.
XX
AC ABQ47501;

FT /*tag= a
FT /product= "alpha-2AAR"
FT replace(753,c)
FT /*tag= b
XX WO200179561-A2.
XX 25-OCT-2001.
XX 17-APR-2001; 2001WO-US12575.
XX 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX Liggett SB, Small KM;
XX WPI; 2001-611728/70.
DR P-PSDB; AAM52123.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
PS Disclosure; page 152; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcgctag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, BHT933 and
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR variant
CC gene.
XX
SQ Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;
Query Match 99.9%; Score 1168.4; DB 23; Length 1350;
Best Local Similarity 99.9%; Pred. No. 2.7e-183;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 361 ATCGTGACCTGTGGCCATCAGCCTGGACCGTACTGTCCATCACAAGGCCATCGAG 420
QY 241 TACAACCTGAAGCGCAGCGCCGCGGCATCAAGGCCATCATCACCCTGTGGTCATC 300
Db 421 TACAACCTGAAGCGCAGCGCCGCGGCATCAAGGCCATCATCACCCTGTGGTCATC 480
QY 301 TCGGCCGTATCTCTCCCGCGGCTCATCTCCATCGAAGAAAGGCGCGCGCGGC 360
Db 481 TCGGCCGTATCTCTCCCGCGGCTCATCTCCATCGAAGAAAGGCGCGCGCGGC 540
QY 361 CCGCAGCCGGCCGAGCGCGGCTGGAGATCAACGACCAGAAAGTGTACGTCTCTCTCG 420
Db 541 CCGCAGCCGGCCGAGCGCGGCTGGAGATCAACGACCAGAAAGTGTACGTCTCTCTCG 600
QY 421 TGCATCGGCT 480
Db 601 TGCATCGGCT 660
QY 481 CAGATCGCCAAAGCGTCCGACCCCGCGTGGCCACCAGCCGCGCGGGGTCCGAGCGCTCGCC 540
Db 661 CAGATCGCCAAAGCGTCCGACCCCGCGTGGCCACCAGCCGCGCGGGGTCCGAGCGCTCGCC 720
QY 541 GCGCCGCGGGGGGCGACCGAGCGCAGGCCCAACAGGCTGTGGCCCCCGAGCGCGCGGGC 600
Db 721 GCGCCGCGGGGGGCGACCGAGCGCAGGCCCAACAGGCTGTGGCCCCCGAGCGCGGGC 780
QY 601 CCGGGGGCGCAGAGCGCGAACCCTGCCCCACCCAGCTCAACGCGCGCCCTGGCGAGCCC 660
Db 781 CCGGGGGCGCAGAGCGCGAACCCTGCCCCACCCAGCTCAACGCGCGCCCTGGCGAGCCC 840
QY 661 GCGCCGCGGGGGGCGCGCAGACCCAGCGCGCTGGACCTGGAGAGAGCTCGTCTTCGAGC 720
Db 841 GCGCCGCGGGGGGCGCGCAGACCCAGCGCGCTGGACCTGGAGAGAGCTCGTCTTCGAGC 900
QY 721 CACGCCGAGCGGCTCCAGGGCCCCCGCAGACCCGAGCGCGGCTCCCGGGGCAAGGCAAG 780
Db 901 CACGCCGAGCGGCTCCAGGGCCCCCGCAGACCCGAGCGCGGCTCCCGGGGCAAGGCAAG 960
QY 781 GCGCCGAGCGAGCTGAAGCGCGGGCGCAGCGCTGCCGCGCGCGCGCGCGCGCGCGAGC 840
Db 961 GCGCCGAGCGAGCTGAAGCGCGGGCGCAGCGCTGCCGCGCGCGCGCGCGCGCGAGC 1020
QY 841 GGGATCGGAGCGCGGCTGCAGGGCGCGGGGGGAGAGCGCGTGGGGCTGCCAAGCGCTCG 900
Db 1021 GGGATCGGAGCGCGGCTGCAGGGCGCGGGGGGAGAGCGCGTGGGGCTGCCAAGCGCTCG 1080
QY 901 CGCTGGCGCGGGCGCGCAACCGCGAGAGCGCTTCACGTTGCTGCTGGCGCTGTCATC 960
Db 1081 CGCTGGCGCGGGCGCGCAACCGCGAGAGCGCTTCACGTTGCTGCTGGCGCTGTCATC 1140
QY 961 GGAAGTTCGT 1020
Db 1141 GGAAGTTCGT 1200
QY 1021 TGTCTCCGTGCCAGCAGCGCTTCAAAATCTTCTGTGTGTGTGTGTGTGTGTGTGTGT 1080
Db 1201 TGTCTCCGTGCCAGCAGCGCTTCAAAATCTTCTGTGTGTGTGTGTGTGTGTGTGTGT 1260
QY 1081 TTGAACCCGGTCTATCTACACCATCTTCAACACGAGTTTCCGCGCGCTTCAAGAGATC 1140
Db 1261 TTGAACCCGGTCTATCTACACCATCTTCAACACGAGTTTCCGCGCGCTTCAAGAGATC 1320
QY 1141 CTCTGTGGGGGGGAGACAGAGAGGAGTCGTG 1170
Db 1321 CTCTGTGGGGGGGAGACAGAGAGGAGTCGTG 1350

RESULT 3
ABQ47500/c
ID ABQ47500 standard; DNA; 1733 BP.
XX
AC ABQ47500;

XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI: 2001-611728/70.
DR P-PSDB; AAM52122.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
XX a polymorphic site -
PS
PS Example 7; Page 151; 163pp; English.

CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (999gcg9gcg) or (B) (99gcg9gcgtag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR gene
CC (GenBank Accession AF281308).
XX
XX

SO Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;

Query Match 100.0%; Score 1170; DB 23; Length 1350;
Best Local Similarity 100.0%; Pred. No. 1.5e-183;
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCGCGCGCTCAAGGCGGCCCAAAACCTCTTCTGGTGTCTTGCCCTGCGCGACATC 60
DB 181 AGCGCGCGCTCAAGGCGGCCCAAAACCTCTTCTGGTGTCTTGCCCTGCGCGACATC 240
OY 61 CTGTGGCCAGCTCGTCATCCCTTTCTCGCTGGCCCAAGAGGTATGGGCTACTGTAC 120
DB 241 CTGTGGCCAGCTCGTCATCCCTTTCTCGCTGGCCCAAGAGGTATGGGCTACTGTAC 300
OY 121 TTGGCAAGGCTTGTGCGAGATCTAACCCTGGCGCTGACGTGCTTCTGACGTGCTCC 180
DB 301 TTGGCAAGGCTTGTGCGAGATCTAACCCTGGCGCTGACGTGCTTCTGACGTGCTCC 360
OY 181 ATCGTGACCTGTGCGCATCAGCCTGGACCGCTACTGTCCATCACAGGCCATCGAG 240
DB 361 ATCGTGACCTGTGCGCATCAGCCTGGACCGCTACTGTCCATCACAGGCCATCGAG 420
OY 241 TACAACCTGAAGCGCAGCGCGCGCATCAAGGCCATCATCATACCGTGTGGTATC 300
DB 421 TACAACCTGAAGCGCAGCGCGCGCATCAAGGCCATCATCATACCGTGTGGTATC 480
OY 301 TCGGCGGTATCTCTTCCCGCGCTCATCTCCATCGAGAAGAGGGCGCGCGCGC 360
DB 481 TCGGCGGTATCTCTTCCCGCGCTCATCTCCATCGAGAAGAGGGCGCGCGCGC 540
OY 361 CCGCAGCGCGCGCGCGCTGCGAGATCAACGACGAGAGTGTACGTATCTCTG 420
DB 541 CCGCAGCGCGCGCGCGCTGCGAGATCAACGACGAGAGTGTACGTATCTCTG 600

OY 421 TGCATCGGCTCTTCTTCTGCTCCCTGCTCATCATGATCTGTCTACGTGCGCATCTAC 480
DB 601 TGCATCGGCTCTTCTTCTGCTCCCTGCTCATCATGATCTGTCTACGTGCGCATCTAC 660
OY 481 CAGATCGCCAAAGCGTGGCACCCCGCTGCGCACCCAGCCCGGGGTCCGGACCGCGTCC 540
DB 661 CAGATCGCCAAAGCGTGGCACCCCGCTGCGCACCCAGCCCGGGGTCCGGACCGCGTCC 720
OY 541 GCGCGCGCGGGGGGACCGAGCGCAGGCCCAACGCTGTGGCCCGGAGCGCAGCGCGGC 600
DB 721 GCGCGCGCGGGGGGACCGAGCGCAGGCCCAACGCTGTGGCCCGGAGCGCAGCGCGGC 780
OY 601 CCGGGGGGGCGAGAGCGCGAACCCTGCCCCACCTCAACGGGCGCCCTGGCGAGCCC 660
DB 781 CCGGGGGGGCGAGAGCGCGAACCCTGCCCCACCTCAACGGGCGCCCTGGCGAGCCC 840
OY 661 GCGCGCGCGGGCGCGCGACACCGAGCGCTGACCTGAGAGAGAGCTCTTCCGAC 720
DB 841 GCGCGCGCGGGCGCGCGACACCGAGCGCTGACCTGAGAGAGAGCTCTTCCGAC 900
OY 721 CACGCCAGCGGCTCCAGGGCCCCCGACACCCGAGCGCGTCCCGGGGCAAGGCAAG 780
DB 901 CACGCCAGCGGCTCCAGGGCCCCCGACACCCGAGCGCGTCCCGGGGCAAGGCAAG 960
OY 781 GCCCGAGCGAGCGTGAAGCCGGCGGACAGCCTGCCGCGCGCGGGCGCGGCGGACG 840
DB 961 GCCCGAGCGAGCGTGAAGCCGGCGGACAGCCTGCCGCGCGGGCGCGGCGGCGGACG 1020
OY 841 GGGATCGGAGCGCGGCTGCAGGGCGGGGGAGGAGCGCGCTCGGCGTCCCAAGCGTGC 900
DB 1021 GGGATCGGAGCGCGGCTGCAGGGCGGGGGAGGAGCGCGCTCGGCGTCCCAAGCGTGC 1080
OY 901 CGCTGGCGCGCGCGGAGAACCGGAGAAAGCGTTCTACAGTTCGTGCGCGGTGTCATC 960
DB 1081 CGCTGGCGCGCGCGGAGAACCGGAGAAAGCGTTCTACAGTTCGTGCTGCGGTGTCATC 1140
OY 961 GGAGTGTCTGTGTGTGCTGCTTCCCTTCTTCTTCAACCTACACGCTCACGCGCGTGGG 1020
DB 1141 GGAGTGTCTGTGTGTGCTGCTTCCCTTCTTCTTCAACCTACACGCTCACGCGCGTGGG 1200
OY 1021 TGTCCGTGCCACGACGCGCTTCAAAATCTTCTTCTGTGCTGCGCTACTGCAACAGCTCG 1080
DB 1201 TGTCCGTGCCACGACGCGCTTCAAAATCTTCTTCTGTGCTGCGCTACTGCAACAGCTCG 1260
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DB 1261 TTGAACCCGCTCATCTACACCATCTTCAACACGAGTTCCGCGCGCGCTTCAAGAGATC 1320
OY 1141 CTCTGTGGGGGGGACAGAGAGCGGATCGT 1170
DB 1321 CTCTGTGGGGGGGACAGAGAGCGGATCGT 1350

RESULT 2
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ID AAI99918 standard; DNA; 1350 BP.
XX
AC AAI99918;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2AAR variant encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.
XX
OS Homo sapiens.
XX
FH Key
FT CDS Location/Qualifiers
1..1353

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 11:01:28 ; Search time 335.892 Seconds
(without alignments)
7844.310 Million cell updates/sec

Title: US-09-636-259B-1
Perfect score: 1170
Sequence: 1 agcgcgcgcgtcaagcgcgc.....gggacaaggagcgcgctcgtg 1170

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1170	100.0	1350	23	AAI99917	Human alpha-2AAR e
2	1168.4	99.9	1350	23	AAI99918	Human alpha-2AAR v
3	804.2	68.7	1733	24	ABQ47500	Oligonucleotide fo
4	804.2	68.7	1733	24	ABQ47501	Oligonucleotide fo
5	804.2	68.7	7353	24	ABL32073	Human immune syste
6	804.2	68.7	7353	24	AAD28363	Human chemically t
7	725.2	62.0	1733	24	ABQ47498	Oligonucleotide fo
8	725.2	62.0	1733	24	ABQ47499	Oligonucleotide fo
9	725.2	62.0	7353	24	ABL32072	Human immune syste

10	725.2	62.0	7353	24	AAD28362	Human chemically t
11	485.4	41.5	1383	23	AAI99931	Human alpha-2CAR e
12	472.4	40.4	1371	23	AAI99933	Human alpha-2CAR v
13	468.8	40.1	1382	15	AAQ64890	Human derived adre
14	402.6	34.4	1344	22	AAD04761	Human alpha2B-adre
15	402.2	34.4	1344	23	AAI99906	Human alpha-2BAR t
16	400.8	34.3	1353	22	AAD04762	Human alpha2B-adre
17	399.2	34.1	1353	23	AAI99905	Human alpha-2BAR t
18	380	32.5	2064	12	AAQ14151	Human alpha 2 beta
19	380	32.5	2064	18	AAI59499	Human alpha-2b adr
20	302.2	25.8	4850	24	AAD28395	Human chemically t
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23	228.4	19.5	6904	24	AAD28365	Human chemically t
24	201.6	17.2	4850	24	AAD28394	Human chemically t
25	186	15.9	1140	18	AAT88392	Corn barnacle G-pr
26	162.4	13.9	1845	21	AAZ98400	Canine betal-adren
27	162.4	13.9	1845	24	ABK40732	Dog betal-adrenoce
28	155.4	13.3	3125	23	ABL13003	Drosophila melanog
29	155.4	13.3	3335	13	AAQ21928	Drosophila melanog
30	155.4	13.3	6313	23	ABL13002	Human betal-adreno
31	151.4	12.9	1637	22	AAF61182	Human betal-adreno
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34	151.4	12.9	1637	22	AAF61185	Human betal-adreno
35	151.4	12.9	1637	22	AAF61186	Human betal-adreno
36	151.4	12.9	1637	22	AAF61187	Human betal-adreno
37	151.4	12.9	1637	22	AAF61188	Human betal-adreno
38	151.4	12.9	1637	22	AAF61189	Human beta-adrener
39	151.4	12.9	1723	21	AAA38338	Human betal-adreno
40	151.4	12.9	1723	21	AAZ98399	Prostate cancer-as
41	151.4	12.9	1723	24	ABK92208	Human betal-adreno
42	151.4	12.9	1723	24	ABK40731	Drosophila melanog
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44	150.8	12.9	1038	23	ABL19931	Rhesus monkey beta
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ALIGNMENTS

RESULT 1	
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ID	AAI99917 standard; DNA: 1350 BP.
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AC	AAI99917;
XX	
DT	18-FEB-2002 (first entry)
XX	
DE	Human alpha-2AAR encoding DNA.
XX	
KW	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW	polymorphic site; allelic variant; cardiovascular disease;
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW	phosphorylation; inositol phosphate; alpha-2AAR;
KW	GenBank Accession AF281308; chromosome 10; ds.
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OS	Homo sapiens.
XX	
FH	Key
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FT	Location/Qualifiers
FT	CD5
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PN	WO200179561-A2.
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PD	25-OCT-2001.
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PF	17-APR-2001; 2001WO-US12575.
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 Db 351 TTTGGTAAGTGTGGTGGAGATCTATTGGCTCTCGACGTGCTTTTGGCAGTCGTC 410
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 Db 411 ATAGTGACCTGTGGCCATCAGCCTTGACCCGTACTGTCCATTCACGACGACGCCATCGAG 470
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 QY 421 TGCATCGGCTCTCTTCTGCTGCTCCCTGCTCATGATCTGCTACGTGCGCATCTAC 480
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 QY 481 CAGATCGCCCAAGCGTCCGACCCCGCTGCCACCCAGCGCGCGGGTCCGAGCGCGTCGCC 540
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DEFINITION	Mouse alpha-2 adrenergic receptor,	complete cds.	
ACCESSION	M99377		
VERSION	M99377.1	GI:191882	
KEYWORDS	alpha-2 adrenergic receptor.		
SOURCE	Mus musculus (strain 129/Sv)	DNA.	
ORGANISM	Mus musculus		

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 1454)	Link, R., Daunt, D., Barsh, G., Chruscinski, A. and Kobilka, B.	Cloning of two mouse genes encoding alpha 2-adrenergic receptor subtypes and identification of a single amino acid in the mouse alpha 2-C10 homolog responsible for an interspecies variation in antagonist binding
Mol. Pharmacol.	42 (1), 16-27 (1992)	
JOURNAL	92342131	
MEDLINE	1353249	
PUBMED		

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				Gaps 0.

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QY 61 CTGGTGCCACGCTGTCATCCCTTTCTGCTGCGCAACGAGTCATGGGCTACTGTAC 120
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JOURNAL Submitted (20-NOV-1996) Cell Biology, UMDNJ-SOM, 2 Medical Ctr.
Dr., Stratford, NJ 08084, USA

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DB 601 TCCATCGGCTCTTCTGCGCCTTGCCTCATGATCTGTTACGTGCGTATCTAC 660
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RESULT 14

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LOCUS Rat alpha-2-adrenergic receptor protein (RG20) gene, complete cds.
DEFINITION M62372
ACCESSION M62372.1 GI:206615
VERSION alpha-2-adrenergic receptor; transmembrane protein.
KEYWORDS Rattus norvegicus (strain Sprague-Dawley) adult liver DNA.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1380)
AUTHORS Lanier,S.M., Downing,S., Duzic,E. and Homcy,C.J.
TITLE Isolation of rat genomic clones encoding subtypes of the alpha
2-adrenergic receptor. Identification of a unique receptor subtype
JOURNAL J. Biol. Chem. 266 (16), 10470-10478 (1991)
MEDLINE 91244823
PUBMED 1645350

FEATURES source

gene location/Qualifiers
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1. .1353
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1. .1353
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KWCEIYLALDVLFTSSIVHLCAISLDRYMSITQAIENLKRTPRIKAIIVTWVI

PUBMED 8573196
REFERENCE 2 (bases 1 to 2291)
AUTHORS Richman,J.G.
TITLE Direct Submission
JOURNAL Submitted (26-APR-1995) Jeremy G. Richman, University of Arizona,
Pharmacology and Toxicology, College of Pharmacy, Room 235, Tucson,
AZ 85721, USA

FEATURES Location/Qualifiers
source 1..2291

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/clone="(GP) alpha-2A"
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BASE COUNT 456 a 593 c 716 g 526 t
ORIGIN

Query Match 83.7%; Score 979.4; DB 10; Length 2291;
Best Local Similarity 90.9%; Pred. No. 1.1e-119;
Matches 1066; Conservative 0; Mismatches 101; Indels 6; Gaps 2;

OY 1 AGCCGGCGCTCAAGCGCCCCAAAACCTCTTCTGCTGCTCTGCGCTCGCGCCGACATC 60
DB 229 AGCCGGCGCTCAAGCGCCCCAGAACCCTTCTGCTGCTCTGCGCTCGCGCCGACATC 288
OY 61 CTGTGGCCACGCTCGTCACTCCCTTCTCGCTGGCCAAAGAGTATGGGCTACTGTGTA 120
DB 289 CTGTGGCCACGCTCGTCACTCCCTTCTCTGCTGGCCAAAGAGTATGGGCTACTGTGTA 348
OY 121 TTGGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGACGTGCTTCTTGACAGTCGTCC 180
DB 349 TTGGTAAGGCGTGTGCGAGATCTACCTGGCGCTCGACGTGCTTCTTGACAGTCGTCC 408
OY 181 ATCGTGACCTGTGGCCATCAGCCTGAGCGGCTACTGTGCATCACAAGGCCATCGAG 240
DB 409 ATCGTGACCTGTGGCTATCAGCCTGAGCGGCTACTGTGCATCACAAGGCCATCGAG 468
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DB 469 TACAACCTGAAGCGCAGCTCCGCGCGCATCAAGGCCATCATCGTCACCGTGTGGGTATC 528
OY 301 TCGCGCGTCACTCTCTCCCGCGCTCATCTCCATCGAGAAGAGGGCGGGCGGGCGGC 360
DB 529 TCGCGCGTCACTCTCTCCCGCGCTCATCTCTTGTG--AGAAAGCGGGCGGGCGGGG 585
OY 361 CCGCAGCGCGCGCAGCGCGCTGCGAGATCAAGCAGCAGAGTGTAGCTCATCTCGTCG 420
DB 586 CAGCAGCCTGGCGAGCGCGCTGCGAGATCAAGCAGCAGAGTGTAGCTCATCTCTCC 645
OY 421 TGCATCGGCTCTCTTCTGCTCCCTGCTCATCATGATGCTGCTTACGTGCGCATCTAC 480
DB 646 AGCATCGGCTCTCTTCTGCGGCCCTGCTCATCATGATGCTGCTTACGTGCGCATTTAC 705
OY 481 CAGATCGCCAAGCGTGCACCGCGCTGCCACCCAGCGCGGGTCCGAGCGC---CGTC 537
DB 706 CAAATAGCCAAGCGCGCGCGCTGCCACCCAGCGCGAGGTCCGAGCCACACGCC 765
OY 538 GCCGCGCGCGCGGGGGCAGCGCAGGCCCAAAGGCTGGGCGCGCGAGCGCAGCGCG 597
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OY 598 GGCCCGGGGGCCAGAGGCCGAACCGCTGCCACCACAGCTCAACGGCGCCCTGGCGAG 657
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DB 946 GAGCAGCAGAGCGGCCCCCGGGGGCCGACAGCGGCTGAGAGAGAGAGCTCGTCTCG 1005
OY 778 AAGGCCGAGCGAGCCAGGTGAAGCCGGCGCAGACCTCGCGCGCGGGCGGGCGGCG 837
DB 1006 AAGCGCGCGCGAGCCAGGTGAAGCCCCGCGAGAGTCTGCCCCCGCGCGCGGGCGG 1065
OY 838 ACGGGATCGGAGCGCGCGCTGCAGGGCGGGGAGAGAGCGCGTCCGGCGCTGCCAAGCG 897
DB 1066 GCGGGGTCCGGACTTCGGGGTCCGGCGGGGAGAGAGCGTGGCGGGCGGCTAAGCGG 1125
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DB 1186 ATCGGGGTGTCTGTGTGTGCTGTTCCTTCTTCTTACCTTACAGCGCTCAGCGCGG 1245
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DB 1246 GGCTGTCTCGGTGCGCGCAGCGCTTTCAAAGTCTTCTTCTGTGCTTACTGCAACAGC 1305
OY 1078 TCGTTGAACCGGTCATCTACACCATCTTCAACACAGATTCGCGCGCTTCAAGAAG 1137
DB 1306 TCCTGAACCGGTCATCTACACCATCTTCAACACAGACTTCGCGCGCTTCAAGAAG 1365
OY 1138 ATCCTCTGTGCGGGGAGACAGGAAGCGGATCGTG 1170
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RESULT 13
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LOCUS R079031 1552 bp mRNA linear ROD 14-JUN-2000
DEFINITION Rattus norvegicus alpha2D adrenergic receptor mRNA, complete cds.
ACCESSION U79031
VERSION U79031.1 GI:3282234
KEYWORDS

SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1552)
AUTHORS Chalberg,S.C., Duda,T., Rhine,J.A. and Sharma,R.K.
TITLE Molecular cloning, sequencing and expression of an alpha
2-adrenergic receptor complementary DNA from rat brain
Mol. Cell. Biochem. 97 (2), 161-172 (1990)
PUBMED 91125329
2177834

REFERENCE 2 (bases 1 to 1552)
AUTHORS Wypijewski,K., Duda,T. and Sharma,R.K.
TITLE Structural, genetic and pharmacological identity of the rat alpha
2-adrenergic receptor subtype cA2-47 and its molecular
characterization in rat adrenal, adrenocortical carcinoma and
bovine retina
Mol. Cell. Biochem. 144 (2), 181-190 (1995)
PUBMED 95349560
7623790

JOURNAL MEDLINE 7623790
PUBMED 95349560
REFERENCE 3 (bases 1 to 1552)
AUTHORS Venkataraman,V., Duda,T.M. and Sharma,R.K.
TITLE Direct Submission

KEYWORDS alpha-2A-adrenergic receptor.
SOURCE Porcine liver DNA.
ORGANISM Sus scrofa
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
AUTHORS 1 (bases 1 to 1728)
Guyer,C.A., Horstman,D.A., Wilson,A.L., Clark,J.D., Kragoe,E.J., Jr. and Limbird,L.E.
JOURNAL Unpublished (1990)
REFERENCE 2 (bases 70 to 1582)
AUTHORS Guyer,C.A., Horstman,D.A., Wilson,A.L., Clark,J.D., Cragoe,E.J. Jr. and Limbird,L.E.
TITLE Cloning, sequencing, and expression of the gene encoding the porcine alpha 2-adrenergic receptor. Allosteric modulation by Na⁺, H⁺, and amiloride analogs
JOURNAL J. Biol. Chem. 265 (28), 17307-17317 (1990)
MEDLINE 91009167
PUBMED 2170371
COMMENT Draft entry and computer-readable sequence for [J. Biol. Chem. (1990) In press] kindly submitted by C.A.Guyer, 02-AUG-1990.
FEATURES
source location/Qualifiers
1..1728
/organism="Sus scrofa"
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130..1482
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BASE COUNT 268 a 590 c 562 g 308 t
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Query Match 84.1%; Score 984.4; DB 4; Length 1728;
Best local Similarity 90.1%; Pred. No. 2.6e-120;
Matches 1054; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
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Db 310 AGCCGCGGCTCAAGCGCCCAAGAACCTCTCTGCTGTGTCTCTGCGCTCGGGCGACATC 369
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Db 370 CTAGTGGCCACGCTCTCATCCCTTCTCTGCTGGCCCAAGAGTCTAGGGCTACTGTGTAC 429
QY 121 TTCGGCAAGGCTTGGTGGAGATCTACCTGGCGCTGACGCTGCTCTTCTGCAGCTGTCC 180
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QY 181 ATCTGTACACTGTGGCCATCAGCCTGACCGCTACTGTCCATCACACAGGCCATCGAG 240
Db 490 ATCTGTACACTGTGTGCCATCAGCTTGGATCGTACTGTCCATCACCCAGGCCATAGAG 549
QY 241 TACAACCTGAAGCGCAGCCCGCCGCATCAAGGCCATCATCATCACCCTGTGGGTATC 300
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QY 301 TCGGCGTCACTCTCTTCCCGCGCTCATCTCCATCGAGAAGAAGGGCGGCGGCGGC 360
Db 610 TCGGCGTCACTCTCTTCCCGCGCTCATCTCCATCGAGAAGAAGGCGGCGGCGGC 669
QY 361 CCGCAGCCGCGCGAGCGCGCTGGAGATCAACGACCAAGAGTGGTACGTCTCTGTG 420
Db 670 CAGCAGCCGCGCGAACCAGCGCTGGAGATCAACGACCAAGAGTGGTACGTCTCTGTG 729

QY 421 TGCATCGGCTCTCTTCTGCGTCCCTGCTCATCATGATCTCTGTCTACGTGGCATCTAC 480
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QY 481 CAGATCGCCCAAGCGTTCGACCCCGCTGCACCCAGCCGCGGGTCCGAGCCGCTCGCC 540
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Db 850 GCGCTGCGGGGGGGCGCGGAGCGGACCCCAATGGCTTAGGCCCGGAGCGCGCTGGGT 909
QY 601 CCGGGGGCGCGAGAGGCGCAACCGCTGCCACCCAGCTCAACGCGGCCCTGGCGAGCCC 660
Db 910 CGCGTGGCGCGGAGGCGCGAGCCGCTAACCCGTCCAGCTCAACGCTGCCCCGGGGAGCCC 969
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Db 970 GCGCCCGCTGGGGCCCCCGGACCGCTGACGGGCTGGACCTCGAGAGAGACTCTCTGTGAG 1029
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CPU25722 2291 bp DNA linear ROD 05-SEP-2001
LOCUS Cavia porcellus alpha-2A adrenoceptor gene, complete cds.
DEFINITION
ACCESSION U25722
VERSION U25722.1 GI:818874
KEYWORDS
SOURCE
ORGANISM
Cavia porcellus.
Cavia porcellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
REFERENCE 1 (bases 1 to 2291)
AUTHORS Svensson,S.P., Bailey,T.J., Porter,A.C., Richman,J.G. and Regan,J.W.
TITLE Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B, and alpha 2C adrenoceptor subtypes. Radioligand binding and functional coupling to a CAMP-responsive reporter gene
JOURNAL J. Biochem. Pharmacol. 51 (3), 291-300 (1996)
MEDLINE 96152573

OY 1080 GTTGAAACCCGGTCACTACACCATCTTCAACCAAGATTTCCGGCCGCTTCAAGAAGAT 1139
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Db 3337 GTTGAACCCGGTCACTACACCATCTTCAACCAAGATTTCCGGCCGCTTCAAGAAGAT 3396
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OY 1140 CCTGTGCGGGGGGACAGAGCGGATCGTG 1170
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Db 3397 CCTGTGCGGGGGGACAGAGCGGATCGTG 3427
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RESULT 10
HUMADRA
LOCUS HUMADRA 1521 bp DNA linear PRI 30-OCT-1994
DEFINITION Human platelet alpha-2-adrenergic receptor gene, complete cds.
ACCESSION M18415
VERSION M18415.1 GI:178191
KEYWORDS alpha-2-adrenergic receptor; alpha-adrenergic receptor.
SOURCE Human (lambda-EMBL 3 library) DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1521)
AUTHORS Kobilka,B.K., Matsui,H., Kobilka,T.S., Yang-Feng,T.L., Francke,U.,
Caron,M.G., Lefkowitz,R.J. and Regan,J.W.
TITLE Cloning, sequencing, and expression of the gene coding for the
human platelet alpha 2-adrenergic receptor
JOURNAL Science 238 (4827), 650-656 (1987)
MEDLINE 88042789
PUBMED 2823383
FEATURES
source location/Qualifiers
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/db_xref="taxon:9606"
/map="10q23-q25"
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/translation="MGSLOPDAGNMSWNGTEAPGGGARATPYSLOVTLTVCLAGLLM
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BASE COUNT 223 a 546 c 499 g 253 t
ORIGIN Chromosome 10q23-q25.
Query Match 97.4%; Score 1139; DB 9; Length 1521;
Best Local Similarity 99.4%; Pred. No. 1.4e-140;
Matches 1164; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
OY 1 AGCCGGCGGCTCAAGCGCCCCCAAAACCTCTTCTGTGTCTGGCCTCGCGGACATC 60
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Db 239 AGCCGGCGGCTCAAGCGCCCCCAAAACCTCTTCTGTGTCTGGCCTCGCGGACATC 298
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OY 61 CTGTGGCCACGCTGTCATCCCTTCTCGCTGGCCAACGAGTTCATGGCTACTGTGAC 120
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Db 299 CTGTGGCCACGCTGTCATCCCTTCTCGCTGGCCAACGAGTTCATGGCTACTGTGAC 358
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OY 121 TTGGGCAAGGCTGTGTGCGAGATCTACCTGGCGCTCGACGTCTTCTTGCACGTCGCC 180
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Db 359 TTGGGCAAGACTGTGTGCGAGATCTACCTGGCGCTCGACGTCTTCTTGCACGTCGCC 418
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OY 181 ATCGTGACACTGTGTGCGCATCAGCCTGGACCGCTACTGTGTCATCACACAGGCGCATCGAG 240
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Db 419 ATCGTGACACTGTGGCCCATCAGCCTGGACCGCTACTGTTCATCACACAGGCCATCGAG 478
OY 241 TACAACCTGAAGCGACGCGCGCGCGCGCATCAAGGCCATCATCATCACCCTGTGGTCATC 300
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Db 779 GCGCGCGCGGGGGGACCGAGCGCGAGGCCCAACGCTGTGGCCCCGAGCGCAGCGCGGC 838
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OY 601 CCGGGGGCGCGAGAGCGCGAACCGCTGCCACCCAGCTCAACGCGCGCCCTGGCGAGCCC 660
Db 839 CCGGGGGCGCGAGAGCGCGAACCGCTGCCACCCAGCTCAACGCGCGCCCTGGCGAGCCC 898
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OY 661 GCGCGCGCGGGGGCGCGGACACCGAGCGCGCTGTGAGAGAGAGCTCGCTTCCGAC 720
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OY 721 CACGCCGAGCGGCTTCAGGGGCCCCGACAGCCCGAGCGCGGTCCCGGGGGGCAAGGCAAG 780
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OY 841 GGGATCGGGAGCGCGCTTCAGGGGCGCGGGGAGGAGCGCGCTCGCGGCTGCCAAGCGCTCG 900
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OY 901 CGCTGGCGCGGGC-GGCAGAACCGCGAGAACCGCTTCACGTTCTGCTGGCGCTGTGTCAT 959
Db 1138 CGCTGGCGCGGGGCGAGAACCTCGAGAACCGCTTCACGTTCTGCTGGCGCTGTGTCAT 1197
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OY 960 CGGAGTGTCTGTTGTGTGCTGTGTTCCCTTCTTCTACCTACACGCTACGCGCGCTCGG 1019
Db 1198 CGGAGTGTCTGTTGTGTGCTGTGTTCCCTTCTTCTACCTACACGCTACGCGCGCTCGG 1257
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OY 1020 GTGCTCCGTGCCACGACGCGCTTCAAAATCTTCTTCTGCTGCTACTGCAACAGCTC 1079
Db 1258 GTGCTCCGTGCCACGACGCGCTTCAAAATCTTCTTCTGCTGCTACTGCAACAGCTC 1317
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OY 1080 GTGAACCCGCTCATCTACACCATCTTCAACCAAGATTTCCGGCGCTTCAAGAAGAT 1139
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OY 1140 CCTGTGTGGGGGGACAGGAAGCGGATCGTG 1170
Db 1378 CCTGTGTGGGGGGACAGGAAGCGGATCGTG 1408
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LOCUS PIGA2AR 1728 bp DNA linear MAM 27-APR-1993
DEFINITION Porcine alpha2a-adrenergic receptor (PORA2AR) gene, complete cds.
ACCESSION J05652
VERSION J05652.1 GI:164303

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OY	1021	TGCTCCGTGCACGACGCTCTTCAAATTCCTCTGGTTGGCTACTGCAACAGCTCG	1080
Dd	1201	TGCTCCGTGCACGACGCTCTTCAAATTCCTCTGGTTGGCTACTGCAACAGCTCG	1260
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Dd	1261	TTGAACCCCGTCATCTACACCATTCTTCAACCACGATTCGCCGCGCCTTCAAGAAGATC	1320
OY	1141	CTCTGTGGGGGACAGAGCGGATCGTG	1170
Dd	1321	CTCTGTGGGGGACAGAGCGGATCGTG	1350

RESULT 9	
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LOCUS	3604 bp DNA linear PRI 30-OCT-1994
DEFINITION	Human alpha 2 adrenergic receptor gene, complete cds.
ACCESSION	M23533
VERSION	M23533.1 GI:178195
KEYWORDS	adrenergic receptor; alpha-2 andrenergic receptor.
SOURCE	Human DNA.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 3604)
AUTHORS	Fraser,C.M., Arakawa,S., McCombie,W.R. and Venter,J.C.
TITLE	Cloning, sequence analysis, and permanent expression of a human

JOURNAL J. Biol. Chem. 264 (20), 11754-11761 (1989)
MEDLINE 89308571
PUBMED 2568356
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by W.R.McCombie, 30-MAR-1989.

	Location/Qualifiers
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RESULT 8
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LOCUS 1353 bp DNA linear PRI 07-FEB-2001
DEFINITION Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.
ACCESSION AF316894
VERSION AF316894.1 GI:12698667
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE An asn to lys polymorphism in the third intracellular loop of the agonist-promoted G1 coupling
J. Biol. Chem. 275 (49), 38518-38523 (2000)

JOURNAL MEDLINE 20536293
PUBMED 10948191
REFERENCE 2 (bases 1 to 1353)
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA

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Best Local Similarity 99.9%; Pred. No. 1.9e-144;
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DEFINITION	Sequence 25 from Patent WO0179561.		
ACCESSION	AX350513		
VERSION	AX350513.1	GI:18616108	
KEYWORDS	human.		
SOURCE	ORGANISM	Homo sapiens	
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		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1	liggett,S.B. and Small,K.M.	
AUTHORS		Alpha-2 adrenergic receptor polymorphisms	
TITLE		Patent: WO 0179561-A 25 25-OCT-2001;	
JOURNAL		liggett, Stephen B. (US) ; Small, Kersten M. (US)	
FEATURES		location/Qualifiers	
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BASE COUNT	199 a	489 c	442 g	220 t	ORIGIN
Query Match	99.9%	Score 1168.4;	DB 6;	Length 1350;	
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AL158163
LOCUS AL158163 204908 bp DNA linear PRI 13-DEC-2001
DEFINITION Human DNA sequence from clone RP11-348N5 on chromosome 10, complete.
ACCESSION AL158163
VERSION AL158163.11 GI:17384427
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 204908)
AUTHORS Johnson,C.
TITLE Direct Submission

JOURNAL
COMMENT
Submitted (13-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
On Dec 5, 2001 this sequence version replaced gi:16944857. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr10
RP11-348N5 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6

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Best Local Similarity 100.0%; Pred. No. 5.2e-145;
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Db 195750 AGCGCGCGCTCAAGCGCGCCCAAAACCTCTCTGCTGCTCTGCGCTGCGCGGACATC 195809
QY 61 CTGTGGCCACGCTGTCATCCCTTCTCGCTGGCCAAAGAGTCACTGGGCTACTGTAC 120
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Db 195810 CTGTGGCCACGCTGTCATCCCTTCTCGCTGGCCAAAGAGTCACTGGGCTACTGTAC 195869
QY 121 TTGGGCAAGGCTTGGTGAGATCTACCTGGCGCTGCAGCTGCTCTTGCACGTCGCC 180
|||||
Db 195870 TTGGGCAAGGCTTGGTGAGATCTACCTGGCGCTGCAGCTGCTCTTGCACGTCGCC 195929
QY 181 ATCGTGACCTGTGCGCATGACCTTGACCGCTACTGCTCATCACAGGCCATCGAG 240
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Db 195930 ATCGTGACCTGTGCGCATGACCTTGACCGCTACTGCTCATCACAGGCCATCGAG 195989
QY 241 TACAACCTGAAGCGACGCGCGCGCGCATCAAGGCCATCATCATCACCCTGTGGTCATC 300
|||||
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QY 361 CCGGAGCCGCGCGAGCGCGCTGCGAGATCAACGACGAGAGTGCTACGTCATCTCGTCG 420
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QY	121	TTCCGCAAGGCTTGGTGCAGATCTACCTGGCGCTCGACGTGCTCTTCTGCAGTCGTCC	180
Db	2385	TTCCGCAAGGCTTGGTGCAGATCTACCTGGCGCTCGACGTGCTCTTCTGCAGTCGTCC	2444
QY	181	ATCGTGACCTGTGCGCCATCAGCCTTGAGCCGCTACTGTCCATCACAACAGGCCATCGAG	240
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QY	241	TACAACCTGAAGCGCAGCGCCCGCCGCATCAAGGCCATCATCACCGTGTGGTTCATC	300
Db	2505	TACAACCTGAAGCGCAGCGCCCGCCGCATCAAGGCCATCATCACCGTGTGGTTCATC	2564
QY	301	TCGGCCGTCATCTCCTTCCCGCCGCTCATCTCCATCGAGAAGAGGGCGCGCGCGGC	360
Db	2565	TCGGCCGTCATCTCCTTCCCGCCGCTCATCTCCATCGAGAAGAGGGCGCGCGCGGC	2624
QY	361	CCGAGCCGCGCGAGCCGCGCTGCGAGATCAACGACGAGAGTGTACGTATCTCTCG	420
Db	2625	CCGAGCCGCGCGAGCCGCGCTGCGAGATCAACGACGAGAGTGTACGTATCTCTCG	2684
QY	421	TGCATCGGCTCTTCTTCTGCTCCCTGCTCATCATGATCCTGTCTACGTCCGATCTAC	480
Db	2685	TGCATCGGCTCTTCTTCTGCTCCCTGCTCATCATGATCCTGTCTACGTCCGATCTAC	2744
QY	481	CAGATCGCAAGCGTTCGACCCCGCTGCGACCCAGCCGCGCGGGTCCGGAGCGCCGTGCC	540
Db	2745	CAGATCGCAAGCGTTCGACCCCGCTGCGACCCAGCCGCGGGTCCGGAGCGCCGTGCC	2804
QY	541	GCGCCGCGCGGGGCGACGCGCAGCGCCAGCGGTCTGGGCCCGCGAGCGCAGCGCGGC	600
Db	2805	GCGCCGCGCGGGGCGACGCGCAGCGCCAGCGGTCTGGGCCCGCGAGCGCAGCGCGGC	2864
QY	601	CCGGGGGCGCAGAGCGCCGAACCGCTGCCCAACCTCAACGCGCCCTTGCGAGGCC	660
Db	2865	CCGGGGGCGCAGAGCGCCGAACCGCTGCCCAACCTCAACGCGCCCTTGCGAGGCC	2924
QY	661	GCGCCGCGCGGGCGCGCGCAGACCGAGCGCTGAGCTGAGGAGAGCTGCTCTCCGAC	720
Db	2925	GCGCCGCGCGGGCGCGCGCAGACCGAGCGCTGAGCTGAGGAGAGCTGCTCTCCGAC	2984
QY	721	CACGCCGAGCGGCTCAAGGGCCCGCAGACCCGAGCGCGGTCCCGGGGCAAGGCAAG	780
Db	2985	CACGCCGAGCGGCTCAAGGGCCCGCAGACCCGAGCGCGGTCCCGGGGCAAGGCAAG	3044
QY	781	GCCCGAGCGAGCCAGGTGAAGCCGGGCGACAGCCTGCCGCGCGCGCGCGCGGCGAGC	840
Db	3045	GCCCGAGCGAGCCAGGTGAAGCCGGGCGACAGCCTGCCGCGCGCGCGCGGCGAGC	3104
QY	841	GCGATCGGGAACCGCGGCTGCAAGGGCCGGGAGAGAGCGGCTCGGGCTGCCAAGCGTGC	900
Db	3105	GCGATCGGGAACCGCGGCTGCAAGGGCCGGGAGAGAGCGGCTCGGGCTGCCAAGCGTGC	3164
QY	901	CGGTGGCGCGGGGCGCGGAGAAACCGCGAAGAGCGCTTCAAGTGTGCTGGCGGTGATC	960
Db	3165	CGGTGGCGCGGGGCGCGGAGAAACCGCGAAGAGCGCTTCAAGTGTGCTGGCGGTGATC	3224
QY	961	GGAGTGTTCGT	1020
Db	3225	GGAGTGTTCGT	3284
QY	1021	TGCTCCGTGCCACGACGCTCTTCAAAATCTTCTTCTGTGCTGGCTACTGCAACAGTGC	1080
Db	3285	TGCTCCGTGCCACGACGCTCTTCAAAATCTTCTTCTGTGCTGGCTACTGCAACAGTGC	3344
QY	1081	TTGAACCCGGTCACTATACACCATCTTCAACACGATTTCCGCGCGCTTCAAGAAGATC	1140
Db	3345	TTGAACCCGGTCACTATACACCATCTTCAACACGATTTCCGCGCGCTTCAAGAAGATC	3404
QY	1141	CTCTGTGGGGGACAGGAAGCGGATCTG 1170	
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RESULT	5	AF284095	3653 bp	mRNA	linear	PRI 27-MAR-2001
LOCUS						
DEFINITION						
ACCESSION						
VERSION						
KEYWORDS						
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Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	AGCCGGCGCTCAAGGCGCCCCAAAACCTTCTCCTGGTGTCTCTGGCCCTGGCCGACATC	60	
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QY	61	CTGTGGCCACGCTCGTCAATCCCTTTCTCGCTGGCCCAACGAGGTCAATGGCTACTGTAC	120	
Db	759	CTGTGGCCACGCTCGTCAATCCCTTTCTCGCTGGCCCAACGAGGTCAATGGCTACTGTAC	818	
QY	121	TTCGGCAAGGCTTGGTGGAGATCTACCTGGGCTCGACGTGCTTCTGCACGTGCTC	180	
Db	819	TTCGGCAAGGCTTGGTGGAGATCTACCTGGGCTCGACGTGCTTCTGCACGTGCTC	878	
QY	181	ATCGTGCACCTGTGGCCATCAGCCTGGAACCGCTACTGGTCCATCACAGGCCATGAG	240	
Db	879	ATCGTGCACCTGTGGCCATCAGCCTGGAACCGCTACTGGTCCATCACAGGCCATGAG	938	
QY	241	TACAACCTGAAGCGACGCGCGCGCGCCGATCAAGGCCATCATCACCGTGGGTATC	300	
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QY	301	TCGGCCGTCAATCTCTTCCCGCGCTATCTCCATCGAGAAAGAGGCGCGCGCGGC	360	
Db	999	TCGGCCGTCAATCTCTTCCCGCGCTATCTCCATCGAGAAAGAGGCGCGCGCGGC	1058	
QY	361	CCGACGCGCGCGAGCGCGCGCTGCGAGATCAACGACCAGAGAGTGTCATCTGTCG	420	
Db	1059	CCGACGCGCGCGAGCGCGCGCTGCGAGATCAACGACCAGAGAGTGTCATCTGTCG	1118	
QY	421	TGCATCGGCTCTCTCTGCTCCCTGCTCATCATGATCTGCTCTACGTGGCATCTAC	480	
Db	1119	TGCATCGGCTCTCTCTGCTCCCTGCTCATCATGATCTGCTCTACGTGGCATCTAC	1178	
QY	481	CAGATCGCCAAGCGTCGCACCCGCGTGGCCACCCAGCCCGCGGGTCCGGACCGCTGCC	540	
Db	1179	CAGATCGCCAAGCGTCGCACCCGCGTGGCCACCCAGCCCGCGGGTCCGGACCGCTGCC	1238	
QY	541	GCGCGCGCGGGGGGACCCGAGCGCGCAAGGCCCAACGGTCTGGGCCCCGAGCGCGCGGC	600	
Db	1239	GCGCGCGCGGGGGGACCCGAGCGCGCAAGGCCCAACGGTCTGGGCCCCGAGCGCGGC	1298	
QY	601	CCGGGGGGCGCAGAGGCCGAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAGCCC	660	
Db	1299	CCGGGGGGCGCAGAGGCCGAACCGCTGCCACCCAGCTCAACGGCGCCCTGGCGAGCCC	1358	
QY	661	GCGCGCGCGGGGGCGCGCGCACCGAGCGCTGAGAGAGAGCTGCTTCCGAC	720	
Db	1359	GCGCGCGCGGGGGCGCGCGCACCGAGCGCTGAGAGAGAGCTGCTTCCGAC	1418	
QY	721	CACGCCGAGCGGCTCCAGGGCCCCCGCAGAGCCGAGCGCGTCCCGCGGCAAGCAAG	780	
Db	1419	CACGCCGAGCGGCTCCAGGGCCCCCGCAGAGCCGAGCGCGTCCCGCGGCAAGCAAG	1478	
QY	781	GCCCCGAGCGAGCCAGGTGAAGCCGGGGGACAGCTGCGCGCGCGCGGGGGGCGACG	840	
Db	1479	GCCCCGAGCGAGCCAGGTGAAGCCGGGGGACAGCTGCGCGCGCGGGGGGCGACG	1538	
QY	841	GCGATCGGGAGCGCGGCTGACGGGGCGGAGAGCGCGTCCGGGCTGCCAAGCGTGC	900	
Db	1539	GCGATCGGGAGCGCGGCTGACGGGGCGGAGAGCGCGTCCGGGCTGCCAAGCGTGC	1598	
QY	901	CGCTGGCGGGGGCGGAGAACCGGAGAGCGCTTCAAGTTCGTGCTGGCGTGGTATC	960	
Db	1599	CGCTGGCGGGGGCGGAGAACCGGAGAGCGCTTCAAGTTCGTGCTGGCGTGGTATC	1658	
QY	961	GGAAGTTCGTGCTGCTGCTTCTTCTTCACTACAGCTCAGCGCGCTGGG	1020	
Db	1659	GGAAGTTCGTGCTGCTGCTTCTTCTTCACTACAGCTCAGCGCGCTGGG	1718	
QY	1021	TGCTCCGTGCAAGCAGCTCTTCAATTTCTTCTTCTGTTGGCTACTGCAACAGCTCG	1080	
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QY	1081	TTGAACCCGGTCACTACACCATCTTCAACCAGATTTCCGCGCGCTTCAAGAGATC	1140	
Db	1779	TTGAACCCGGTCACTACACCATCTTCAACCAGATTTCCGCGCGCTTCAAGAGATC	1838	
QY	1141	CTCTGTGGGGGACAGGAAGCGGATCGTG	1170	
Db	1839	CTCTGTGGGGGACAGGAAGCGGATCGTG	1868	

RESULT 4	AY032736	3612 bp	DNA	linear	PRI 12-MAY-2001
LOCUS	AY032736				
DEFINITION	Homo sapiens alpha-2A adrenergic receptor (ADR2AR) gene, complete cds.				
ACCESSION	AY032736				
VERSION	AY032736.1	GI:14029162			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens.				
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 3612)				
TITLE	Human alpha-2A adrenergic receptor gene and the genotype of -1296 nucleotide and motionsickness				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 3612)				
AUTHORS	Liu, L. and Yuan, L.				
TITLE	Direct Submission				
JOURNAL	Submitted (17-Apr-2001) Key Laboratory of Molecular Biology, General Hospital of Airforce, Fucheng Road No. 30, Beijing 100036, China				

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BASE COUNT	555 a	1278 c	1136 g	643 t
ORIGIN				

Query Match	100.0%;	Score 1170;	DB 9;	Length 3612;
Best Local Similarity	100.0%;	Pred. No. 1e-144;		
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

QY	1	AGCCGGCGCTCAAGGCGCCCCAAAACCTTCTCCTGGTGTCTCTGGCCCTGGCCGACATC	60	
Db	2265	AGCCGGCGCTCAAGGCGCCCCAAAACCTTCTCCTGGTGTCTCTGGCCCTGGCCGACATC	2324	
QY	61	CTGTGGCCACGCTCGTCAATCCCTTTCTCGCTGGCCCAAGAGGTCAATGGCTACTGTAC	120	
Db	2325	CTGTGGCCACGCTCGTCAATCCCTTTCTCGCTGGCCCAAGAGGTCAATGGCTACTGTAC	2384	

Query Match		100.0%;	Score 1170;	DB 9;	Length 1353;
Best Local Similarity		100.0%;	Pred. No. 1.2e-144;		
Matches 1170;		Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
OY	1	AGCCGCGGCTCAAGGCGCCCAAAACCTCTTCCGTGTGTCTCTGGCCTCGGCGACATC	60		
Db	181	AGCCGCGGCTCAAGGCGCCCAAAACCTCTTCTGTGTCTCTGGCCTCGGCGACATC	240		
OY	61	CTGTGGCCACGCTCGTCATCCCTTTTCTCGCTGGCCCAAGAGTTCATGGGCTACTGGTAC	120		
Db	241	CTGTGGCCACGCTCGTCATCCCTTTTCTCGCTGGCCCAAGAGTTCATGGGCTACTGGTAC	300		
OY	121	TTGCGCAAGGCTGTGTCGAGATCTACCTGGCGCTGCAGCTGCTCTTCTGCAGCTGCTCC	180		
Db	301	TTGCGCAAGGCTGTGTCGAGATCTACCTGGCGCTGCAGCTGCTCTTCTGCAGCTGCTCC	360		
OY	181	ATCGTGACCTGTGCGCCATCAGCCTGGACCGCTACTGGTCCATTCACACAGGCCATCGAG	240		
Db	361	ATCGTGACCTGTGCGCCATCAGCCTGGACCGCTACTGGTCCATTCACACAGGCCATCGAG	420		
OY	241	TACAACCTGAAGCGCACGCGCGCCGATCAAGGCCATCATCATCCTGTGGGTATC	300		
Db	421	TACAACCTGAAGCGCACGCGCGCCGATCAAGGCCATCATCATCCTGTGGGTATC	480		
OY	301	TGCGCCGTCACTCTTCCCGCGCTCATCTCCATCGAAGAGAGGCGCGCGCGCGC	360		
Db	481	TGCGCCGTCACTCTTCCCGCGCTCATCTCCATCGAAGAGAGGCGCGCGCGCGC	540		
OY	361	CCGCAAGCCGCGGAGCGCGCTGCGAGATCAACGACAGAGTGATGTCATCTGTCG	420		
Db	541	CCGCAAGCCGCGGAGCGCGCTGCGAGATCAACGACAGAGTGATGTCATCTGTCG	600		
OY	421	TGCAATCGGCTCTTCTTCGCTTCCCTGCTCATCATGATCCTGTCTACTGCGCATCTAC	480		
Db	601	TGCAATCGGCTCTTCTTCGCTTCCCTGCTCATCATGATCCTGTCTACTGCGCATCTAC	660		
OY	481	CAGATCGCCAAGCGTCCGACCCGCGTGCACCCAGCCGCGGGTCCGAGCGCGTCCG	540		
Db	661	CAGATCGCCAAGCGTCCGACCCGCGTGCACCCAGCCGCGGGTCCGAGCGCGTCCG	720		
OY	541	GCGCGCGCGGGGGGCGACCGAGCGGCGCAACGGTCTGGCCCCGAGCGGAGCGCGGGC	600		
Db	721	GCGCGCGCGGGGGGCGACCGAGCGGCGCAACGGTCTGGCCCCGAGCGGAGCGCGGGC	780		
OY	601	CCGGGGGGGCGAGAGGCGCGGCTGCCACCCAGCTCAACGGCGCCCTGCGGAGCGCC	660		
Db	781	CCGGGGGGGCGAGAGGCGCGGCTGCCACCCAGCTCAACGGCGCCCTGCGGAGCGCC	840		
OY	661	GCGCGCGCGGGGGCGCGCGCGAGCGCGCTGACCTGGAGGAGAGCTGCTTCCGAC	720		
Db	841	GCGCGCGCGGGGGCGCGCGCGAGCGCGCTGACCTGGAGGAGAGCTGCTTCCGAC	900		
OY	721	CACGCGAGCGGCTCCAGGGGCGCGGAGACCCGAGCGCGGTCCCGGGCAAGGCAAG	780		
Db	901	CACGCGAGCGGCTCCAGGGGCGCGGAGACCCGAGCGCGGTCCCGGGCAAGGCAAG	960		
OY	781	GCCCGAGCGGCGAGGTGAAGCCGCGGCGACAGCCTGCCGCGCGCGGGCGGCGGACG	840		
Db	961	GCCCGAGCGGCGAGGTGAAGCCGCGGCGACAGCCTGCCGCGCGCGGGCGGCGGACG	1020		
OY	841	GGGATCGGAGCGCGGCTGCAGGGCGGGGGAGGAGCGCGCTGGGCGCTGCCAAGCGCTG	900		
Db	1021	GGGATCGGAGCGCGGCTGCAGGGCGGGGAGGAGCGCGCTGGGCGCTGCCAAGCGCTG	1080		
OY	901	CGCTGGCGGCGGCGAGAACCGCGAGAGCGCTTCACGTTCTGCTGGCGTGTCTATC	960		
Db	1081	CGCTGGCGGCGGCGAGAACCGCGAGAGCGCTTCACGTTCTGCTGGCGTGTCTATC	1140		
OY	961	GGAGTGTCTGT	1020		
Db	1141	GGAGTGTCTGT	1200		

OY	1021	TGCTCCGTGCCACGACGCGCTCTTCAAAATTTCTTCTGTGCTCGGCTACTGCAACAGCTCG	1080
Db	1201	TGCTCCGTGCCACGACGCGCTCTTCAAAATTTCTTCTGTGCTCGGCTACTGCAACAGCTCG	1260
OY	1081	TTGAACCCGGTCACTTACACCATCTTCAACCAAGATTTCCGCGCGCCTTCAAGAAGATC	1140
Db	1261	TTGAACCCGGTCACTTACACCATCTTCAACCAAGATTTCCGCGCGCCTTCAAGAAGATC	1320
OY	1141	CTCTGTGGGGGACAGGAAGCGGATCTG	1170
Db	1321	CTCTGTGGGGGACAGGAAGCGGATCTG	1350
RESULT 3			
LOCUS	AF262016	1941 bp	DNA linear PRI 22-AUG-2000
DEFINITION	Homo sapiens adrenergic receptor alpha-2A gene, complete cds.		
ACCESSION	AF262016		
VERSION	AF262016.2 GI:9864781		
KEYWORDS	.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1941)		
TITLE	Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C., Beschl,M. and Agabiti Rosel,E. A search for genetic variability in the human alpha-2 adrenergic receptor on chromosome 10		
JOURNAL	Unpublished		
AUTHORS	2 (bases 1 to 1941)		
TITLE	Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C., Beschl,M. and Agabiti Rosel,E.		
JOURNAL	Direct Submission		
AUTHORS	Submitted (29-APR-2000) Medical and Surgical Sciences, University of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy		
TITLE	3 (bases 1 to 1941)		
JOURNAL	Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C., Beschl,M. and Agabiti Rosel,E.		
AUTHORS	Direct Submission		
TITLE	Submitted (22-AUG-2000) Medical and Surgical Sciences, University of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy		
JOURNAL	Sequence update by submitter		
AUTHORS	On Aug 22, 2000 this sequence version replaced gi:9837145.		
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Query Match	100.0%; Score 1170; DB 9; Length 1941;		
Best Local Similarity	100.0%; Pred. No. 1.1e-144;		

FEATURES Liggett, Stephen B. (US) ; Small, Kersten M. (US)
source location/Qualifiers
1.1350 /organism="Homo sapiens"
BASE COUNT 199 a 490 c 441 g 220 t
ORIGIN

Query Match 100.0%; Score 1170; DB 6; Length 1350;
Best Local Similarity 100.0%; Pred. No. 1.2e-144;
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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LOCUS Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.
DEFINITION AF281308.1 GI:9652209
ACCESSION AF281308
VERSION AF281308.1
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Granlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling
JOURNAL J. Biol. Chem. 275 (49), 38518-38523 (2000)
MEDLINE 20556293
PUBMED 10948191

REFERENCE
AUTHORS Small,K.M., Forbes,S.L., Bridges,K.M. and Liggett,S.B.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA
FEATURES
source location/Qualifiers
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Gencore version 5.1.3
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Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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9	1147	98.0	3604	9	HUMADRA2R	HUMADRA2R	M23533 Human alpha
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13	955.6	81.7	1552	10	RRU79031	RRU79031	U79031 Rattus norv
14	944.4	80.7	1380	10	RATRG20	RATRG20	M62372 Rat alpha-2
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38	403.8	34.5	22842	9	AC092603	AC092603 Homo sapi	X57659 R. norvegic
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ALIGNMENTS

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LOCUS AX350512 Sequence 24 from Patent WO0179561.
DEFINITION AX350512
ACCESSION AX350512
VERSION AX350512.1 GI:18616107
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
REFERENCE 1
AUTHORS Liggett,S.B. and Small,K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 24 25-OCT-2001;


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RESULT 15
US-10-166-101-6
; Sequence 6, Application US/10166101
; Publication No. US20030008823A1
; GENERAL INFORMATION:
; APPLICANT: Weinschenk, Richard L.
; APPLICANT: Branchek, Theresa
; APPLICANT: Hartig, Paul
; TITLE OF INVENTION: DNA Encoding A 5-HT1F Receptor And Uses Thereof
; FILE REFERENCE: 39318-c
; CURRENT APPLICATION NUMBER: US/10/166,101
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/246,075
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 08/483,222
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/117,006
; PRIOR FILING DATE: 1994-08-22
; PRIOR APPLICATION NUMBER: PCT/US93/00149
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: 07/817,920
; PRIOR FILING DATE: 1992-01-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 6
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-166-101-6

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Query Match	23.38;	Score 555;	DB 9;	Length 390;
Best Local Similarity	30.28;	Pred. No. 4.2e-28;		
Matches 138; Conservative	59;	Mismatches 154;	Indels 106;	Gaps 12;

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Db      283  -----SPVYVNQVK----- 291
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Db      292  ---VRVSDALLEKKKILMAARERKATKTLGIIILGAFIYCWLEPFFIISLVMPICKDACWFH 347
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Job time : 15.5 secs

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RESULT 13
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; Sequence 4, Application US/10185991
; Publication No. US20030022900A1
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, et al.
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
; TREAT BENIGN PROSTATIC HYPERPLASIA
;
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/185,991
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/444,783
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
;
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 4:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
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; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-185-991-4

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Best Local Similarity 29.1%; Pred. No. 1.1e-28;
Matches 130; Conservative 81; Mismatches 133; Indels 103; Gaps 8;

OY	10 NASWNGTEAPGGCARATPYSLQVTLTVCLAGLLMLLTVEGNLVITIAFTSRALKAPON	69
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OY	70 LFLVSLASADILVA TLVIPFSLANEVMGWYFGKAWCEIYLALDYLFCTSSIVHLC AISL	129
Dd	82 YFIVNLAMADLLSTFYLPFSALAEVLGIWLGRI FCDIMAAVDYLCCTASILSCAIS I	141
OY	130 DRYWSITOAI EYNMKRTPPRIKAII TVWVISAVISFPPLISI EKKG GGGGPQA--EP	186
Dd	142 DRYIGVRYSLOYP TLTTRKAILALLSWAVLSTVISIGPLL-----GWKEP APNDK	193
OY	187 RCEINDOKWYVI SSCIGSFPA PCLMILYVRITYOIAKRTRVPSPRRGPD AVAAPPGGT	246
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RESULT 14
US-10-052-589-2
; Sequence 2, Application US/10052589
; Patent No. US20020133832A1
; GENERAL INFORMATION:
; APPLICANT: Perez, Dianne
; APPLICANT: Zuscik, Michael
; TITLE OF INVENTION: Model systems for neurodegenerative and cardiovascular disorders
; FILE REFERENCE: 26473/04200
; CURRENT APPLICATION NUMBER: US/10/052,589
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 09/568,255
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Mesocricetus sp.
US-10-052-589-2

```

	Query Match	23.5%;	Score 560;	DB 12;	Length 497;	
	Best Local Similarity	29.1%;	Pred. No. 2.6e+28;			
	Matches 136;	Conservative 81;	Mismatches 133;	Indels 118;	Gaps	
QY	4 LQPD-----AGNASW-----NGTEAPGGGARATPYSLOVT--LTLVCLAGLMLITV 48					
Db	1 MNPDLDTGHTNSAPAQMGEKDKANFTGPNOTSSNSTLPQLDVTTRAISVGVLGAFLFAI 60					
QY	49 FGNVLVIIVFTSRALKAPQNLEFLVSASADILVATLVIPESLANEVMGYWFEGRAWCEI 108					
Db	61 VGNILVLLSVACNRHLRTPNPFIVNLAIADLLSFVEPSATLEVLGMYWLGRIFCDI 120					
QY	109 YIALDVLECTSSIVHLCALISLDRTWSITQAIEYNLKTRPRRIKAILITVWVISAVISFPP 168					
Db	121 WAAVDVLCCTASILSLCAISIDIRIGVRYSLOQPTLVTRKAALLLSVWVLSTVISIGP 180					

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;; PRIOR FILING DATE: 1995-06-07
;; PRIOR APPLICATION NUMBER: 08/117,006
;; PRIOR FILING DATE: 1994-08-22
;; PRIOR APPLICATION NUMBER: PCT/US93/00149
;; PRIOR FILING DATE: 1993-01-08
;; PRIOR APPLICATION NUMBER: 07/817,920
;; PRIOR FILING DATE: 1992-01-08
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: PatentIn Ver. 2.0 - beta
;; SEQ ID NO 5
;; LENGTH: 376
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-166-101-5
```

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Query Match      24.4%; Score 580; DB 9; Length 376;
Best Local Similarity 31.2%; Pred. No. 1.1e-29;
Matches 138; Conservative 66; Mismatches 152; Indels 86; Gaps 9;
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```
OY 4 LQPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLLTFVGNVLIYAVTSRA 63
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 11 LPEASNRSLNATETSEAMPRTLQALKISLAVV--LSVITLATVLSNAFVLTILLTRK 68
OY 64 LKAPQNLFLVSLASADILVATLVIPESLANEVMGYWYFGKAWCEIYLADVLCTSSIVH 123
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 69 LHPNANYLIGSLATDILVSLVPMISMAYTITHTWNEFGIICDIWLSSDITCCTASILH 128
OY 124 LCAISLDYWSITQAIEXNLRTPRRIKAIITVWVISAVISFPPLISIEKGGGGGPQP 183
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 129 LCVIALDRYWAITDALEYSKRRTAGHAATMIAIWAISICISIPLEWRQAKA-----QE 183
OY 184 AEPRCIN-DQKWYVSSCIGSEFAPCLIMILVYVRIYQIAKRTRVPPSRGPDAAVAP 242
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 184 EMSDCLVNTSQISYTYSTCGAFYIPSVLLIYGRYRARNRILNPPSLYGRFTTA- 242
OY 243 PGCTERRPGLGPERSAGPGCAEAEPPLTQNLGAPGEPAPGPRDTDALDLESSSSSDHA 302
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 243 -----HLITGSG-----SSLCSLNSSLHEGHS 264
OY 303 ERPPGRRRPERGPRGKGKARASQVKGDSLPRRPGATGIGTPAGPGEERVGAAKASRW 362
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 265 HSAGSPL-----FENHVKIKILADSALER-----KRISAA----- 293
OY 363 RGRQNRKRTFVLAVVIGVVCWPFEEFTYTLTAV--GCSVPRTLEKFFWFGYCNS 419
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 294 -----REKATKILGIIIGAFITICWLPFEVSVLVPICRDCSWIHGCLDFFTWLGLYNS 348
OY 420 SLNPVIYTIENHDFRRAFKIL 441
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 349 LINPIITYVFNEEFROAFQKIV 370
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RESULT 11
US-10-005-010-4
; Sequence 4, Application US/10005010
; Patent No. US20020115149A1
; GENERAL INFORMATION:
; APPLICANT: Weinschank et al, Richard L.
; TITLE OF INVENTION: Method of obtaining A Composition Comprising A 5-HT1D
; FILE REFERENCE: 36536-BA
; CURRENT APPLICATION NUMBER: US/10/005,010
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/371,705
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-010-4
```

```
Query Match      24.3%; Score 577.5; DB 12; Length 390;
Best Local Similarity 30.6%; Pred. No. 1.6e-29;
Matches 140; Conservative 60; Mismatches 152; Indels 105; Gaps 11;
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```
OY 6 PDAGNASW----NGTEAPGGARATPY-----SLQVTLTVCLAGLMLLTFVGNVLIY 55
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 12 PPAGSETWPPQANLSSAPSONCSAKDYIYQDSISLPWKVLLVMLALITLATLSNAFVI 71
OY 56 IAVTSRALKADQNLFLVSLASADILVATLVIPESLANEVMGYWYFGKAWCEIYLADVL 115
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 72 ATVYRTRKLRHPNANYLIASLAVTDILVSLVPMISTMTVTGRTILGQVCDFWLSSDIT 131
OY 116 FCTSSIVHLCAISLDYWSITQAIEXNLRTPRRIKAIITVWVISAVISFPPLISIEK 175
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132 CCTASILHLCVIALDRYWAITDAVEYSAKRTPKRAAVMIALVWVESISISLPFFWRQAK 191
OY 176 GGGGPQPAEPRCIN-DQKWYVSSCIGSEFAPCLIMILVYVRIYQIAKR-TRVPPSR 233
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 192 A-----EEEVSECVVNTDILYTVYSVGAFYFPTLLLIYGRYVEARSRIKQTPNR 246
OY 234 RG-----PDAAVAPPGCTERRPGLGPERSAGPGCAEAEPPLTQNLG-APGEPAPGPRD 287
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 247 TGKRLTRAQILITDPSGTS-----VTSINSRVPDPVPSGSG--- 282
OY 288 TDALDLESSSSSDHAERPPGPRRPERGPRGKGKARASQVKGDSLPRRPGATGIGTPAA 347
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 283 -----SPVYVNOVK----- 291
OY 348 GPGEERVGAAKASRWGRQNRKRTFVLAVVIGVVCWPFEEFTYTLTAV--GCSVP 404
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 292 -----VRVSDALLEKKKLMARERATKTIIGAFITICWLPFEIISLVMPICKACWGH 347
OY 405 RTLEKFFWFGYCNSSLNPVIYTIENHDFRRAFKIL 441
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 348 LAIFDFFTWLGLYNSLINPIITYMSNEDFKQAFHKLI 384
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```
RESULT 12
US-09-951-622-10
; Sequence 10, Application US/09951622
; Patent No. US20020106734A1
; GENERAL INFORMATION:
; APPLICANT: Daniel R. Soppet et al.
; TITLE OF INVENTION: ADRENERGIC RECEPTOR
; FILE REFERENCE: PF128D2C1
; CURRENT APPLICATION NUMBER: US/09/951,622
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/339,244
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: 09/030,582
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 08/467,568
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US94/09051
; PRIOR FILING DATE: 1994-08-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 517
; TYPE: PRT
; ORGANISM: human
US-09-951-622-10
```

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Query Match      24.1%; Score 573.5; DB 10; Length 517;
Best Local Similarity 29.3%; Pred. No. 3.8e-29;
Matches 131; Conservative 81; Mismatches 132; Indels 103; Gaps 8;
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OY 10 NASWNGTEAPGGARATPYSLQVTLTVCLAGLMLLTFVGNVLIYAVTSRALKAPQN 69
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 22 NANFTGPNOTSSNSTLPOLDITRAISVGLVGAFFILFAIVGNILVITISVACNRHLRTPTN 81
OY 70 LFLVSLASADILVATLVIPESLANEVMGYWYFGKAWCEIYLADVLCTSSIVHLCAISL 129
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```


[illegible]

```

RESULT 6
US-09-884-430-8
; Sequence 8, Application US/09884430
; Patent No. US20020151046A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Santiago, Immaculada Slllos
; TITLE OF INVENTION: 52871, A NOVEL HUMAN G PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR AND USES THEREOF
; FILE REFERENCE: MNI-165
; CURRENT APPLICATION NUMBER: US/09/884,430
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: USSN 60/212,331
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: USSN 60/269,758
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-884-430-8

```

Query Match	27.2%;	Score 648;	DB 10;	Length 601;
Best Local Similarity	32.7%;	Pred. No. 9.5e-34;		
Matches 164;	Conservative 75;	Mismatches 161;	Indels 102;	Gaps 14.

QY	31	QVTLTVLVCAGLMLLTFVEGNVLVITAVFTSRALKAPQNLFLVSLASADILVATLVIPFS	90
Db	108	EALLTALVLS-VIIVLTIIGNILVILSVFTYKPLRIVQNFVLVLAVADLVALLVLEPN	166
QY	91	LANEVMGYWYFGKAWCEIYALADVICTSSIVHLCAISLDRAWSTITQAIENLKRTPRRI	150
Db	167	VAYSILGRMEFGIHLCKLMLTCDVLCCTSSILNLCAIALDRWAITDPINYAQKRYGRV	226
QY	151	KAIITVWVISAVISFPPLISIEKKGGGGQPAAE---PCEIINDQKWYVISSCTIGSFF	206
Db	227	LLLISGWWLSTLSSPLI-----GWNDWPDEFTSATPPCELLTSQRGYVITYSSIGSFF	279
QY	207	APCLIMLVYVRIYQIAKRRTRVPSPSRGPDVAAPPGCTERRPNGLGPERSAGPGCAEA	266
Db	280	IPLAIMTVYIEIFVATRRLRERARANKLNTIALK--STIELEPMANSSPVAASNGSKS	337
QY	267	EPLPTQL-----NGAPGEPAAGP-----	285
Db	338	RLLASWLCGGRDRAQFATPMIQNDQESISSETHQPDQSSKAGPHGNSDPQQQHVVLVYKK	397
QY	286	----RDTDAL-----DLESSSSSDHAER-----PPGPRRPERGPRGCKARA-	323
Db	398	SRRAKTKDSIKHGKTRGGRKSSSSSTCEPHGEQOLLPAGDGGSCQPGCGHSGGKSDAE	457
QY	324	-----SQVAPGDSLPRRGP-GATGIGTPAAGPGEERVGAAK---ASRW	362
Db	458	ISTESGSDPKGCIQVCVTAQADEQTSKLTPPOSSTGYAAAVSVPLOKKTSGVANOFEIEKQ	517

[illegible]

RESULT 7
US-10-166-101-3

```

; Sequence 3, Application US/10166101
; Publication No. US20030008823A1
; GENERAL INFORMATION:
; APPLICANT: Weinsbank, Richard L.
; APPLICANT: Branchek, Theresa
; APPLICANT: Hartig, Paul
; TITLE OF INVENTION: DNA Encoding A 5-HT1F Receptor And Uses Thereof
; FILE REFERENCE: 39318-C
; CURRENT APPLICATION NUMBER: US/10/166,101
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/246,075
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 08/483,222
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/117,006
; PRIOR FILING DATE: 1994-08-22
; PRIOR APPLICATION NUMBER: PCT/US93/00149
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: 07/817,920
; PRIOR FILING DATE: 1992-01-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentln Ver. 2.0 - beta
; SEQ ID NO 3
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-166-101-3

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Query Match	24.9%;	Score 594;	DB 9;	Length 422;
Best Local Similarity	34.2%;	Pred. No. 1.6e-30;		
Matches 164; Conservative	62;	Mismatches 158;	Indels 96;	Gaps 20.

[illegible]

```

; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Nyyss"nen, Kristiina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kauphanen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; TITLE OF INVENTION: protein, and uses thereof
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT APPLICATION NUMBER: US/09/825,923
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422,985
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-923-2

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Query Match	47.28;	Score 1124;	DB 10;	Length 447;
Best Local Similarity	53.28;	Pred. No. 1.1e-63;		
Matches 243; Conservative	49;	Mismatches 103;	Indels 62;	Gaps 14;

QY	27	PYSLOVTLTVLCIAGLIMLLTVEGNVLIIAVFTSRALKAPONLFLVSLASADILVATLV	86
		: : : : : : : : :	
Db	6	PYSVQATAIAAAITFLLFTTFGNALVILAVALTSRSLRAPONLFLVSLAADIIVATLI	65
QY	87	IPESLANEVMGYWFGKAWCEIYLALDVLECTSSIVHLCAISLDRYWSITOAIERYNLRT	146
		: : : :	
Db	66	IPESLANELGMYFERRTWCCEVYIALDVLCTSSIVHLCAISLDRYWAVSRALEYNSKRT	125
QY	147	PRRIKAIIITWWIVSAVISFPPLISIEKKGGGGGPQP-AEPRCETNDOKWYVISCIGSF	205
		: : : : :	
Db	126	PRRIKCIIITWVILAAVISLPPLI---YKGDOGPOPRGRPOCKLNQEAMWYILASSIGSF	181
QY	206	FAPCLIMILVVYRIVOYIAKRTRVRPPSRBGDAVAAPPGCITERENGLPERSAGPGCAE	265
		: : : :	
Db	182	FAPCLIMILVYLRIVLIAKRV-----SNRRGBRAKGGPGOGESKOPR--PDHGALASAK	233
QY	266	AEDLPT-----QLNG----APGEPAFA-GPRDTDALDEES-----SS	298
		: : :	
Db	234	LPAIASVASAREVNCHSKSTGEKEGETPEBGTGRALPPSWAALPNSGOGOKEGVCGASP	293
QY	299	SDHAERPPGPRPERGPRGCKGARASOVKPGD--SLPRRGPG-----ATGITPAAGPGE	351
		: :	
Db	294	EDEAE-----EEEEEECEBPQAVPVSPASACSPLOQPQGSRYLATLIRGOVLLTGRG-	345
QY	352	ERVGAAKASRWGRQ--NREKRTFVLAVVIGVFVVCWFPEFFTYLLTAV--GCSVPRT	406
		: :	
Db	346	--VGAIGGWWRRAQLTREKRTFVLAVVIGVFVLCWFPEFFFSYGALICPKHKCVPHG	403
QY	407	LKFEEFWFGYCNSLNPIVYTIIFNHDFRAAFKILCR	443
		: :	
Db	404	LFOEFFWIGYCNSLNPIVYTIIFNODFRARFRILCR	440

RESULT 5
US-09-782-980-84
; Sequence 84, Application US/097829980
; Patent No. US20020072089A1
; GENERAL INFORMATION:

```

; APPLICANT: Khodadoust, Mehran M.
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Busfield, Samantha J.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gu, Wei
; APPLICANT: White, David
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDST, LRSG, AND
; TITLE OF INVENTION: STMST PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNT-121CP
; CURRENT APPLICATION NUMBER: US/09/782,980
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US00/02125
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/448,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/276,400
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: 60/117,580
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,195
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/014,348
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/086,892
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/296,208
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 09/063,950
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 09/561,381
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,810
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/087,121
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/672,721
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/049,799
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 84
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; OS-09-782-980-84

```

Query Match	27.2%;	Score 648;	DB 10;	Length 601;
Best Local Similarity	32.7%;	Pred. No. 9.5e-34;		
Matches 164;	Conservative 75;	Mismatches 161;	Indels 102;	Gaps 14;

QY	31	QVTLTVLVLACGLMLLTVEGNVLVIATFTSRALKAPQNLEVLVSASADILVAATVPIS	90
Db	108	EALLTALVLS-VIIVLTIGNILVILSVFTYKPLRIVQNEFFIVSLAVADLTVALLVLPEN	166
QY	91	LANEVMGYWYFGKAWCEIYLALDVELECTSSIVHLCAISLDKRWYSITQAIEYNLKRRTPRRI	150
Db	167	VAYSILGRWEFEGHCLKMLTCDVLCTCSSILNLCAIALDRIMAITDPINYAQKRIVGRAV	226
QY	151	KAITTTVVVISAVISPPPLISIEKKGGGQPAPAE---PCEINDOKWYVISSCTIGSFF	206
Db	227	LLISGVWLSTLISSPPLI-----GWNDWPDEFTSATPCELITSORGYVIYSSLSGSFF	279
QY	207	APCLIMILVYVRIOIAKRRTRVPPSRRGPDAAVAPPGCTERRDNGLGPERSAGPGGAEA	266
Db	280	IPLAIMTIYIEIFVATRRLRERARANKLNTIALK--STELBPMANSSPVAAASNBSGSKS	337
QY	267	EPULPTQL-----NGAPGEPAAPAGP-----	285
Db	338	RLIASWLCCGRBRAQFATPMIQNDQESISSETHQPODDSSKAGPHGNSDPQQOHHVVVLVKK	397

Db 234 LPALASVASAREVNGHSHKSTGEKEGETPEDTGTTRALPPSWALPNSGQKGCGVCGASP 293
QY 299 SDHAERPPGPRRPERGPRGCKARASQVKPGD--SLPRRPG-----ATGIGTPAAGPGE 351
Db 294 EDEAE-----EEEEEEECPEQAVPVSPASACSPPLQOPQGSRYLATLRGQVLLGRG- 348
QY 352 ERVGAAKASRWGRQ--NREKRTFVLAVVIGVFWCWFPEFFTYTLTAV---GCSVPRT 406
Db 349 --VGAIGGQWRRRAQLTREKRTFVLAVVIGVFWCWFPEFFSYSGLAICPKHCKVPHG 406
QY 407 LKFEFFWFGYCNSSLNPVIYITIFNHDFFRAFKILCR 443
Db 407 LQOFFFWIGYCNSSLNPVIYITIFNODFRRAFRRIICR 443

RESULT 2

US-09-825-923-4
; Sequence 4, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Nyysanen, Kristiina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kauhanen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; TITLE OF INVENTION: protein, and uses thereof
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT APPLICATION NUMBER: US/09/825,923
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422,985
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-923-4

Query Match 47.2%; Score 1124.5; DB 10; Length 450;
Best Local Similarity 53.2%; Pred. No. 1e-63;
Matches 243; Conservative 49; Mismatches 106; Indels 59; Gaps 14;

QY 27 PYSLOVTLTVCLAGLMLLTVEGNVLIIVAVTSRAKAPQNLFLVSLASADILVATLV 86
Db 6 PYSVQATAIAAATFLILFTIFGNALVILAVLTSRLRAPQNLFLVSLAADIIVATLI 65
QY 87 IPFSLANEVGYWYFGKAWCEIYALDVLECTSSIVHLCAISLDRYWSITQAIENLKRT 146
Db 66 IPFSLANEVGYWYFRTWCEYIALDVLECTSSIVHLCAISLDRYWAVSRALEYNSKRT 125
QY 147 PRRIKAITTVWVIVSAVISFPPPLISIEKKGCGPOP-AEPRCEINDQKWYVSSCIGSF 205
Db 126 PRRIKAITTVWVIVSAVISFPPPLISIEKKGCGPOP-AEPRCEINDQKWYVSSCIGSF 181
QY 206 FAPCLIMILVYVRIYQIAKRRTVRPPSRGPDVAAPPGGTERPNGLGERSAGPGGAE 265
Db 182 FAPCLIMILVYVRIYQIAKRRTVRPPSRGPDVAAPPGGTERPNGLGERSAGPGGAE 233
QY 266 AEPLPT-----QLNG---APGEPAPA-GPRDTDALDLES-----SS 298
Db 234 LPALASVASAREVNGHSHKSTGEKEGETPEDTGTTRALPPSWALPNSGQKGCGVCGASP 293

QY 299 SDHAERPPGPRRPERGPRGCKARASQVKPGD--SLPRRPG-----ATGIGTPAAGPGE 351
Db 294 EDEAE-----EEEEEEECPEQAVPVSPASACSPPLQOPQGSRYLATLRGQVLLGRG- 348
QY 352 ERVGAAKASRWGRQ--NREKRTFVLAVVIGVFWCWFPEFFTYTLTAV---GCSVPRT 406
Db 349 --VGAIGGQWRRRAQLTREKRTFVLAVVIGVFWCWFPEFFSYSGLAICPKHCKVPHG 406
QY 407 LKFEFFWFGYCNSSLNPVIYITIFNHDFFRAFKILCR 443
Db 407 LQOFFFWIGYCNSSLNPVIYITIFNODFRRAFRRIICR 443

RESULT 3

US-10-077-870-2
; Sequence 2, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 09/3-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-870-2

Query Match 47.2%; Score 1124; DB 9; Length 447;
Best Local Similarity 53.2%; Pred. No. 1.e-63;
Matches 243; Conservative 49; Mismatches 103; Indels 62; Gaps 14;

QY 27 PYSLOVTLTVCLAGLMLLTVEGNVLIIVAVTSRAKAPQNLFLVSLASADILVATLV 86
Db 6 PYSVQATAIAAATFLILFTIFGNALVILAVLTSRLRAPQNLFLVSLAADIIVATLI 65
QY 87 IPFSLANEVGYWYFGKAWCEIYALDVLECTSSIVHLCAISLDRYWSITQAIENLKRT 146
Db 66 IPFSLANEVGYWYFRTWCEYIALDVLECTSSIVHLCAISLDRYWAVSRALEYNSKRT 125
QY 147 PRRIKAITTVWVIVSAVISFPPPLISIEKKGCGPOP-AEPRCEINDQKWYVSSCIGSF 205
Db 126 PRRIKAITTVWVIVSAVISFPPPLISIEKKGCGPOP-AEPRCEINDQKWYVSSCIGSF 181
QY 206 FAPCLIMILVYVRIYQIAKRRTVRPPSRGPDVAAPPGGTERPNGLGERSAGPGGAE 265
Db 182 FAPCLIMILVYVRIYQIAKRRTVRPPSRGPDVAAPPGGTERPNGLGERSAGPGGAE 233
QY 266 AEPLPT-----QLNG---APGEPAPA-GPRDTDALDLES-----SS 298
Db 234 LPALASVASAREVNGHSHKSTGEKEGETPEDTGTTRALPPSWALPNSGQKGCGVCGASP 293
QY 299 SDHAERPPGPRRPERGPRGCKARASQVKPGD--SLPRRPG-----ATGIGTPAAGPGE 351
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QY 352 ERVGAAKASRWGRQ--NREKRTFVLAVVIGVFWCWFPEFFTYTLTAV---GCSVPRT 406
Db 346 --VGAIGGQWRRRAQLTREKRTFVLAVVIGVFWCWFPEFFSYSGLAICPKHCKVPHG 403
QY 407 LKFEFFWFGYCNSSLNPVIYITIFNHDFFRAFKILCR 443
Db 404 LQOFFFWIGYCNSSLNPVIYITIFNODFRRAFRRIICR 440

RESULT 4
US-09-825-923-2
; Sequence 2, Application US/09825923

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 12:02:50 ; Search time 12.5 Seconds
(without alignments)
919.760 Million cell updates/sec

Title: US-09-636-259B-3
Perfect score: 2381
Sequence: 1 MGSIQPDAGNASWNGTEAPG.....HDFRRAFKKILCRGDRKRIV 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1124.5	47.2	450	9 US-10-077-870-4	Sequence 4, Appli
2	1124.5	47.2	450	10 US-09-825-923-4	Sequence 4, Appli
3	1124	47.2	447	9 US-10-077-870-2	Sequence 2, Appli
4	1124	47.2	447	10 US-09-825-923-2	Sequence 2, Appli
5	648	27.2	601	10 US-09-782-980-84	Sequence 84, Appli
6	648	27.2	601	10 US-09-884-430-8	Sequence 8, Appli
7	594	24.9	422	9 US-10-166-101-3	Sequence 3, Appli
8	589	24.7	451	10 US-09-993-844-6	Sequence 6, Appli
9	585.5	24.6	377	12 US-10-005-010-2	Sequence 2, Appli
10	580	24.4	376	9 US-10-166-101-5	Sequence 5, Appli
11	577.5	24.3	390	12 US-10-005-010-4	Sequence 4, Appli
12	573.5	24.1	517	10 US-09-951-622-10	Sequence 10, Appli
13	566.5	23.8	520	9 US-10-185-991-4	Sequence 4, Appli
14	560	23.5	497	12 US-10-052-589-2	Sequence 2, Appli
15	555	23.3	390	9 US-10-166-101-6	Sequence 6, Appli
16	553.5	23.2	572	9 US-10-185-991-2	Sequence 2, Appli
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18	545.5	22.9	466	10 US-09-951-622-11	Sequence 11, Appli
19	542.5	22.8	501	10 US-09-951-622-9	Sequence 9, Appli

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21	505	21.2	400	10 US-09-895-211-4	Sequence 4, Appli
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25	496.5	20.9	445	9 US-09-349-755-5	Sequence 5, Appli
26	496.5	20.9	445	9 US-09-166-334-5	Sequence 5, Appli
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35	464	19.5	478	9 US-10-029-009-10	Sequence 10, Appli
36	464	19.5	498	9 US-10-029-009-22	Sequence 22, Appli
37	463	19.4	460	10 US-09-782-980-82	Sequence 82, Appli
38	463	19.4	460	10 US-09-884-430-6	Sequence 6, Appli
39	461.5	19.4	279	10 US-09-864-761-36992	Sequence 36992, A
40	460	19.3	359	10 US-09-951-622-13	Sequence 13, Appli
41	452.5	19.0	445	10 US-09-989-861-16	Sequence 16, Appli
42	444	18.6	388	10 US-09-989-861-8	Sequence 8, Appli
43	441.5	18.5	359	10 US-09-989-861-19	Sequence 19, Appli
44	441	18.5	460	9 US-10-166-101-4	Sequence 4, Appli
45	435	18.3	387	10 US-09-989-861-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-077-870-4
; Sequence 4, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077, 870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-077-870-4

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Best Local Similarity	53.2%;	Pred. No.	1e-63;				
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						Gaps	14;
QY	27	PYSLOVTLTVLCIAGLIMLTFVGNVLIIVFTSRALKAPQNLFLVSLASADILVATLV	86				
DB	6	PYSVQATAIAIAAITFLILFTIFGNALVILAVLTSRSIRAPQNLFLVSLAADIIVATLI	65				
QY	87	IPESLANEVMGYWYFGKAWCEIYLALDYLFCTSSIVHLCAISLDRYWSITQAIENYLNKRT	146				
DB	66	IPESLANELTGYWYFRRTWCEVYLALDYLFCTSSIVHLCAISLDRYWAVSRALYNSKRT	125				
QY	147	PRRIKAIITVWVISAVISFPLPISIEKGGGGGPOP-AEPRCEINDQKWYVISSCIGSF	205				
DB	126	PRRIKCIITVWLIIVAVISLPLI---YKDGQGPQPRGRPOCKLNQEAWIILASSIGSF	181				
QY	206	FAPCLIMILVYVRIQIAKRTRVPPSRGPDVAVAAPPGGTERPNGLPERSAGPGGAE	265				
DB	182	FAPCLIMILVLRIVLIAKR-----SNRRGPRAKGPGGEGSKQPR---PDHGALASAK	233				
QY	266	AEPLPT-----QLNG---APGEPAFA-GPRDTDALDLES-----SS	298				


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; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
;
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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PCT-US93-08528-20

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Best Local Similarity	53.0%;	Pred. No. 4e-52;		
Matches 221; Conservative	41;	Mismatches 55;	Indels 100;	Gaps 14;

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1 APPLICATION NUMBER: US/07/676,174A
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3 FILING DATE: 19910328
4
5 CLASSIFICATION: 435
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7 ATTORNEY/AGENT INFORMATION:
8
9 NAME: Scott, Watson T.
10
11 REGISTRATION NUMBER: 26,581
12
13 REFERENCE/DOCKET NUMBER: WTS/5683/79117/KIK
14
15 TELECOMMUNICATION INFORMATION:
16
17 TELEPHONE: (202)861-3000
18
19 TELEFAX: (202)822-8944
20
21 TELEX: 6714627 CUSH
22
23 INFORMATION FOR SEQ ID NO: 2:
24
25 SEQUENCE CHARACTERISTICS:
26
27 LENGTH: 601 amino acids
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29 TYPE: AMINO ACID
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31 TOPOLOGY: linear
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33 MOLECULE TYPE: protein
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35 US-07-676-174A-2

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Query Match	27.2%;	Score 648;	DB 1;	Length 601;
Best Local Similarity	32.7%;	Pred. No. 3.6e-30;		
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OY	91	LANEVNGWYEGKAWCEIYLALDYLECTSSIVHLCAISLDRIYSTQAIEYNLKRTPRI	150
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Dd	167	VAYSILGRWEFGIHLCKLMWLCVDLCTSSIINLCAIALDRYWAITDPINYAQKRTVGRV	226
OY	151	KAIITFWAVISAVISFPPLISIEKKGGGQPQAE---PRCEINDQKWVISSCIGSFF	206
	:	: :	
Dd	227	LLISGWLLSLLISSPPLI-----GWNDMPDEFTSATPCELTSQRGYVIYSSLSGFFE	279
OY	207	APCLIMLVYVRIVQIAKRTRVPSPRRGDVAVAPPGGTERRPNGLGPERSAGPGGAEA	266
	:	: :	
Dd	280	IPLAIMTIVYEIFVATRRLERARANKLNTIALK--STLEPMANSSPYAASNSGSKS	337
OY	267	EPLPTQL-----NGAPEPAPAGR-----	285
	:	: :	
Dd	338	RLLASWLCCGRDRAQFATPMIONDESISSETHQPODSSKAGPHGNSDPQOHHVVLYVK	397
OY	286	----RDTDAL-----DLLESSSDHAER-----PPGRRPERGPRGKGKARA-	323
	:	: :	
Dd	398	SRRAKTKDSIKHCKTRGGRKSQSSTCEPHGEQULLPAGDGSCQPGGHSGGKSDAE	457
OY	324	-----SQVKPGDSLPRRG-PATGICTPAAGGEERVGAAK---ASRW	362
	:	: :	
Dd	458	ISTESGSDPKGCIOVCYTQADEQTSLKLTPPOSSGVAAVSVTPLQKTSGVNQFIEEKQ	517
OY	363	RGRONREKREFTVLAVVIGVFVWCWFPEFFTYTLTAVGCSV--PRTLFK-FFEWEGYCNS	419
	:	: :	
Dd	518	KISLSKERRAARTLGIIIMGVFVICWLPFLMYILDF-CQTCPCPTNKFKNFIWTMGYINS	576
OY	420	SLNPVIYTIENHDFRRAFKKIL	441
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Dd	577	GLNPVIYTIENLDYRRAFRKLL	598

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Search completed: February 14, 2003, 13:48:20
Job time : 18.5 secs
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Db	139	IVHLCAISLDRWYSVTGAVEYNLKRTPRVKATIVAVMIIISAVISFPPLVSLYRQPDGA-	197
QY	181	PQPAEPRCETINDQKVVYVVISSCIGSFPAPLIMILVYVRIYQIAKRTRVPPSRRGPDVA	240
Db	198	---AYPQCGLNDETWYILSSCIGSFFAPCLIMGLVYARIYVAKRRTRTLSEKRAP---V	251
QY	241	APPGGTERRRNGLGPERSAGPGAE---AEP LPTQLNGAPGEPAAGPRDTDALDLEES	297
Db	252	GPDGASPTTENGIG---AAAGEARTGTARPR-----PTWARTR-----	287
QY	298	SSDHAERP----PGRRPERGPRGCKAKARASQVKPGDSLPRRGPGATIGTPAAGGEHR	353
Db	288	---AAQRPREGAPGPLR--RGRRRRAGAG-----GAGGADGQGAGPGAAQ	328
QY	354	VGAAKASRWRC-----RQNRKRTFVLAVYIG	381
Db	329	SGALTASRSPGPGGRLSRASSRSVEFTLSRRRRARASSVCRKRYAQAREKRTFVLAVWVG	388
QY	382	VFVVVCMPEFFFTYLTITAV---GCSVPRTLKFFFWFGYCNSSINLPVITYTIFNHDFRAFK	438
Db	389	VFVLCMPEFFFTYSLYIGICREACQVGPGLFKFFFWIGYCNSSINPLVLYTVFNQDFRASFK	448
QY	439	KILCRGDRK 447	
Db	449	HILFRRRRR 457	

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RESULT 11
US-08-118-270-19
; Sequence 19, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-118-270-19

```

Query Match	44.08%	Score 1046.5;	DB 1;	Length 330;
Best Local Similarity	50.78%	Pred. No. 4e-53;		
Matches 216;	Conservative 38;	Mismatches 55;	Indels 117;	Gaps 9;

OY	36	LVCGLMLTLVTEGNNLVIIIAVETSRALKAPONLFLVSLASADILVATLVIPESLANEV	95
Dd	4	LAADVGFLLIVETVGNVLNVIANVLTSRALRAPQNLFLVASIASADILVATLVMPFSLANEI	63
OY	96	MGYWYFGKAWCEIYLALDVLCTSSIVHLCALSIDRYMSITQAIEYNLKRTPRKAIIII	155
Dd	64	M-YWYEGQWCGVYLAIDLFCFSSIVHLCAISLDRYWSVTQAVEYNLKRTPRVKATIV	122
OY	156	TWVVISAVISFPPLISIEKKGGGGPQPAEPRCEINDOKWYVISSCIGSFAPCLIMILY	215
Dd	123	AVWLISAIVISEPPLVSlyRQPDGA---AYPQCGLNDETMYILLSCIGSFFAPCLLYLV	178
OY	216	YVRIOYIAKRTRRVPPSRRGPDVAVAPPGETERRPNGLBPERSAGPGGAEAEPDLTQLNG	275
Dd	179	YARIYRVAKRRTRLSEKRAP-----VGPDGAS---PTENG	212
OY	276	APGEPAACPRDTDALDLESSSSSDHAERPPGPRRPERGPBGKGKARASQVKPGDSLPRR	335
Dd	213	L-----	213
OY	336	GPGATGIGTPAACGPEERVGA--ASRWGR-----QNREKRFTFLAVVIGFEV	384
Dd	214	-----CAAAGEARTGTARFLSRRRRARSSVCRKKAQAREKRFTEVLAL---VFV	260
OY	385	VCMFPPEFFTYTLTAV---GCSVPRTLKEFFFWGYCNSSLNPVIYTIENHDFRAAFKIL	441
Dd	261	LCWFPEFFIYSLYGICREACQVPGLFRFFFWIGYCNSSLNPVIYTVFNQDFRPSEFKIL	320
OY	442	CRGDRK	447
Dd	321	FRRRRR	326

RESULT 12
PCT-US93-08528-19
Sequence 19, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NETMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:

Db 361 XXXXXXXXREKRFTEVLAVIGVFCWPFPEFTYTLTAVGCSVPRTLFKFFFWGYNSS 420

QY 421 LNPVIYTIFFNHFRAFKILC 442

Db 421 LNPVIYTIFFNHFRAFKILC 442

RESULT 9

US-08-760-936-11

; Sequence 11, Application US/08760936

; Patent No. 5856443

; GENERAL INFORMATION:

; APPLICANT: MacLennan, A. John

; TITLE OF INVENTION: Molecular Cloning and Expression of

; G-PROTEIN COUPLED RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: US

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/760,936

; FILING DATE: December 6, 1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Pace, Doran R.

; REGISTRATION NUMBER: 38,261

; REFERENCE/DOCKET NUMBER: MAC-100C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 352-375-8100

; TELEFAX: 352-372-5800

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 450 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant

; MOLECULE TYPE: protein

; US-08-760-936-11

Query Match 61.5%; Score 1465; DB 2; Length 450;

Best Local Similarity 68.6%; Pred. No. 6.9e-77;

Matches 303; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 1 MGSLOPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLLTVEGNVLIIVFT 60

Db 1 MGSLOPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLLTVEGNVLIIVFT 60

QY 61 SRALKAPONLFLVSLASADILVATLVIPFSLANEVMGYWYFGKAWCEIYALDVLCTSS 120

Db 61 SRALKAPONLFLVSLASADILVATLVIPFSLANEVMGYWYFGKAWCEIYALDVLCTSS 120

QY 121 IVHLCAISLDRYWSITQAIENLKRTPRIKAIITVWVISAVISFPPLISIEKKGCGG 180

Db 121 IVHLCAISLDRYWSITQAIENLKRTPRIKAIITVWVISAVISFPPLISIEKKGCGG 180

QY 181 PQPAEPRCEINDQKWIYISSCISGFAPCLIMILVYRIYQIAKRTRVPPSRGPDAVA 240

Db 181 PQPAEPRCEINDQKWIYISSCISGFAPCLIMILVYRIYQIAKRTRVPPSRGPDAVA 240

QY 241 APGGTERRPNGLPERSAGPGGAEPLEPTQLNGAPGEPAPAGPRDPTDALDESSSSD 300

Db 241 XX 300

QY 301 HAERPPGPRPERGPRGKGKARASQVPGDSLPRRGPGATGIGTPAAGGEERVGAKAS 360

Db 301 XX 360

QY 361 RWRGRONREKRFTEVLAVIGVFCWPFPEFTYTLTAVGCSVPRTLFKFFFWGYNSS 420

Db 361 XXXXXXXXREKRFTEVLAVIGVFCWPFPEFTYTLTAVGCSVPRTLFKFFFWGYNSS 420

QY 421 LNPVIYTIFFNHFRAFKILC 442

Db 421 LNPVIYTIFFNHFRAFKILC 442

RESULT 10

US-08-194-338-4

; Sequence 4, Application US/08194338

; Patent No. 5474898

; GENERAL INFORMATION:

; APPLICANT: Venter, John C.

; APPLICANT: Fraser, Claire M.

; APPLICANT: McComb, William R.

; TITLE OF INVENTION: OCTOPAMINE RECEPTOR

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobe, Martens, Olson and Bear

; STREET: 620 Newport Center Drive, Sixteenth Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: USA

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/194,338

; FILING DATE: 08-FEB-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/676,174

; FILING DATE: 28-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Israel, Ned A.

; REGISTRATION NUMBER: 29,655

; REFERENCE/DOCKET NUMBER: NIH101.001DVI

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 235-8550

; TELEFAX: (619) 235-0176

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 461 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: Internal

US-08-194-338-4

Query Match 48.2%; Score 1146.5; DB 1; Length 461;

Best Local Similarity 50.9%; Pred. No. 1e-58;

Matches 249; Conservative 41; Mismatches 98; Indels 101; Gaps 12;

QY 10 NASWNGTEAPGGARAT-----PYSLOVTLTVCLAGLMLLTVEGNVLIIVFT 60

Db 19 NAGAGGERGSGGVANASGSGWPPRGQYSAGAVAGLAAYVGFIVFTVGNVLIIVFT 78

QY 61 SRALKAPONLFLVSLASADILVATLVIPFSLANEVMGYWYFGKAWCEIYALDVLCTSS 120

Db 79 SRALKAPONLFLVSLASADILVATLVIPFSLANEVMGYWYFGKAWCEIYALDVLCTSS 138

QY 121 IVHLCAISLDRYWSITQAIENLKRTPRIKAIITVWVISAVISFPPLISIEKKGCGG 180

PCT-US93-08528-22
; Sequence 22, Application PC/RUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-08528-22

Query Match 64.2%; Score 1529; DB 5; Length 334;
Best Local Similarity 71.8%; Pred. No. 1.2e-80;
Matches 301; Conservative 10; Mismatches 22; Indels 86; Gaps 3;
QY 33 TLTVLCIAGLMLLTVEGNVLTIAVFTSRALKAPQNLFLVSLASADILVATLVIPFSLA 92
Db 1 TLTVLCIAGLMLLTVEGNVLTIAVFTSRALKAPQNLFLVSIASADILVATLVIPFSLA 60
QY 93 NEVMGYWYFGKAWCEIYIALDVLEFCTSSIVHLCAISLDYWSITQAI EYNLKRTPRIKA 152
Db 61 NEVM-YWYFGKAWCEIYIALDVLEFCTSSIVHLCAISLDYWSITQAI EYNLKRTPRIKA 119
QY 153 IITVWVISAVISFP-LISTEKKGGGGPOPAEPCEINDQKWYVISSCISFEAPCLI 211
Db 120 IIVYVWVISAVISFPPLISTEKKGAGGGOQPAEPSCINDQKWYVISSSISGFEAPCLI 179
QY 212 MLVYVRIYQIAKRTRVPPSRGPDVAVAPPGGTERRPNGLGPERSAGPGGAEPPLPT 271
Db 180 NMLVYVRIYQIAKRTRVPPSRGPDACAPPGADRRPNNAVGP ERGAGTAG----- 231
QY 272 QLNGAPGEPAPAGPRDTALDLESSSSSDHAERPGRPRPERGPRGKGAKARASQYKPGDS 331
Db 232 ----- 231
QY 332 LPRRGPGATGIGTPAAGPGGEERYGAAKASRWGRGRONREKRTFVLAVVIGVVCWMPFF 391
Db 232 -----GQGEERAGAKASRWGRGRONREKRTFVIAVIGVVCWMPFF 275
QY 392 FTYTTLAVGCSVPRTLFEKFFWFGYCNSSLNPVITYTIENHDFRAFKKILCRGDKRIY 450
Db 276 FTYTTLAVGCPVPYQLFNFFWFGYCNSSLNPVITYTIENHDFRAFKKILCRGDKRIY 334

RESULT 8
US-08-196-989B-11
; Sequence 11, Application US/08196989B
; Patent No. 5585476
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,989B
; FILING DATE: 15-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: MAC-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-196-989B-11

Query Match 61.5%; Score 1465; DB 1; Length 450;
Best Local Similarity 68.6%; Pred. No. 6.9e-77;
Matches 303; Conservative 0; Mismatches 139; Indels 0; Gaps 0;
QY 1 MGSLQPDAGNASWNGTEAPGGGARATPYSLQVTLTVLCIAGLMLLTVEGNVLTIAVFT 60
Db 1 MGSLQPDAGNASWNGTEAPGGGARATPYSLQVTLTVLCIAGLMLLTVEGNVLTIAVFT 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANVMGYWYFGKAWCEIYIALDVLEFCTSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANVMGYWYFGKTWC EYIALDVLEFCTSS 120
QY 121 IVHLCAISLDYWSITQAI EYNLKRTPRIKAIITVWVISAVISFPPLISTEKKGGGG 180
Db 121 IVHLCAISLDYWSITQAI EYNLKRTPRIKAIITVWVISAVISFPPLISTEKKGGGG 180
QY 181 POPAEPCEINDQKWYVISSCISGFEAPCLIMLVYVRIYQIAKRTRVPPSRGPDVA 240
Db 181 POPAEPCEINDQKWYVISSCISGFEAPCLIMLVYVRIYQIAKRTRVPPSRGPDVA 240
QY 241 APPGTERRPNGLGPERSAGPGGAEPPLPTQLNGAPGEPAPAGPRDTALDLESSSSD 300
Db 241 XXX 300
QY 301 HAERPGRPRPERGPRGKGAKARASQYKPDLSLPRGPATGIGTPAAGPGGEERVGA AKAS 360
Db 301 XXX 360
QY 361 RWRGRONREKRTFVLAVVIGVVCWMPFFFTYTLTAVGCSVPRTLFEKFFWFGYCNSS 420

```

; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-08528-21

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Query Match          64.8%; Score 1543; DB 5; Length 330;
Best Local Similarity 74.4%; Pred. No. 1.9e-81;
Matches 311; Conservative 7; Mismatches 12; Indels 88; Gaps 6;

QY 33 TLTLVCLAGLMLTFEGNVLIIVFTSRALKAPQNLFLVSLASADILVATLVIPFSLA 92
Db 1 TLTLVCLAGLMLTFEGNVLIIVFTSRALKAPQNLFLVSLASADILVATLVIPFSLA 58
QY 93 NEVMGYWYFGKAWCEIYLALDLVLFCTSSIVHLCALISLDRYWSITQAI EYNLKRTPRRIKA 152
Db 59 NEVMGYWYFGKAWCEIYLALDLVLFCTSSIVHLCALISLDRYWSITQAI EYNLKRTPRRIKA 117
QY 153 IITVWVISAVISFPPLISIEKKGGGQPAEPCEINQKWIYISSCIGSFAPCLIM 212
Db 118 IITVWVISAVISFPPLISIEKKGGGQPAEPCEINQKWIYISSCIGSFAPCLIM 177
QY 213 ILVYVRIYQIAKRRTRVPPSRRGPDVAAPPGGTERPNGLGPERSAAGPGAEAEPLPTQ 272
Db 178 -LVYVRIYQIAKRRTRVPPSRRGPDVAAPPGGTERPNGLGPERSAAGPGAEAEPLPTQ 227
QY 273 LNGAPGEPAPAGPRDLDLLESSSSSDHAERPPGPRRPERGPRGKGKARASQVKPGDSL 332
Db 228 -----GRGRS-----ASGL 236
QY 333 PRRGPGATGIGTPAAGGGEERVGAAKASRWGRGRONREKRTFVLAVVIGVFVWCWPFPEF 392
Db 237 PRRRAGA-----GGQNRKREFTFVIAVVIIGVFVWCWPFPEF 272
QY 393 TYTLTAVGCSVPRTLKFFFWFGYCNSSLNPIYITIFNHFRAAFKKILCRGDRKRIV 450
Db 273 TYTLTAVGCSVPRTLKFFFWFGYCNSSLNPIYITIFNHFRAAFKKILCRGDRKRIV 330

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RESULT 6
US-08-118-270-22
; Sequence 22, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.

```

```

; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-118-270-22

```

```

Query Match          64.2%; Score 1529; DB 1; Length 334;
Best Local Similarity 71.8%; Pred. No. 1.2e-80;
Matches 301; Conservative 10; Mismatches 22; Indels 86; Gaps 3;

QY 33 TLTLVCLAGLMLTFEGNVLIIVFTSRALKAPQNLFLVSLASADILVATLVIPFSLA 92
Db 1 TLTLVCLAGLMLTFEGNVLIIVFTSRALKAPQNLFLVSLASADILVATLVIPFSLA 60
QY 93 NEVMGYWYFGKAWCEIYLALDLVLFCTSSIVHLCALISLDRYWSITQAI EYNLKRTPRRIKA 152
Db 61 NEVM-YWYFGKAWCEIYLALDLVLFCTSSIVHLCALISLDRYWSITQAI EYNLKRTPRRIKA 119
QY 153 IITVWVISAVISFPPLISIEKKGGGQPAEPCEINQKWIYISSCIGSFAPCLIM 211
Db 120 IITVWVISAVISFPPLISIEKKGGGQPAEPCEINQKWIYISSCIGSFAPCLIM 179
QY 212 MILVYVRIYQIAKRRTRVPPSRRGPDVAAPPGGTERPNGLGPERSAAGPGAEAEPLPT 271
Db 180 NHLVYVRIYQIAKRRTRVPPSRRGPDACSAPPGCADRRPNVAGPERGAGTAG----- 231
QY 272 QLNGAPGEPAPAGPRDLDLLESSSSSDHAERPPGPRRPERGPRGKGKARASQVKPGDS 331
Db 232 ----- 231
QY 332 LPRRGPGATGIGTPAAGGGEERVGAAKASRWGRGRONREKRTFVLAVVIGVFVWCWPFPEF 391
Db 232 -----GQGEERAGGAAKASRWGRGRONREKRTFVLAVVIGVFVWCWPFPEF 275
QY 392 FTYTLTAVGCSVPRTLKFFFWFGYCNSSLNPIYITIFNHFRAAFKKILCRGDRKRIV 450
Db 276 FTYTLTAVGCPVPYQLNFNFWFGYCNSSLNPIYITIFNHFRAAFKKILCRGDRKRIV 334

```

```

RESULT 7

```

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,971B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-465-971B-4
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Query Match          69.9%; Score 1665; DB 2; Length 358;
Best Local Similarity 74.0%; Pred. No. 2.2e-88;
Matches 339; Conservative 4; Mismatches 7; Indels 108; Gaps 7;
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QY 1 MGSLOPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLLTVEGNVLIAVET 60
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Db 1 MGSLOPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLLTVEGNVLIAVET 60

QY 61 SRALKAPQNLFLV-SLASADILVA--TLVIPESLANEVMGYWYFGKAWCEIYLALDVLFC 117
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 SRALKAPQNLFLVXSLASADILVAXXTLVIPESLANEVMGYWYFGKAWCEIYLALDVLFC 120

QY 118 TSSIVHLCALISLDRWYSITQAIENYLNKTRPRRIKAIITVWVISAVISEPPLISIEKKG- 176
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 TSSIVHLCALISLDRWYSITQAIENYLNKTRPRRIKAIITVWVISAVISEPPLISIEKKGx 180

QY 177 -GGGPPQPAEPRCIEINDQKWYVSSCIGSFEAPCLIMILVYVRIYQIAKRTRVPPSRRG 235
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 XGGGGPPQPAEPRCIEINDQKWYVSSCIGSFEAPCLIMILVYVRIYQIAKRTRVPPSRRG 240

QY 236 PDAVAAPPGETERRPENGLPERSAGPGGAEAEPPLTQLNGAPGEPAPAGPRDTALDLEE 295
   |||||||||||:
Db 241 PDAVAAPPGETLQ----- 252

QY 296 SSSSDHAERPPGRRRPERGPRGKGKARASQVKGPGDSLPRRGPGATGIGTPAAGPEERVG 355
   |||:|:|:|
Db 253 -----GGRGS-----ASGLPRRRAGA----- 268

QY 356 AAKASRWGRGRQNRKRTFVLAVVIGVFVVCWPEFFFTYTLTAVGCSVPRTLKFFFWEG 415
   | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 269 -----GGQNRKRTFVLAVVIGVFVVCWPEFFFTYTLTAVGCSVPRTLKFFFWEG 320

QY 416 YCNSSLNPVIYITFNHDERRAFKKI--LCRGDRKRIV 450
   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 321 YCNSSLNPVIYITFNHDERRAFKKIXXLCRGDRKRIV 358
```

```
RESULT 4
US-08-118-270-21
Sequence 21, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
```

```
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-21
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Query Match          64.8%; Score 1543; DB 1; Length 330;
Best Local Similarity 74.4%; Pred. No. 1.9e-81;
Matches 311; Conservative 7; Mismatches 12; Indels 88; Gaps 6;
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QY 33 TLLVCLAGLMLLVEGNVLIIAVFTSRALKAPQNLFLVSLASADILVATLVIPESLA 92
   |||||:| : |||||||||||||||||||||||||||||||||||||||||||
Db 1 TLLVLCIA--CLSLTFEGNVLTIIAVFTSRALKAPQNLFLVSLASADILVATLVIPESLA 58

QY 93 NEVMGYWYFGKAWCEIYLALDVLFC TSSIVHLCALISLDRWYSITQAIENYLNKTRPRRIKA 152
   ||| ||||||| |||||||||||||||||||||||||||||||||||||||
Db 59 NEVMGYWYFGK-WCEIYLALDVLFC TSSIVHLCALISLDRWYSITQAIENYLNKTRPRRIKA 117

QY 153 IITVWVISAVISFPPLISIEKKGGGGPPQPAEPRCIEINDQKWYVSSCIGSFEAPCLIM 212
   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 118 IITVWVISAVISFPPLISIEKKGGGGPPQPAEPRCIEINDQKWYVSSCIGSFEAPCLIM 177

QY 213 ILVYVRIYQIAKRTRVPPSRRGPDAVAAPPGETERRPENGLPERSAGPGGAEAEPPLTQ 272
   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 178 -LVYVRIYQIAKRTRVPPSRRDPDAVAAPPGETERRPENGLPERSAGPG----- 227

QY 273 LNGAPGEPAPAGPRDTALDLESSSSSDHAERPPGRRRPERGPRGKGKARASQVKGPGDSL 332
   |||:|:|
Db 228 -----GGRGS-----ASGL 236

QY 333 PRRGPGATGIGTPAAGPEERVGAAKASRWGRGRQNRKRTFVLAVVIGVFVVCWPEFF 392
   ||| || | ||||||||||| | |||||||||||
Db 237 PRRRAGA-----GGQNRKRTFVLAVVIGVFVVCWPEFF 272

QY 393 TYTLTAVGCSVPRTLKFFFWEGYCNSSLNPVIYITFNHDERRAFKKILCRGDRKRIV 450
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 273 TYTLTAVLCSPRTLKFFFWEGYCNSSLNPVIYITFNHDERRAFKKILCRGDRKRIV 330
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RESULT 5
PCT-US93-08528-21
Sequence 21, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
```


;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
US-08-444-734A-8

Query Match 92.9%; Score 2211; DB 1; Length 450;
Best Local Similarity 93.8%; Pred. No. 1.9e-119;
Matches 422; Conservative 2; Mismatches 26; Indels 0; Gaps 0;

QY 1 MGSLOPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLLTVEGNVLIIVFTS 60
Db 1 MGSLOPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLLTVEGNVLIIVFTS 60
QY 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEMGYWYFGKAWCEIYLALDVLCTSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEMGYWYFGKAWCEIYLALDVLCTSS 120
QY 121 IYHLCALISLDYWSITQAIENYLNKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGGG 180
Db 121 IYHLCALISLDYWSITQAIENYLNKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGGG 180
QY 181 PQPAEPRCEINDQKWYVIVSSCIGSEFAPCLIMILVYVRIYQIAKRRTVPPSRGPDVAV 240
Db 181 PQPAEPRCEINDQKWYVIVSSCIGSEFAPCLIMILVYVRIYQIAKRRTVPPSRGPDVAV 240
QY 241 APPGCTERRPGLPERSAGPGGAEAELPTQLNGAPGEPAPAGPRDTDALDLESSSSD 300
Db 241 APPGCTERRPGLPERSAGPGGAEAELPTQLNGAPGEPAPAGPRDTDALDLESSSSD 300
QY 301 HAERPPGRRPERGPRGKGKARASQVKPGDSLPRRGPGATGIGTPAAGPGEERVAKAAS 360
Db 301 HAERPPGRRPERGPRGKGKARASQVKPGDSLPRRGPGATGIGTPAAGPGEERVAKAAS 360
QY 361 RWRGRONREKRTFVLAVVIGVFWVCMFPFFFTYTLTAVGCSVPRTLKFFFWGFCYCNSS 420
Db 361 AGAGGONREKRTFVLAVVIGVFWVCMFPFFFTYTLTAVGCSVPRTLKFFFWGFCYCNSS 420
QY 421 LNPVIYTYTFNHDFRAFKKILCRGDKRKIV 450
Db 421 LNPVIYTYTFNHDFRAFKKILCRGDKRKIV 450

RESULT 2
US-08-194-338-5
; Sequence 5, Application US/08194338
; Patent No. 5474898
; GENERAL INFORMATION:
; APPLICANT: Venter, John C.
; APPLICANT: Fraser, Claire M.
; APPLICANT: McCombie, William R.
; TITLE OF INVENTION: OCTOPAMINE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobb, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,338
; FILING DATE: 08-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,174
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.

;
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH101.001DV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
US-08-194-338-5

Query Match 91.1%; Score 2170; DB 1; Length 450;
Best Local Similarity 92.9%; Pred. No. 4.1e-117;
Matches 416; Conservative 3; Mismatches 29; Indels 0; Gaps 0;

QY 3 SLOPDAGNASWNGTEAPGGARATPYSLQVTLTVCLAGLMLLTVEGNVLIIVFTSR 62
Db 3 SLOPDAGNASWNGTEAPQOARATPYSLQVTLTVCLAGLMLLTVEGNVLIIVFTSR 62
QY 63 ALKAPQNLFLVSLASADILVATLVIPFSLANEMGYWYFGKAWCEIYLALDVLCTSSIV 122
Db 63 ALKAPQNLFLVSLASADILVATLVIPFSLANEMGYWYFGKAWCEIYLALDVLCTSSIV 122
QY 123 HLCALISLDYWSITQAIENYLNKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGGGPQ 182
Db 123 HLCALISLDYWSITQAIENYLNKRTPRRIKAIITVWVISAVISFPPLISIEKKGGGGGPQ 182
QY 183 PAEPRCEINDQKWYVIVSSCIGSEFAPCLIMILVYVRIYQIAKRRTVPPSRGPDVAVAP 242
Db 183 PAEPRCEINDQKWYVIVSSCIGSEFAPCLIMILVYVRIYQIAKRRTVPPSRGPDVAVAP 242
QY 243 PGCTERRPGLPERSAGPGGAEAELPTQLNGAPGEPAPAGPRDTDALDLESSSSDHA 302
Db 243 PGCTERRPGLPERSAGPGGAEAELPTQLNGAPGEPAPAGPRDTDALDLESSSSDHA 302
QY 303 ERPPGRRPERGPRGKGKARASQVKPGDSLPRRGPGATGIGTPAAGPGEERVAKAASRW 362
Db 303 ERPPGRRPERGPRGKGKARASQVKPGDSLPRRGPGATGIGTPAAGPGEERVAKAASRW 362
QY 363 RGRONREKRTFVLAVVIGVFWVCMFPFFFTYTLTAVGCSVPRTLKFFFWGFCYCNSSLN 422
Db 363 AOGONREKRTFVLAVVIGVFWVCMFPFFFTYTLTAVGCSVPRTLKFFFWGFCYCNSSLN 422
QY 423 PVYTYTFNHDFRAFKKILCRGDKRKIV 450
Db 423 PVYTYTFNHDFRAFKKILCRGDKRKIV 450

RESULT 3
US-08-465-971B-4
; Sequence 4, Application US/08465971B
; Patent No. 5942414
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 12:02:49 ; Search time 15.5 Seconds
(without alignments)
854.214 Million cell updates/sec

Title: US-09-636-259B-3
Perfect score: 2381
Sequence: 1 MGSLQPDAGNASWNGTEAPG.....HDFRRAFKKILCRGDRKRIV 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2211	92.9	450	1 US-08-444-734A-8	Sequence 8, Appli
2	2170	91.1	450	1 US-08-194-338-5	Sequence 5, Appli
3	1665	69.9	358	2 US-08-465-971B-4	Sequence 4, Appli
4	1543	64.8	330	1 US-08-118-270-21	Sequence 21, Appli
5	1543	64.8	330	5 PCT-US93-08528-21	Sequence 21, Appli
6	1529	64.2	334	1 US-08-118-270-22	Sequence 22, Appli
7	1529	64.2	334	5 PCT-US93-08528-22	Sequence 22, Appli
8	1465	61.5	450	1 US-08-196-989B-11	Sequence 11, Appli
9	1465	61.5	450	2 US-08-760-936-11	Sequence 11, Appli
10	1146.5	48.2	461	1 US-08-194-338-4	Sequence 4, Appli
11	1046.5	44.0	330	1 US-08-118-270-19	Sequence 19, Appli
12	1046.5	44.0	330	5 PCT-US93-08528-19	Sequence 19, Appli
13	1029	43.2	330	1 US-08-118-270-20	Sequence 20, Appli
14	1029	43.2	330	5 PCT-US93-08528-20	Sequence 20, Appli
15	648	27.2	601	1 US-07-676-174A-2	Sequence 2, Appli
16	624.5	26.2	443	1 US-07-626-618A-18	Sequence 18, Appli
17	624.5	26.2	443	1 US-08-333-977-18	Sequence 18, Appli
18	619.5	26.0	415	1 US-08-194-338-10	Sequence 10, Appli
19	618	26.0	444	1 US-07-626-618A-19	Sequence 19, Appli
20	618	26.0	444	1 US-08-333-977-19	Sequence 19, Appli
21	616	25.9	444	1 US-07-781-254A-1	Sequence 1, Appli
22	594	24.9	422	1 US-07-817-920-3	Sequence 3, Appli
23	594	24.9	422	1 US-08-370-542-3	Sequence 3, Appli
24	594	24.9	422	1 US-08-117-006-3	Sequence 3, Appli
25	594	24.9	422	1 US-08-216-594-3	Sequence 3, Appli
26	594	24.9	422	1 US-08-542-358-3	Sequence 3, Appli
27	594	24.9	422	2 US-08-157-185-13	Sequence 13, Appli

28	594	24.9	422	3 US-08-281-526B-13	Sequence 13, Appli
29	594	24.9	422	3 US-09-018-351-3	Sequence 3, Appli
30	594	24.9	422	4 US-09-332-837-13	Sequence 13, Appli
31	594	24.9	422	5 PCT-US93-00149-3	Sequence 3, Appli
32	591.5	24.8	443	1 US-08-444-734A-3	Sequence 3, Appli
33	585.5	24.6	377	2 US-08-461-812-2	Sequence 2, Appli
34	585.5	24.6	377	2 US-08-157-185-14	Sequence 14, Appli
35	585.5	24.6	377	3 US-08-281-526B-14	Sequence 14, Appli
36	585.5	24.6	377	4 US-09-450-790A-14	Sequence 14, Appli
37	585.5	24.6	377	4 US-09-332-837-14	Sequence 14, Appli
38	585	24.6	375	1 US-08-370-542-5	Sequence 5, Appli
39	585	24.6	375	1 US-08-542-358-5	Sequence 5, Appli
40	585	24.6	375	3 US-09-018-351-5	Sequence 5, Appli
41	585	24.6	376	1 US-07-817-920-5	Sequence 5, Appli
42	585	24.6	376	1 US-08-117-006-5	Sequence 5, Appli
43	585	24.6	376	1 US-08-216-594-5	Sequence 5, Appli
44	585	24.6	376	5 PCT-US93-00149-5	Sequence 5, Appli
45	582	24.4	467	1 US-08-056-051-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-444-734A-8
; Sequence 8, Application US/08444734A
; Patent No. 5610282
; GENERAL INFORMATION:
; APPLICANT: Sibley, David R.
; APPLICANT: Monsma, Frederick J.
; APPLICANT: Mahan, Lawrence C.
; APPLICANT: McVittie, Loris D.
; TITLE OF INVENTION: cDNA encoding the rat D1 dopamine
; TITLE OF INVENTION: receptor linked to adenylyl cyclase activation and
; TITLE OF INVENTION: expression of the receptor protein in plasmid-transfected
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,734A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,917
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/548,714
; FILING DATE: 06-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: NIH065.001FW1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 760-0404
; TELEFAX: (714) 760-9502
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

CC vascular contraction of coronary arteries which is clinically expressed
CC as coronary heart disease (CHD), unstable chronic angina pectoris which is
CC clinically expressed as Prinzmetal's variant form or acute myocardial
CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.

PN WO200179561-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-US12575.
 XX
 PR 17-APR-2000; 2000US-0551744.
 PR 10-AUG-2000; 2000US-0636259.
 PR 19-OCT-2000; 2000US-0692077.
 XX
 PA (LIGG/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 XX
 PI Liggett SB, Small KM;
 XX
 DR WPI; 2001-611728/70.
 DR N-PSDB; AAI99906.
 XX
 XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 PS Claim 20; Page 147-149; 163pp; English.
 XX
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcgctgag) at
 CC positions 961-972 of (IIIV). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, BHT933 and
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the third intracellular loop of
 CC the human alpha-2BAR variant protein, the sequence is deleted for the 3
 CC amino acid polymorphic site at residues 301-303 (EEE) of the wildtype
 CC protein (AAM52117).
 CC
 XX
 XX
 SQ Sequence 447 AA;

 Query Match 47.2%; Score 1124; DB 22; Length 447;
 Best Local Similarity 53.2%; Pred. No. 1.1e-77;
 Matches 243; Conservative 49; Mismatches 103; Indels 62; Gaps 14;

 QY 27 PYSLOYTLTLVCLAGLMLTLTFEGNVLIIVFTSRALKAPQNLFLVSLASADILVATLV 86
 |||:| : | :| :||| |||:| |||:|||||||:|||||:
 Db 6 PYSYQATAAIAAAITFLILFTTFGNALVILAVLTSRSLRAPQNLFLVSLAADILVATLI 65

 QY 87 IPFSLANEVWGMYFGKAWCEIYALDVLCTSSIVHLCAISLDRYWSITQAIENLKRT 146
 |||||:||||| : |||:|||||||:|||||||:|||||:
 Db 66 IPFSLANELLGWYFRRTWCEVYALDVLCTSSIVHLCAISLDRYWAVSRAL EYNSKRT 125

 QY 147 PRRIKAITTWVISAVISFPPLISIEKGGGGGPQ-AEPRCEINDQKWYVSSICIGSF 205
 ||||| ||:||||:||||| |||| | |||| |:||:| :||:| ||||
 Db 126 PRRIKAITTWLIAAVISLPLI---YKDGQGPQPRGRPQCKLNQEAWYIIASSIGSF 181

 QY 206 FAPCLIMLVYVRIOIAKRTRVPPSRKCPDAVAAPPGTERRPNGLDPERSAGPGAE 265
 |||||||||:||||| |||| :||||| | | :||| :| :|
 Db 182 FAPCLIMLVYLRILIYIAKR-----SNRRGPRAKGGPGGEGSKQPR--PDHGALASAK 233

QY	266	AEPLPT-----QLNG--APGEPAPA-GPRD	TALDLEES-----SS	298
		:	:	
Db	234	LPALASVASAREVNGHSHKSGCEKEGETPEDTGT	RALPPSWAALPNSGQGQKEGVCASP	293
QY	299	SDHAERPPGPRRPERGPRGKGAKARASQVKPGD--	SLPRRPG-----ATGIGTPAAGPGE	351
			:	
Db	294	EDEAEE-----EEEEEECEBPQAVPSPASACSP	LQDPQGSRLVATLRGQVLLGRG-	345
QY	352	ERYGAAKASRWGRGRQ--NREKFTFVLAVVIGVF	VWCWPFPEFTYTLTAV--GCSVPRT	406
Db	346	--VGAIGGQWRRRRRQQLTREKFTFVLAVVIGVF	LCWPFPEFTSYSLGALCPKHCKVPHG	403
QY	407	LEKFEFFWFGYCNSSLNPVITYTTFNHD	FRAFKILCR	443
		:		:
Db	404	LFQFFFWIGYCNSSLNPVITYTTFNOD	FRAFRILCR	440
RESULT 15				
ID	AAE00989	standard; Protein; 447 AA.		
AC	AAE00989;			
XX	04-JUL-2001	(first entry)		
DE	Human	alpha2B-adrenoceptor (alpha2B-AR)	variant protein.	
XX	Human;	cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;		
KW	glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;			
KW	norepinephrine; epinephrine; therapy; vascular contraction; variant;			
KW	coronary artery; coronary heat disease; CHD; chronic angina pectoris;			
KW	acute myocardial infarction; AMI; Prinzmetal's variant.			
XX	Homo sapiens.			
XX	Key	Location/Qualifiers		
FT	Region	298..306		
FT		/note="Glutamic acid repeat"		
XX	WO200129082-A1.			
XX	26-APR-2001.			
XX	20-OCT-2000; 2000WO-FI00913.			
PR	22-OCT-1999; 99US-0422985.			
XX	(JUVA-) JUVANTIA PHARMA LTD OY.			
XX	Snapiir A', Heinonen P', Alhopuro P', Karvonen M', Koulu M', Pesonen U';			
PI	Scheinin M', Salonen JT', Tuomainen T', Lakka TA', Nyssönen K';			
PI	Salonen R', Kaunanen J', Valkonen V';			
XX	WPI: 2001-300318/31.			
DR	N-PSDB; AAD04761.			
XX	New DNA molecule encoding variant specific adrenoceptor protein with			
PT	deletion of specific amino acids located in the third intracellular			
PT	loop of the polypeptide, for treating vascular contraction of coronary			
PT	arteries			
PS	Claim 8; Page 26-27; 37pp; English.			
XX	The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) variant			
CC	protein. Alpha2B-AR has a glutamic acid repeat element (amino acids			
CC	298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino			
CC	acids 294-311), located in the third intracellular loop of the receptor			
CC	polypeptide. The variant is obtained by deletion of three glutamates from			
CC	the Glu repeat (amino acids 307-309). Alpha2B-AR gene is located on			
CC	chromosome 2. Alpha2-AR mediate many of the physiological effects of the			
CC	catecholamines, norepinephrine and epinephrine. An antagonist of			
CC	alpha2B-adrenoceptor is useful for treating a mammal suffering from			
CC	vascular contraction of coronary arteries and a disease involving			


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OY 206 FAPCLIMILVYVRIYQIAKRRTRVPPSRGPDAAVAPPGCTERRRPNGLGPERSAGPGCAE 265
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 FAPCLIMILVYVRIYLIAKR-----SNRRGPRAKGPGGQESKQPR--PDHGALASAK 233
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 266 AEP LPT-----QLNG---APGEPAPA-GPRDTALDLEES-----SS 298
      | : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 234 LPALASVASAREVNGHSHKSTGEKEGETPEDTGTALPPSMAALPNSGGQKEGYCGCASP 293
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 299 SDHAERPPGPRRPERGPRGKGKARASQVKPGD--SLPRRPG-----ATGIGTPAAGPGE 351
      ||| ||| | : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 294 EDEAEE-----EEEEEEECPEQAVPVSPASACSPLOQPQGSRYLATLRGOYLLGRG- 348
      ||| ||| | : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 352 ERVGAAKASRWGRQ--NREKRTFVLAIVIGVFVVCMPPEFFTYTLTAV--GCSVPRT 406
      ||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 349 --VGAIGGQMMRRRAQLTREKRTFVLAIVIGVFVLCWPEFFFSYSLGAICPRHCKVPHG 406
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 407 LFKFFWFGYCNSSLNPVITYTFNHDFRRAFKKILCR 443
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 407 LFOFFFWGICNSSLNPVITYTFNODFRRAFRILCR 443
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 13
AAE00990
ID AAE00990 standard; Protein; 450 AA.

AC AAE00990;

DT 04-JUL-2001 (first entry)

Human alpha2B-adrenoceptor (alpha2B-AR) protein.

KW Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
 KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
 KW norepinephrine; epinephrine; therapy; vascular contraction;
 KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
 KW acute myocardial infarction; AMI; Prinzmetal's variant.
 XX
 OS *Homo sapiens*.

Homo sapiens.

	Key	Location/Qualifiers
FH	Region	298..309
FT		/note= "Glutamic acid repeat"
FT		
xx		

PN WO200129082-A1.

PD 26-APR-2001.

PF 20-OCT-2000; 2000WO-FI00913.

PR 22-OCT-1999; 99US-0422985.

(JUVVA-) JUVANTIA PHARMA LTD OY.

Salonen R, Kauphanen J, Valkonen V;
Schelén M, Salonen JT, Tuomala T, Lakka TA, Nyyssönen K;
Simpola A, Heinonen P, Alhopuro P, Karvonen M, Koulou M, Pesonen U;

DR WPI; 2001-300318/31.
DR N-PSDB; AAD04762.

PT New DNA molecule encoding variant specific adrenoreceptor protein with
PT deletion of specific amino acids located in the third intracellular
PT loop of the polypeptide, for treating vascular contraction of corona
PT arteries -

PS Disclosure; page 29-31; 37pp; English.

Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 294-311), located in the third intracellular loop of the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2. Alpha2-AR

mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries which is clinically expressed as coronary heart disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in gene therapy.

SD Sequence 450 AA;

Query Match	47.28;	Score 1124.5;	DB 22;	Length 450;
Best Local Similarity	53.28;	Pred. No. 1e-77;		
Matches 243;	Conservative 49;	Mismatches 106;	Indels 59;	Gaps 14

QY 27 PYSLQVTLTVCLAGLLMLTFVGNLVIIAIVFTSRALKAPQNLEFVSASADILVATLV 866
|||:| | : |||:||||| |||:||||| |||:||||| |||:||||| |||:
Db 6 PYSVQATAAIAAITFLILFTFGNALVIIAVLFSTRAPQNLEFVSLAAADIVATLI 65

```
QY      87 IPFSLANEVMGYWFGKAWCEIYLALDVECTSSIVHLCAISLDRYWSITQAIEYNLKR 146
        |||||::|||| : ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
Db       66 IPFSLANELGMYFRRTWCVEYLLALDVECTSSIVHLCAISLDRYAVSRALEYNSKR 125
```

```
QY 147 PRRIKAIITVWVWISAVISFPPLISIEKKGGGGGPQ-APRCLEINDQKWYVISSCIGSF 205
      ||||| :|||:|:|:| ||| | ||||| :|||:|:|:| |||||
Db 126 PRRIKCIITVWVWLAAVISLPPLI---YKGDQGPQPRGRPQCKLQNEAWYILASSIGSF 181
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QY 206 FAPCLIMLVYRVIYQIAKRRTRVPPSRRGDVAVAPPGCTERRBNGLGPERSAGPGAE 265
    ||||| ||||| :||| | | :| :|
Db 182 FAPCLIMLVLRILYLIAR-----SNRGPRAKGGPGQGESKOPR---PDHGALASAK 233
```

QY 266 AEPLPT-----QLNG--APGEPAPA-GPRDTDALDLEES-----SS 298

Db 234 LPALASVASAREVNGSHSKSTGEKEGETPEDTGTALPSPWALPNSGGQKEGVCASP 293

QY 299 SDHAERPGRPRPERGPRGKGAKARASQYKPGD--SLPRRCPC----ATGIGTPAAGCE 351

DB 294 EDEAEE---EEEEEEEEECEPQAVPVSPASACSPPLQOPGSRVLATLRGVLGRG- 348

QY 352 ERVGAAKASRRGR--NREKRFVLAVVIGVFVCWPEPFETTYTLTAV--GCSVPRT 406
||| ||| |||||||||:|||||:| |
Db 349 --VGALGGWMRRRAQLTREKRFEVLAVVIGFVLCWFPEFFSYSLGAICPKHCAVPHG 406

QY 407 LKFEFFWEGYCNSSLNPVIYITFNHDFRRAFKILICR 443
 ||:||||| ||||||||||||| |||||:|||||
 Db 407 LKQFEFFWEGYCNSSLNPVIYITFNQDFRRAFRITICR 443

RESULT 14
AAM52118
ID AAM52118 standard; Protein; 447 AA.
....

AC AAM52118;

DT 18-FEB-2002 (first entry)

Human alpha-2BAR third intracellular loop variant.

KW human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity
KW phosphorylation; inositol phosphate; alpha-2BAR.

OS Homo sapiens.

FH	Key	Location/Qualifiers
FT	Domain	170..193

FT	/label= transmembrane_domain
FT	307..309
Region	

FT	/label= polymorphic_site
FT	370..393
Domain	

```

2 2 370.1555
2 2 domain
XX /label= transmembrane_domain

```


DR N-PSDB; AAI99931.

XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting a
PT polymorphic site -

PS Claim 78; Page 158-160; 163pp; English.

CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIV)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcggtgag) at
CC positions 961-972 of (IIR). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2CAR protein,
CC the sequence includes a 4 amino acid polymorphic site at residues 321-324
CC (GAGP), absent in the alpha-2CAR variant protein (AAM52126).

XX Sequence 461 AA;

Query Match 48.9%; Score 1164.5; DB 22; Length 461;
Best Local Similarity 51.9%; Pred. No. 9.3e-81;
Matches 252; Conservative 38; Mismatches 101; Indels 95; Gaps 11;

OY 10 NASWNGTEAPGCGARAT-----PYSLOVTLTLVCLAGLMLLTVEGNAVIAVET 60
DB 19 NASGAGERGSGGVANASGASWGPGRQYSAGAVAGLAAVGFLIVFTVGNVLVIAVL 78
OY 61 SRALKAPQNLFLVSLASADILVATLVIPESLANVMGWYFGKAWCEIYLADVLECTSS 120
DB 79 SRALRAPQNLFLVSLASADILVATLVIPESLANELMAYWYFGQWCGVYLADVLECTSS 138
OY 121 IVHLCAISLDRYWSITQAIENYLNKTRPRRIKAIITVWVISAVISFPPLISTEKKGGGG 180
DB 139 IVHLCAISLDRYWSVTQAVEYNLKRTPRRVKATIVAWLISAVISFPPLVSLYRQPDGA- 197
OY 181 POPAEPRCEINDOKWYVIVISSICISFEAPCLIMILVYVRIYQIAKRRTRVPSRGPDAVA 240
DB 198 ---AVPOGCLNDETWYILSSCISFEAPCLIMGLVYARIYVAKRRTRTLEKRAP---V 251
OY 241 APPGTERRRPNGLGPERISAGPGCAEAEPPLTQNGAPGEPAPAGPRDTALDLESSSSD 300
DB 252 GPDGASPTTENGIG---AAGEART-----GTARPRP-----TWSRTR 287
OY 301 HAERP-----PGRRPERGPRGCKAKARASQVKKPGDSLPRRPGATGIGTPAAGPEERVGA 356
DB 288 AAQRRPGAGAPPLR--RGGRRAAGAE-----GAGGADGGAGPGAAESGA 331
OY 357 AKASRWG-----RQNRKREFTVLAVVIGVFV 384
DB 332 LTASRSPGPGGRLSRASSSVEFFLSRRRRARSSVCRKVAQAAREKREFTVLAVVMGVFV 391
OY 385 VCVPPFFFTYTLTAV---GCSVPRTLKFFFWEGYCNSSINPVITYTIFNHDFFRAFKKIL 441
DB 392 LCVPPFFFTYSLYGICREACQVPGPLKFFFWIGYCNSSINPVITYVFNQDFRPSFKHIL 451
OY 442 CRGDRK 447

DB 452 FRRRRR 457

RESULT 11
AAM52126
ID AAM52126 standard; Protein; 457 AA.

XX AAM52126;

DT 18-FEB-2002 (first entry)

DE Human alpha-2CAR variant protein.

KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2CAR.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain 208..231

FT Domain /label= transmembrane_domain
FT Domain 379..402
FT /label= transmembrane_domain

PN WO200179561-A2.

PD 25-OCT-2001.

PF 17-APR-2001; 2001WO-US12575.

PR 17-APR-2000; 2000US-0551744.

PR 10-AUG-2000; 2000US-0636259.

PR 19-OCT-2000; 2000US-0692077.

PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.

PI Liggett SB, Small KM;

DR WPI; 2001-611728/70.

DR N-PSDB; AAI99933.

PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -

PS Claim 78; Page 160-162; 163pp; English.

CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIV)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcggtgag) at
CC positions 961-972 of (IIR). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate

Db	231	-----	230
QY	361	RWRGRQNRREKRETFVLAVVIGFVVCWPEPPEFTYTLTAVGCSVPRLKFEFFWGYCNS	420
Db	231	-----REKRFTEVIAVIGMFVVCWPEPPEFTYTLTAVGCSVPRLKFEFFWPGYCNS	283
QY	421	LNPVIYTIENHDFERRAFKKILCR	443
Db	284	LNPVIYTLFNFHDFERRAFWKILCR	306
RESULT 9			
ID	AAR54834	standard; Protein; 458 AA.	
XX			
AC	AAR54834;		
XX			
DT	01-FEB-1995	(first entry)	
XX			
DE	Human derived adrenaline alpha 2CII receptor.		
XX			
KW	adrenaline receptor; alpha CII; screening; detection; pharmacology;		
KW	drugs.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 1	/note= "may or may not be present, but is only present if amino acid residues 2-17 are present"	
FT	Peptide	2..17	
FT		/label= N-terminal_peptide	
FT		/note= "may or may not be present"	
XX			
PN	JP06121686-A.		
XX			
PD	06-MAY-1994.		
XX			
PF	12-OCT-1992;	92JP-0272744.	
XX			
PR	12-OCT-1992;	92JP-0272744.	
XX			
PA	(ASAH) ASAH KASEI KOGYO KK.		
XX			
DR	WPI; 1994-185923/23.		
DR	N-PSDB; AAO64890.		
XX			
PT	Adrenaline receptor gene encoding alpha 2CII receptor - for screening drugs reactive to the alpha 2CII receptor		
XX			
PS	Claim 1; Page 9-11; 13pp; Japanese.		
XX			
CC	AAO64890 encodes the amino acid sequence of a polypeptide (AAR54834) that constitutes human derived adrenaline alpha 2CII receptor. The DNA can be used for the study of the pharmacological importance of the gene expression in humans.		
CC			
CC			
XX			
SQ	Sequence	458 AA;	
QY	Query Match	49.4%; Score 1177; DB 15; Length 458;	
Db	Best Local Similarity	52.5%; Pred. No. 1e-81;	
	Matches 253; Conservative	38; Mismatches 101; Indels 90; Gaps 9;	
QY	10 NASWNGTEAPGCGARAT-----PYSIOVTLTLVCLAGLMLTLVFGNVLIIAVFT	60	
Db	19 NASGAGERGSGGVANASGASWGPGRGYSAGAVAGLAAVGFLIVFTVGNVLVIIVLT	78	
QY	61 SRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWFGKAWCEIYALDVLECTSS	120	
Db	79 SRALRAPQNLFLVSLASADILVATLVIPFSLANELMAWYFGQVWCGVYALDVLECTSS	138	
QY	121 IVHLCALSLDRYMSITQAIENYLNKRTPRRIKALITTVWVISAVISFPPLISIEKKGGGG	180	

Db	139	IVHLCAISLDRKWSVTAQAVEYNLKRTPRRVAKTIVAVMWLISAVISFPPLVSLYRQPDGA-	197
QY	181	PQPAEPRCEINDQKWYVISSCIGSFAPCLMILVYVRIYQIAKRRTRVPPSRGPDAVA	240
Db	198	---AYPQCGLNDETWTYIILSSCIGSFAPCLMGLVYARIYRAKLRFTLSEKRAP--	251
QY	241	APPGETERRPNGLGPEERSAGPGGAEAEPPTQNLGANGEPAPAGPRDTDALDESSSSD	300
Db	252	GPDGASPTTENGIGAAGAGENGHCA-----PPPA-----DVEPDESSA	290
QY	301	HAERPPGPRRPERGPRGKGKARASQVKKPGDSLPRRQPGATGIGTPAGPGEERYGAAKAS	360
Db	291	AAE-----RRRRRGALRRG-----GRRRAGAEAGAGADGQGAESGALLTAS	332
QY	361	RWRG-----RQNRKRFTEVLAVVIGVFVWCWF	388
Db	333	RSPGPGRLSRASSRSVVEFLSRRRARRASSVCRRKVAQAAREKRFTEVLAVVMGVFLCWF	392
QY	389	PEFFTYTLTAV---GCSVPRTLKFEFFWFEGYCNSSLNBPVITYTFNHDERRAEKTLICRGD	445
Db	393	PEFFSYSLYGICREACQVPGPLFKFEFFWIGYCNSSLNBPVITYTVENQDFRRSEFKHILFRRR	452
QY	446	RK 447	
Db	453	RR 454	
RESULT	10		
ID	AAM52124	standard; Protein; 461 AA.	
AC	AAM52124;		
DT	18-FEB-2002	(first entry)	
DE	Human alpha-2CAR protein.		
KW	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;		
KW	polymorphic site; allelic variant; cardiovascular disease;		
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;		
KW	phosphorylation; inositol phosphate; alpha-2CAR.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	Region	205..409	
FT	Domain	/note="featured in figure 12"	
FT	Region	208..231	
FT	Region	/label= transmembrane_domain	
FT	Domain	321..324	
FT	Domain	/label= polymorphic_site	
FT	Domain	/note= "Polymorphic site absent in the variant protein (AAM52126)"	
FT	Domain	383..406	
FT	Domain	/label= transmembrane_domain	
PN	WO200179561-A2.		
PD	25-OCT-2001.		
PF	17-APR-2001; 2001WO-US12575.		
PR	17-APR-2000; 2000US-0551744.		
PR	10-AUG-2000; 2000US-0636259.		
PR	19-OCT-2000; 2000US-0692077.		
PA	(LIGG/) LIGGETT S B.		
PA	(SMAL/) SMALL K M.		
PI	Liggett SB, Small KM;		
DR	WPI; 2001-611728/70.		

Query Match 64.2%; Score 1529; DB 17; Length 334;
Best Local Similarity 71.8%; Pred. No. 1e-108;
Matches 301; Conservative 10; Mismatches 22; Indels 86; Gaps 3;

QY	33	TLTLVCLAGLMLLTVEGNVLVIITVTSRALKAPQNLFVSLASADILVATLVIPFSLA	92
Db	1	TLTLVCLAGLMLLTVEGNVLVIITVTSRALKAPQNLFVSLASADILVATLVIPFSLA	60
QY	93	NEVMGYWYFGKAWCEIYLALDVLEFCTSSIVHLCAISLDRYWSTQAIENLKRTPRIKA	152
Db	61	NEVM-YWYFGKWCEIYLALDVLEFCTSSIVHLCAISLDRYWSTQAIENLKRTPRIKA	119
QY	153	IIITWVVISAVISFPP-LISIEKKGGGGPQPAEPRCIENDQKWYVISSCIGSEFAPCLI	211
Db	120	IIITWVVISAVISFPPLLISIEKKGAGGGQQPAEPSCKINDQKWYVISSSIGSEFAPCLI	179
QY	212	MILVYVRIYQIAKRTRVPPSRKGPDAVAAPPGGTERPNGUGPERSAGPGAEAEPLPT	271
Db	180	NHLVYVRIYQIAKRTRVPPSRKGPDAVASAPPGADRPNNAVGERGAGTAG-----	231
QY	272	QLNGAPGEPAPAGPRDTALDLESSSSSDHAERPPGPRPERGPRGKGKARASQVKGDS	331
Db	232	-----	231
QY	332	LPRRGATGIGTPAAGPEERVGAKASRWGRQNRKRTFVLAVVIGVYVQWEPPE	391
Db	232	-----GQGERAGAKASRWGRQNRKRTFVLAVVIGVYVQWEPPE	275
QY	392	FTYTLTAVGCSVPRTLKFKEFWFGYCNSSLNPVIYTFNHDERRAFKKILCRDKRRIV	450
Db	276	FTYTLTAVGCPVPYQLNFNEFWFGYCNSSLNPVIYTFNHDERRAFKKILCRDKRRIV	334

RESULT 8
AAU08334
AAU08334 standard; Protein; 307 AA.
AC AAU08334;
XX 21-MAY-2002 (first entry)
XX Human alpha 2 adrenergic receptor.
DE Human alpha 2 adrenergic receptor.
XX
KW Human; D2 dopamine receptor; RGB-2; antiparkinsonian; hormone secretion;
KW G-protein coupled receptor; schizophrenia; drug addiction;
KW Parkinson's disease; Tourette syndrome; Tardive dyskinesia;
KW receptor; neuroleptic.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Domain	37..59
FT	Domain	/note= "Transmembrane domain I"
FT	Domain	71..96
FT	Domain	/note= "Transmembrane domain II"
FT	Domain	108..129
FT	Domain	/note= "Transmembrane domain III"
FT	Domain	151..173
FT	Domain	/note= "Transmembrane domain IV"
FT	Domain	190..213
FT	Domain	/note= "Transmembrane domain V"
FT	Domain	238..261
FT	Domain	/note= "Transmembrane domain VI"
FT	Domain	269..292
FT	Domain	/note= "Transmembrane domain VII"
PN	US6277591-B1.	
XX	21-AUG-2001.	
PD	07-JUN-1995;	95US-0480390.
PF		
XX		

PR 20-NOV-1989; 89US-0438544.
PR 09-NOV-1992; 92US-0973588.
PR 18-NOV-1988; 88US-0273373.
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Civeilli O, Bunzow JR, Grandy DK, Machida CA;
XX
DR WPI; 2001-540405/60.
XX
PT New isolated mammalian G-protein coupled D2 dopamine receptor
PT polynucleotide, useful in gene therapy and for treating schizophrenia,
PT drug addiction, Parkinson's disease, Tourette syndrome and Tardive
PT dyskinesia
XX
PS Claim 1; Fig 2; 71pp; English.

This invention relates to the nucleotide and polypeptide sequences of an isolated mammalian G-protein coupled D₂ dopamine receptor. This protein binds to G proteins to inhibit cyclic AMP generation and hormone secretion. The nucleotide sequences of the invention are useful as oligonucleotide probes and to screen nucleic acid libraries containing dopamine receptor nucleic acid sequences. These probes are also useful in hybridisation methods to locate the dopamine gene positions in various mammalian chromosomal maps or to determine the levels of mRNA or receptor concentrations in a sample. The nucleic acid sequences can also be used to identify dopamine receptor gene disorders (defective or aberrant genes) and for in vitro diagnostic procedures on DNA samples in given patients. A composition comprising the nucleic acid may be used for increasing the concentration of the receptor or its gene in a sample, or for in vivo uses such as gene therapy to render a defective gene or gene product inactive or to provide an increased concentration of dopamine receptor in a given location. The nucleotide sequences are useful for treating disease conditions associated with abnormalities in the structure, expression or concentration of the dopamine receptor or its gene, where the disease conditions are selected from neurological and other disorders, including schizophrenia, drug addiction, Parkinson's disease, Tourette syndrome, and Tardive dyskinesia. The nucleotide sequence is also useful for preparing the corresponding transgenic animals, in particular nonhuman mammals and to inject oocytes from frogs, which can then be conventionally used in binding or second messenger analyses. This sequence represents the human alpha 2 adrenergic receptor which has homology to the rat D2 dopamine receptor of the invention receptor of the invention.

Sequence 307 AA:
Query Match 61.1%; Score 1454.5; DB 22; Length 307;
Best Local Similarity 65.7%; Pred. No. 4.5e-103;
Matches 291; Conservative 7; Mismatches 8; Indels 137; Gaps 1;

QY	1	MGSLQPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLLTVEGNVLITAVFT	60
Db	1	MGSLQPDAGNASWNGTEAPGGARATPYSLOVTLTVCLAGLMLLTVEGNVLITAVFT	60
QY	61	SRAIKAPQNLFVSLASADILVATLVIPFSLANEVMGYWYFGKAWCEIYLALDVLEFCTSS	120
Db	61	SRAIKAPQNLFVSLASADILVATLVIPFSLANEVMGYWYFGKTWCEIYLALDVLEFCTSS	120
QY	121	IYHLCAISLDRYWSTQAIENLKRTPRIKAIITWVVISAVISFPLSIEKKGGGG	180
Db	121	IYHLCAISIQRYWSTQAIENLKRTPRIKAIITWVVISAVISFPLSIEKKGGGG	180
QY	181	POPAEPRCEINDQKWYVISSCIGSEFAPCLIMLVYVRIYQIAKRTRVPPSRGPDAVA	240
Db	181	POPAEPRCEINDQKWYVISSCIGSEFAPXIIIMLVYVRIYQIAKRTRVP-----	230
QY	241	APPGTERPNGUGPERSAGPGAEAEPLPTQLNGAPGEPAPAGPRDTALDLESSSSSD	300
Db	231	-----	230
QY	301	HAERPPGPRRPERGPRGKGKARASQVKGDSLPRRGATGIGTPAAGPEERVGAKAS	360

Db	228	-	-----GGRS-----ASGL	236
OY	333	PRRGATGIGTPAAGPGEERVGAAKASRWGRONREKRTFLVLAIVGVFVWCWEPFEF	392	
Db	237	PRRAGA-----GGONREKRFTFLVAIVGVFVWCWEPFEF	272	
OY	393	TyTLTAVGCSPRTLKFEFFWFPGYCNSSLNPEVITTFNHDFRAAFKKILCGDRKRIV	450	
Db	273	TyTLFAVLCSVPRLKFEFFWFPGYCNSSLNPEVITTFNHDFRAAFKKILCGDRKRIV	330	
	RESULT 6			
ID	AAR48701	standard; Protein; 334 AA.		
XX	AAR48701;			
AC				
XX	05-JUN-1996	(first entry)		
DT				
DE	G-protein coupled rat alpha-2 adrenergic receptor R20 protein.			
XX				
KM	G-protein coupled receptor; ligand binding assay; transmembrane domain;			
KM	psychotic disorder; schizophrenia; dopamine; CAMP; adenosine; thrombin;			
KW	muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;			
KW	rhodopsin; opsin; odorant; cytomegalovirus.			
XX				
OS	Rattus rattus.			
PB	WO9405695-A1.			
PD	17-MAR-1994.			
PF	09-SEP-1993;	93WO-US08528.		
PR	10-SEP-1992;	92US-0943236.		
PA	(UYN Y) UNIV NEW YORK STATE.			
PI	Murphy RB, Schuster DI;			
DR	WPI; 1994-101120/12.			
PT	Polypeptides of G-coupled receptor proteins (GPRs) - useful for			
PT	binding GPR ligands or modulating GPR binding			
PS	Disclosure; Page 74-75; 160pp; English.			
CC	proteins AAR48685-R48758 represent a range of G-protein coupled receptor			
CC	proteins selected from cAMP, adenosine, muscarinic acetylcholine,			
CC	adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,			
CC	odorant, cytomegaloviral and other G-protein coupled receptors. The			
CC	receptor proteins were used to design polypeptides, pref. based on the			
CC	transmembrane domains, for use in G-protein coupled receptor ligand			
CC	binding assays. The polypeptide fragments retain biological activity			
CC	such as binding a GPR ligand or modulating GPR ligand binding to a GPR			
CC	(see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples			
CC	of polypeptide fragments). The polypeptide fragments can be used in			
CC	compositions for treating subjects suffering from a pathology related to			
CC	a GPR abnormality e.g. a psychotic disorder such as schizophrenia.			
XX				
SQ	Sequence	334 AA;		
	Query Match	64.2%; Score 1529; DB 15; Length 334;		
	Best local Similarity	71.8%; Pred. No. 1e-108;		
	Matches 301; Conservative	10; Mismatches 22; Indels 86; Gaps 3;		
OY	33	TyTLTVCLAGLMLLTVEGNLVIIIAVFTRALKAPQNLFVLSLASADILVATLVIPESLA	92	
Db	1	TyTLTVCIAGLIMLTVEGNLVIIIAVFTRALKAPQNLFVLSIASADILVATLVIPESLA	60	
OY	93	NEVMGYWYEGAWCEIYLALDVLECTSSIVHLCAISLDRYWSITQAITEYNLKRTPRIKA	152	
Db	61	NEVM-YWYFGKWCEIYLALDVLECTSSIVHLCAISLDRYWSITQAITEYNLKRTPRIKA	119	

OY		153	IITVWVISAVISFPP-LISIEKKGGGQPAEP RCEINDOKMYVISSCIGSFAPCLT	211
Dd		120	IIVTWVISAVISFPPLLSIEKKGAGCGQP AEPSCKINDOKMYVISSSIGSFAPCLI	179
OY		212	MILVVRIYQIAKRTRVPSPSRGPDAVA APGCTERRPNGLPERSAGPGAEAPLPT	271
Dd		180	NHLVVRITYQIAKRRTRVPSRGRPDAC SAPPGADRRPNNAVGP ERGAGTAG-----	231
OY		272	QLNGAGEPARAGRDTDALDLESSSDHA ERP RPGRP GRG KARASOV K PGDS	331
Dd		232	-----	231
OY		332	LPRRGATGTGTPAAGPEERVGAKASRM RGQRNREKRFTFLAVVIGVFVCWFPEE	391
Dd		232	-----GQEERAGGAKASRMGRQN REKRFT FVLAVVIGVFVCWFPEE	275
OY		392	FTVTTLTA VGCSVPRTLKEFFFWFGYC NSSLNDPIYTTFNHDFRAFKKITLCRGDR KRIV	450
Dd		276	FTYTLI AVGPCPVPLYLFNF FF WF G YCNSSLNP V I TTF NH DFR AF KK IT LC RG DR KR IV	334
RESULT 7				
ID	AAM02673		AAM02673 standard; peptide; 334 AA.	
XX	AAW02673;			
AC		12-NOV-1996	(first entry)	
DX		G-protein coupled rat alpha-2 adrenergic receptor.		
KX		G-protein coupled receptor; ligand binding assay; transmembrane domain; schizophrenia; dopamine; CAMP; adenosine; thrombin; adrenergic; opsin; muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin; odorant; cytomegalovirus; serotonergic.		
OS	Rattus rattus.			
XX		US5508384-A.		
Pd		16-APR-1996.		
Xx		10-SEP-1992;	92US-0943236.	
Pf		09-SEP-1993;	93US-0118270.	
xx		10-SEP-1992;	92US-0943236.	
pr		(UYN) UNIV NEW YORK STATE.		
pa		Murphy RB,	Schuster DI;	
xx		WPI;	1996-208785/21.	
xX		New dopamine receptor peptide - useful as antipsychotic agent, e.g. for treating schizophrenia		
ps		Disclosure; Column 73-76; 184pp; English.		
cc		Proteins AAW02657-W02730 represent a range of G-protein coupled receptor (GPR) proteins selected from CAMP, adenosine, muscarinic acetylcholine, adrenenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomagaloviral and other GPR proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. CC The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAW02747-W02999 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.		
sQ	Sequence	334	AA;	

```
KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
KW rhodopsin; opsin; odorant; cytomegalovirus.
XX
OS Homo sapiens.
XX WO9405695-A1.
XX
XX 17-MAR-1994.
XX
XX 09-SEP-1993; 93WO-US08528.
XX
XX 10-SEP-1992; 92US-0943236.
XX
XX (UYNY ) UNIV NEW YORK STATE.
XX
XX Murphy RB, Schuster DI;
XX
XX WPI; 1994-101120/12.
XX
XX Polypeptides of G-coupled receptor proteins (GPRs) - useful for
XX binding GPR ligands or modulating GPR binding
XX
XX Disclosure; Page 73-74; 160pp; English.
XX
XX Proteins AAR48685-R48758 represent a range of G-protein coupled receptor
XX proteins selected from cAMP, adenosine, muscarinic acetylcholine,
XX adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
XX odorant, cytomegaloviral and other G-protein coupled receptors. The
XX receptor proteins were used to design polypeptides, pref. based on the
XX transmembrane domains, for use in G-protein coupled receptor ligand
XX binding assays. The polypeptide fragments retain biological activity
XX such as binding a GPR ligand or modulating GPR ligand binding to a GPR
XX (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples
XX of polypeptide fragments). The polypeptide fragments can be used in
XX compositions for treating subjects suffering from a pathology related to
XX a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
XX
SQ Sequence 330 AA;

Query Match 64.8%; Score 1543; DB 15; Length 330;
Best Local Similarity 74.4%; Pred. No. 8.7e-110;
Matches 311; Conservative 7; Mismatches 12; Indels 88; Gaps 6;

OY 33 TLTVCLAGLMLLTVEGNVLIIVFTSRALKAPQNLFVSLASADIVATLVIPFSLA 92
Db 1 TLTVLCIA--CLSLTFEGNVLIIVFTSRALKAPQNLFVSLASADIVATLVIPFSLA 58

OY 93 NEVNGWYFGKAWCEIYALDVLFCSTSSIVHCAISLDRYWSITQATEYNLKRTPRRIKA 152
Db 59 NEVNGWYFGK-WCEIYALDVLFCSTSSIVHCAISLDRYWSITQATEYNLKRTPRRIKA 117

OY 153 IITVWVISAVISFPPLISIEKKGGGGQPAPRCEINDOKWYVISSCIGSFAPCLIM 212
Db 118 IITVWVISAVISFPPLISIEKKGGGGQPAPRCEINDOKWYVISSCIGSFAPCLIM 177

OY 213 ILVYVRIYQIAKRRTRVPPSRGPDAAVAPPGCTERRPNGLGPERSAGPGAEAPLPTQ 272
Db 178 -LVYVRIYQIAKRRTRVPPSRGPDAAVAPPGCTERRPNGLGPERSAGPGG----- 227

OY 273 LINGAPGEPAPAGPRDLDLLESSSSDHAERPPGPRRPERGPRGKGKARASQVKPGDSL 332
Db 228 -----GRGRS-----ASGL 236

OY 333 PRGPGATGIGTPAAGGGEERVAAGAKASRWGRONREKRFTFVLAIVIGVVCWFPEFFF 392
Db 237 PRRRAGA-----GGQNRKRFTFVLAIVIGVVCWFPEFFF 272

OY 393 TYTLTAVGCVPRTLKFFFWFGYCNSSLNPVIYTIFFNHDFRRAFKKILCRGDKRRIY 450
Db 273 TYTLTAVLCVPRTLKFFFWFGYCNSSLNPVIYTIFFNHDFRRAFKKILCRGDKRRIY 330

RESULT 5
```

```
AAW02672
ID AAW02672 standard; peptide; 330 AA.
XX
XX AAW02672;
XX
XX 12-NOV-1996 (first entry)
XX
XX G-protein coupled human alpha-2 C10 adrenergic receptor.
XX
XX G-protein coupled receptor; ligand binding assay; transmembrane domain;
XX schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
XX muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
XX odorant; cytomegalovirus; serotonergic.
XX
XX Homo sapiens.
XX
XX US5508384-A.
XX
XX 16-APR-1996.
XX
XX 10-SEP-1992; 92US-0943236.
XX
XX 09-SEP-1993; 93US-0118270.
XX
XX 10-SEP-1992; 92US-0943236.
XX
XX (UYNY ) UNIV NEW YORK STATE.
XX
XX Murphy RB, Schuster DI;
XX
XX WPI; 1996-208785/21.
XX
XX New dopamine receptor peptide - useful as antipsychotic agent, e.g.
XX for treating schizophrenia
XX
XX Disclosure; Column 71-74; 184pp; English.
XX
XX Proteins AAW02657-W02720 represent a range of G-protein coupled receptor
XX (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,
XX adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
XX odorant, cytomegaloviral and other GPR proteins. The receptor proteins
XX were used to design polypeptides, pref. based on the transmembrane
XX domains, for use in G-protein coupled receptor ligand binding assays.
XX The polypeptide fragments retain biological activity such as binding a
XX GPR ligand or modulating GPR ligand binding to a GPR (see
XX AAW02747-W02999 for examples of polypeptide fragments). The polypeptide
XX fragments can be used in compositions for treating subjects suffering
XX from a pathology related to a GPR abnormality e.g. a psychotic disorder
XX such as schizophrenia.
XX
SQ Sequence 330 AA;

Query Match 64.8%; Score 1543; DB 17; Length 330;
Best Local Similarity 74.4%; Pred. No. 8.7e-110;
Matches 311; Conservative 7; Mismatches 12; Indels 88; Gaps 6;

OY 33 TLTVCLAGLMLLTVEGNVLIIVFTSRALKAPQNLFVSLASADIVATLVIPFSLA 92
Db 1 TLTVLCIA--CLSLTFEGNVLIIVFTSRALKAPQNLFVSLASADIVATLVIPFSLA 58

OY 93 NEVNGWYFGKAWCEIYALDVLFCSTSSIVHCAISLDRYWSITQATEYNLKRTPRRIKA 152
Db 59 NEVNGWYFGK-WCEIYALDVLFCSTSSIVHCAISLDRYWSITQATEYNLKRTPRRIKA 117

OY 153 IITVWVISAVISFPPLISIEKKGGGGQPAPRCEINDOKWYVISSCIGSFAPCLIM 212
Db 118 IITVWVISAVISFPPLISIEKKGGGGQPAPRCEINDOKWYVISSCIGSFAPCLIM 177

OY 213 ILVYVRIYQIAKRRTRVPPSRGPDAAVAPPGCTERRPNGLGPERSAGPGAEAPLPTQ 272
Db 178 -LVYVRIYQIAKRRTRVPPSRGPDAAVAPPGCTERRPNGLGPERSAGPGG----- 227

OY 273 LINGAPGEPAPAGPRDLDLLESSSSDHAERPPGPRRPERGPRGKGKARASQVKPGDSL 332
Db 228 -----GRGRS-----ASGL 236
```


DR N-PSDB; AAI99917.

XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting a
PT a polymorphic site -

PS Claim 48; Page 152-154; 163pp; English.

XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIV)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcggtgag) at
CC positions 961-972 of (IIV). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR protein.

XX Sequence 450 AA;

Query Match 100.0%; Score 2381; DB 22; Length 450;
Best Local Similarity 100.0%; Pred. No. 1.5e-173;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGSLOPDAGNASWNGTEAPGGARATPYSLQVTLTLVCLAGLMLTLVFGNVLTIAVFT 60
Db 1 MGSLOPDAGNASWNGTEAPGGARATPYSLQVTLTLVCLAGLMLTLVFGNVLTIAVFT 60
OY 61 SRALKAPQNLFLVSLASADILVATLVPFSLANVMGYWFGKAWCEIYLALDVLCTSS 120
Db 61 SRALKAPQNLFLVSLASADILVATLVPFSLANVMGYWFGKAWCEIYLALDVLCTSS 120
OY 121 IVHCAISLDRWYSITQAIENYLNKRTPRRIKAIITVWVISAVISFPPLISIEKGGGGG 180
Db 121 IVHCAISLDRWYSITQAIENYLNKRTPRRIKAIITVWVISAVISFPPLISIEKGGGGG 180
OY 181 POPAEPRCEINDOKWYVSISSCIGSFFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDAVA 240
Db 181 POPAEPRCEINDOKWYVSISSCIGSFFAPCLIMILVYVRIYQIAKRRTRVPPSRGPDAVA 240
OY 241 APGGETERRRNGLGPERSAGPGAEAEPLPTQLNGAGGEPAPAGPRDTDALDLESSSSD 300
Db 241 APGGETERRRNGLGPERSAGPGAEAEPLPTQLNGAGGEPAPAGPRDTDALDLESSSSD 300
OY 301 HAERPPGRRRPERGPRGKGRASQVKKPGDSLPRRGATGIGTPAAGPGEERVGAAKAS 360
Db 301 HAERPPGRRRPERGPRGKGRASQVKKPGDSLPRRGATGIGTPAAGPGEERVGAAKAS 360
OY 361 RWRGRQNRKRTFTVLAVVGVFVVCWPFFFFTYTLTAVGCSVPRTLFRFFFWGYNSS 420
Db 361 RWRGRQNRKRTFTVLAVVGVFVVCWPFFFFTYTLTAVGCSVPRTLFRFFFWGYNSS 420
OY 421 LNPVITYTIFNHFRAFKILCRGDRKRIV 450
Db 421 LNPVITYTIFNHFRAFKILCRGDRKRIV 450

RESULT 2
AAMS2123

ID AAM52123 standard; Protein; 450 AA.

XX AAM52123;

XX 18-FEB-2002 (first entry)

DE Human alpha-2AAR variant protein.

KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2AAR.

OS Homo sapiens.

FH Key Location/Qualifiers
FT Misc-difference 251 /note= "Wild-type Asn substituted by Lys"

PN WO200179561-A2.

PD 25-OCT-2001.

PF 17-APR-2001; 2001WO-US12575.

PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.

PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMAL K M.

PI Liggett SB, Small KM;

DR WPI; 2001-611728/70.
DR N-PSDB; AAI99918.

PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -

PS Claim 48; Page 154-155; 163pp; English.

XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIV)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcggtgag) at
CC positions 961-972 of (IIV). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR variant
CC protein.

XX Sequence 450 AA;

Query Match 99.7%; Score 2375; DB 22; Length 450;
Best Local Similarity 99.8%; Pred. No. 4.3e-173;
Matches 449; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 15, 2003, 13:41:57 : Search time 47 Seconds
(without alignments)
1275.804 Million cell updates/sec

Title: US-09-636-259B-3
Perfect score: 2381
Sequence: 1 MGSLOPPDAGNASWNGTEAPG.....HDFRAFAFKKILCRGDRKRIV 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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14: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
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17: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2381	100.0	450	22	AAM52122	Human alpha-2AAR p
2	2375	99.7	450	22	AAM52123	Human alpha-2AAR v
3	1554	65.3	324	10	AAP90552	Hamster beta-2 -ad
4	1543	64.8	330	15	AAR48700	G-protein coupled
5	1543	64.8	330	17	AAW02672	G-protein coupled
6	1529	64.2	334	15	AAR48701	G-protein coupled
7	1529	64.2	334	17	AAW02673	G-protein coupled
8	1454.5	61.1	307	22	AAU08334	Human alpha 2 adre
9	1177	49.4	458	15	AAR54834	Human derived adre
10	1164.5	48.9	461	22	AAM52124	Human alpha-2CAR p

11	1152.5	48.4	457	22	AAM52126	Human alpha-2CAR v
12	1124.5	47.2	450	22	AAM52117	Human alpha-2BAR t
13	1124.5	47.2	450	22	AAE00990	Human alpha2B-adre
14	1124	47.2	447	22	AAM52118	Human alpha-2BAR t
15	1124	47.2	447	22	AAE00989	Human alpha2B-adre
16	1092.5	45.9	487	12	AAR14149	Human alpha 2 beta
17	1092.5	45.9	487	18	AAW11804	Human alpha-2b adr
18	1046.5	44.0	330	15	AAR48698	G-protein coupled
19	1046.5	44.0	330	17	AAW02670	G-protein coupled
20	1029	43.2	330	15	AAR48699	G-protein coupled
21	1029	43.2	330	17	AAW02671	G-protein coupled
22	901	37.8	437	22	AAE99035	Sheep/guinea pig c
23	681.5	28.6	379	18	AAW33185	Corn barnacle G-pr
24	651	27.3	476	18	AAW24089	Balanus amphitrite
25	648	27.2	601	13	AAR21931	D.melanogaster oct
26	648	27.2	601	22	ABB63318	D.melanogaster melanog
27	648	27.2	601	23	AAE17036	D. melanogaster oc
28	648	27.2	601	23	AAE17036	Drosophila melanog
29	626.5	26.3	443	11	AAR05541	Human pituitary do
30	626.5	26.3	443	12	AAR11497	Human dopamine D2 r
31	626.5	26.3	443	20	AAV01600	Human pituitary do
32	626.5	26.3	443	22	AAU76292	Human D2 dopamine
33	626.5	26.3	443	22	AAE69075	Human dopamine rec
34	626.5	26.3	443	23	AAE51019	Human D2 dopamine
35	626	26.3	414	12	AAR11800	Human retinal dopa
36	619.5	26.0	443	22	ABB56348	Non-endogenous hum
37	617.5	25.9	415	11	AAR05539	Rat D2 dopamine re
38	617.5	25.9	415	20	AAV01598	Rat D2 dopamine re
39	616.5	25.9	415	17	AAW09388	Mouse dopamine D2
40	616	25.9	444	12	AAR10544	D2 dopamine recept
41	616	25.9	444	17	AAW09387	Mouse dopamine D2
42	615.5	25.9	415	22	AAU08332	Rat D2 dopamine re
43	615.5	25.9	415	23	AAM51017	Rat D2 dopamine re
44	594	24.9	422	22	AAE70249	HTR1A protein. Ho
45	590	24.8	637	20	AAV13445	Invertebrate octop

ALIGNMENTS

RESULT 1	
AAAM52122	
ID	AAAM52122 standard; Protein; 450 AA.
XX	
AC	AAAM52122;
XX	
DT	18-FEB-2002 (first entry)
XX	
DE	Human alpha-2AAR protein.
XX	
KW	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW	polymorphic site; allelic variant; cardiovascular disease;
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW	phosphorylation; inositol phosphate; alpha-2AAR.
XX	
OS	Homo sapiens.
XX	
PN	WO200179561-A2.
XX	
PD	25-OCT-2001.
XX	
PF	17-APR-2001; 2001WO-US12575.
XX	
PR	17-APR-2000; 2000US-0551744.
PR	10-AUG-2000; 2000US-0636259.
PR	19-OCT-2000; 2000US-0692077.
XX	
PA	(LIGG/) LIGGETT S B.
PA	(SMAL/) SMALL K M.
XX	
PI	Liggett SB, Small KM;
XX	
DR	WPI; 2001-611728/70.